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                                                           "Genome sequence of an obligate intracellular pathogen of Chlamydia trachomatis."; Science 282:754-759(1998).
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MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., F.,
Mitchell W.P., Olinger L., Tatusov R.L.,
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1994) to the SWISS-PROT data bank. -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M., Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 LGWSQSSSASNGGAIQTTQGFTLRNNKGSIYFDSNTATHAGGAINCGYIDIRDNGPVYFL
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                                                                                                              STPMIIFNGRLSIVDENYESVYDSMDLSRGKAEQLILSIETTNDGQLDSNWQSSLNTSLL
NFIELGTEGAPYEKRFWVAGI-SNVLHRSGRENORKFRHVSGGAVVG
                                                                                                                                                                                                                                                            VVFSYNQMS-SDIRTLMGKEHNYIKEAPTTLKFGTLAIEDDAELEIFNIPFTQNPTSLLA
                                      SPPHYGYQGLWTPNWITTTYTITLNNNSSAPTSATSIAEQK-------KTSE
                                                         SP--YGYQGKWTINWSTDDKKATV---SWAKQSFNPTAEQEAPLVPNLLWGSFIDVRPFQ
                                                                                                                                               DRPVV-----LAISDESF---YQNGFLNEDHSYDGILELDAGKDIVISAD-SRSIN-AVQ 473
                                                                                                                                                                                     LGSGATLTVGKHGKLNITNLGVILPIILKEGKSPPCIRVNPQDMTQNTGTGQTPSSTSSI
                                                                                                                                                                                                                      MDLGTSL-VANTESIELTNLEINID-SLRNGKK---IKL------SAATAQKDIRI 423
                                                                                                                                                                                                                                                                                              IVFSGEKLTEAEAKDEKNRTSKLLQN--VAFKNGTVVLKGDVVLSANG--FSQDANSKLI 378
                                                                                                                                                                                                                                                                                                                                 TLSLG-----AKKDTRIYFYDLFQWERVKENTSNNPPSPTSRNTITVNPETEFSGA 456
                                                                                                                                                                                                                                                                                                                                                                     AIDLGTSAKITALRAAQGHTIYFYD-----PITVTGSTSVADALNINSPDTGDNKEYTGT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YATTITLTGNRTLAFINNMSGDCG---GAISADTQISITDTVKGILFENNHTLNHIPYTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGETQSTSCFKNDAA---AGDLNFLGGGFSFTFSNIDATTASGAAIGSEAANK-----
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MW; 445FF4C35D463AE7 CRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                          Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H. Kashinoto K., Kins., Kinura S., Kitagawa M., Kitakawa M., Makino K. Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashinoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1023
 Submitted
                                                                                                                                        MEDLINE-84272624; PubMed-6087316 Carlson J., Fuchs J.A., Messing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; P
Escherichia
                                SEQUENCE OF 925-1198 FROM N.A. STRAIN-K12 / EMG2;
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                                                                                                                        Primary structure of the Escherichia coli ribonucleoside diphosphate
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nce 277:1453-1474(1997).
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O'Keeffe T., Robison K., Church G.M.; (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                   Sci. U.S.A. 81:4294-4297(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        three gene classes.";
Nucleic Acids Res. 23:3554-3562(1995).
-i- SIMILARITY: TO E.COLI YDEK.
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SEQUENCE OF 1180-1250 FROM STRAIN=OV6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borodovsky M., McIninch J., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96032851; PubMed=7567469;
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 186
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                                                                                                                                                           8 LLISLVPTLSMSNLLGAATTE----ELSAS-----NSFDGTTSTTS-----FSSKTS
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DVIFDNNQAYTSTSYSDGDGGAIDVTDNNSDSKHPSGYTIVNN--TAFTNNTAEGYGGAI
                     --LLDNDKYLIQDNFSTGDGGAINCA-----GSLKIANNKSLSFIGNSSSTRGGAI
                                             DVIFSGNVAGGYGGAIYSSGTNDTGAVDLRVTNAM-FRNNIANDGKGGAIYTINNDVYLS
                                                                                       NASGGAVFLQQGAEFSLLPEN--ETGMT----LFANNTVTGEYNNGGAIFAKENSTLNLT
                                                                                                              SATDGTNYVFKD---SVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDAT 107
                                                                                                                                    LLPSMIASLFSANGVAAVTDSCQGYDVKASCQASRQSLSGITQDWSIADGQWLVFSDMIN 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         D90854;
K02672;
                                                                                                                                                                                 174;
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EG12850; YfaL.
                                                                 ----ASGAAIGSEAANKT--VTLSGFSALSFLKSPASTVTNG-LGAINVKGNLS
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BAA16050.1; ALT_INIT.
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LV -> PG (IN REF. 3).

S -> Q (IN REF. 3).
                                                                                                                                                                                          Score 235; DB 1;
Pred. No. 4.7e-06;
                                                                                                                                                                                                                                    AG -> SÅ (IN REF. 3).
A -> R (IN REF. 3).
E -> S (IN REF. 3).
V -> M (IN REF. 3).
PP -> AT (IN REF. 3).
PAYQPYLMAKVGGYLMNLRAANQAFMMERRDHAGGDGQTLNLRVIGG -> LLTSRC (IN REF. 4).
MW; 17F98C05E299FC95 CRC64;
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POTENTIAL.
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P96989;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
00TER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SURFACE PROTEIN ANTIGE)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGE).
                                                            MEDLINE-94040787; PubMed-8224886;
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene encoding
surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
                                                    the S-layer protein prowazekii.";
                                                                                                                                                                                                                                                                                               Rickettsiaceae;
                                                                                                            STRAIN-WILMINGTON;
MEDLINE-92114896; PubMed-1370573;
                                                                                                                                          PARTIAL SEQUENCE
                                                                                                                                                                                                                                         STRAIN-WILMINGTON;
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  MEDLINE=92104668;
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                                       29:95-105(1992).
              OF.
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CLEAVAGE SITE. PubMed=1729180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KTGAGTLELTASGTTQSAVRVEEGTLKGDVADI-LPYAS
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CONFLICT
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"Evidence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettsiae: identification of an avirulent
mutant deficient in processing.";
Infect. Immun. 60:159-165(1992).
-I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
-I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE AN
-I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED B
S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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                                                                                         DVAINELVMENDGSVHLTHNTYLITKTINAANQGKIIVAADPINTDTALADGTNLGSAES
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 IELTNLEINIDSLRNGKKIK-LSAATAQKDIRIDRPVVLAISD---
                               PLSNIHFATKAANGDSILHIGKGVNLYANNITTTDANVGSLHFRSGGTSIVSGTVGGQQG
                                                           LLQNVAF - - - - KNGTVVL - - - KGDVVLSANGFSQDAN - - SKLIMDLGTSLVANT - - -
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                                                                                                                                                                                                                                                                                                     --GKGGAIAIADSGTLSISGD------
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21.0%;
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32 KDA BETA PEPTIDE.

MEMBRANE ANCHOR (POTENTIAL).

H -> N (IN REF. 2).

V -> I (IN REF. 2).

G -> A (IN REF. 2).

G -> S (IN REF. 2).
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Pred. No. 0.00
[9; Mismatches
                                                                                                                      ·NKEYTGTIVFSGEKL-TEAEAKDEKNRTS--K
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(See http://www.isb-sib.ch/announce/

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There are no restrictions ng as its content is in

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_YEAST
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                                                                                                                                                                                                      Kovacech
"EGT2 gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1099
                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND FUNCTION.
MEDLINE-96251274; PubMed-8668141;
Kovacech B., Nasmyth K., Schuster
                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C / FY1676;

MEDLINE=95373280; PubMed=7645347;

Maftahi M., Nicaud J.-M., Levesque H., Gaillan

Maftahi M., Nicaud J.-M., Levesque H., Gaillan

"Sequencing analysis of a 15.4 kb fragment of

identifies the RPD3, PAS8 and KREI loci, five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; 
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGT2 OR YNL327W OR N0320
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                FUNCTION: SEEMS TO BE INVOLVED IN THE CORRECT TIMING OF CELL SEPARATION AFTER CYTOKINESIS, AS SEPARATION OF MUTANT DAUGHTER CELLS IS DELAYED. COULD EITHER BE AN ENZYME NECESSARY FOR GLOCANS-DEGRADATION OF THE CELL WALL AT THE NECK REGION BETWEEN MOTHER AND DAUGHTER CELLS OR A REGULATORY PROTEIN CONTROLLING THIS METABOLIC STEP. EXCLUSIVELY EXPRESSED BETWEEN THE END OF MITOSIS AND EARLY G1; INACTIVATED BEFORE CELLS PASS START.
                                                                                                                                                                   Cell.
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                                                                                                                                                                 Biol. 16:3264-3274(1996)
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GNTAPTAAGKGGAIAIADSGTL--SISGDSGDIIFEGNTIGATGTVS----
                  TSISSSITNTSSVSSTTSSLSSGPFVSNTAVASGSYILTTTTESAQLTEIGSLIPISTIT
                                                        TLSSSSVLESVISSPYLANTTVSGASSASQSTNPPYVSNSTTSSATQLATIAPFAINITG
                                                                   TLSGFSAL-SFLKSP--ASTVTNGLGAINVKGNLSLLDNDKVLIQDNFSTGDGGAINCAG
                                                                                            DNSTTTAVTQSTSTI----AVSSAEKLSSTLSYT
                                                                                                              ENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASG---AAIGSEAANKTV
                                                                                                                                  MSAVSTVSSSSEQASSSSISLSAPSSSNSTFTTPSSSLSATETYSIISSASISVTQASYI
                                                                                                                                                    ISLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFS---SKTSSATDGTNYVFKDSVVI
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Z71603; CAA96259.1;
                                     -SLKIANNKSLS-----FIGNSSSTRGGAI---HTKNLTLSSGGETL----FQ
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11; Mismatches
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POLY-SER.
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POLY-SER.
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                                                                                                                                                                    MEDLINE-92167802; PubMed=1724278; Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor."; mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
00TER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RICRI
            Gilmore R.D. Jr., Joste N., McDonald G.A.;
"Cloning, expression and sequence analysis of the gene encoding
"Cloning, expression and sequence analysis of the gene encoding
120 kD surface-exposed protein of Rickettsia rickettsii.";
Mol. Microbiol 3:1579-1586(1989).

-I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
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Rickettsiaceae;
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                                                                                                  MEDLINE=90136087; PubMed=2515418;
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Rickettsieae; Rickettsia.
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Best Local
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   TLPCSFYGQLSYGHTDHRMKTESLPPPPPTLSTDHTSWGGYVWAGEL - -
                                \texttt{LGVDSVIADGQVIGDQNNIVGLGLGSDNGIIVNATTLYAGISTLNNNQG--TVTLSGGVP}
                                                                 LGFAQLFARDKDYFMNTNFAKTYAGSLR--LQHDASLYSVVSILLGEGGLREILLPYVSK
                                                                                                  GNHHGAVTDT IAFENSSLGAVVFLPRG I PFNDAGNTMPLT I KSTVGNKTAKGFDVPSVVV
                                                                                                                                                                    CVASADGTGIV-----EFVNTGPIT--VTLNKQAAPVNALKQITVSGPGNVVINEIGNA
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                                                                                                                                                                                                                                                                      GKDIVISA-----DSRSINAVQSPYG----YQGKWTINWSTDDKKATVSWAKQSFNPTAE
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                                                                                                                                   -HRSGRENQRKFRHVSGGAVV-----GASTRMP--
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1654 AA;
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32 KDA BETA PEPTIDE.
POLY-THR.
POLY-THR.
MW; D7AB70FB7087F618 CRC64;
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RESULT 7

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Alba H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996).
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P33666; P76087; P76088; P76856; P76857; P76859;
01-FEB-1994 (Rel. 28, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 205.9 KDA PROTEIN IN PAAY-ACPD INTERGENIC
                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moszer I., Glaser P., Danchin A.;
"Multiple IS insertion sequences near the replication terminus
Escherichia coli K-12.";
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"The complete genome sequence Science 277:1453-1474(1997).
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MEDLINE-97426617; PubMed-9278503;
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CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING
THIS PROTEIN IS INTERRUPTED BY A HYBRID ISZD/IS30C ELEMENT
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AE000237; AAC74487.1; ALT_SEQ.
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D90778; BAA18880.1; ALT_SEQ.
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01-JUN-1994 (Rel. 2
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5-LAYER PROTEIN (SI
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J. Biol. Chem. 265:19372-19372(1990).
-!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROCESTICAL FOR VIRULENCE.
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MEDLINE=90354448; PubMed=2387868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                        Gilmore R.D. Jr., Joste N., McDonald G.A.: "Cloning, expression and sequence analysis of the 120 kD surface-exposed protein of Rickettsia ricke Mol. Microbiol. 3:1579-1586(1989).
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                                                                                                                                                                                                                                                               S-LAYER WITH HEXAGONAL SYMMETRY.
DISEASS: RICKETTSIA RICKETTSII IS THE CAUSATIVE AGENT
MOUNTAIN SPOTTED FEVER (RMSF).
MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE
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                                                                                                                                                                                                                                                                                             DGTTSTTSFSSKTSSATDGT--NYVFKDSVVIENVPKTGETQSTSCFKNDAA----AGD
-- VTLNKQAAPVNALKQITVSGPGNVVINEIGNAGNHHGAVTDTIAFENSSLGAVVFLPR
                                                                                                                                                                    NTIGATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGD
                                                            -TYLNYGEGYNLYATNITTTDANY-GSFYFNAGGTNIYSGTYGGQQGNKFNTVALENG
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                                            -YQGKWTINWSTDDKKATVSWAKQSFNPTAEQEAP-----LVPNLLWGSFIDVRPFQ
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22.5%;
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Pred. No. 0.0013;
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-!- SUBCELLULAR LOCATION: OUTER MEMBRANE (POTENTIAL).
                                           EMBL; U36840; AAA79815.1; ALT_SEQ.
EMBL; ABC00350; AAC75695.1;
EMBL; D90889; BAA16514.1; ALT_INIT.
EMBL; D90890; BAA16518.1; ALT_INIT.
                                                                                                                                                                                                                   This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YPJA_ECOLI STANDARD; PRT; 1569 AA.
p52143; P76610; P77017; P77019;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 98.4 KDA PROTEIN IN ALPA-GABD INTERGENIC REGION (F949).
                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                        modified
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Bacteria; Proteol
              Hypothetical
                                EcoGene;
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Query Match Best Local Similarity

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Score 188. Pred. No.

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Length

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                                                                                                                                                                                                                                  Rickettsiaceae;
NCBI_TaxID=783;
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                           Rickettsia rickettsii.
                                    between
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                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                         WVAGISNVLHRSGRENQRKFRHVS-----GGAVVGAST
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                                                 GGAV--IKATTKLTNAASVLTLTNANAV---LTGAVDNTTGGDNVGVLNLNGA-----
                                                                           NWSTDDKKATVSWAKQSFNPTAEQEAPLVPNLLWGSFIDVRPFQNFIELGTEGAPYEKRF 544
                                                                                                     SVLTLTNANAVLTGAIDNTTGGDNVGVLNLN-GALSQVTGDIGNTNSLATISVGAGTATL
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                                              the
                                                                                                                      INTEGER. IMMUN. 60:159-165(1992).

INFECT. IMMUN. 60:159-165(1992).

-!- FUNCTION: THE 120 KDA SURFACE EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE PACTOR AND/OR IMMUNOGEN DURING INFECTION.
-!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE A FUNCTION: CELL WALL. THIS BACTERIUM IS COVERED
                                                                                                                                                                                                                          IDENTIFICATION OF CLEAVAGE SITE.

MEDLINE=92104668; PubMed=1729180;

Hackstadt T., Messer R., Cieplak W. Jr., Peacock M.G.;

"Evidence for proteolytic cleavage of the 120-kilodalton outer

membrane protein of rickettsiae: identification of an avirulent
deficient in processing.";

Infort Tempus 60.180.186.186.190.2
                                                                                                                                                                                                                                                                                                                                                                                Ching W.M., Carl M., Dasch G.A.; "Mapping of monoclonal antibody binding sit the S-layer protein antigens of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moron C.G., Yu X.J., Walker D.H.; "Sequence analysis of ompB of Rickettsia prowazekii."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface-layer protein of Rickettsia prowazekii: presence truncated identical homolog in Rickettsia typhi."; Proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).
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            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restroy non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                               WITH HEXAGONAL SYMMETRY.
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.E., Ching W.M.,
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32 KDA BETA PEPTIDE:
V -> A (IN STRAIN BREINL).
Y -> D (IN STRAIN BREINL).
A -> S (IN STRAIN BREINL).
AA -> VC (IN REF. 1).
TYOGAPLILGA -> INSRSSSYHLVS (:
T'OGAPLILGA -> INSRSSSYHLVS (:
T -> I (IN REF. 1).
D -> G (IN REF. 2).
T -> S (IN REF. 2).
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-3000 (Rel. 40, Last annotation update)
01-CCT-3000 (Rel. 39, Created)
01-CCT-3000 (Rel. 39, Last sequence update)
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-i- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR-
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
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ween the Swiss Institute of Bioinformatics and the Embi outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED
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01-FEB-1995 (Rel. 31, Created) 
01-NOV-1997 (Rel. 35, Last sequence update) 
01-OCT-2000 (Rel. 40, Last annotation updat
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                                                  Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R
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Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
Yamamoto Y., Horiuchi T.;
Yamamoto Y., Horiuchi T.;
Takeda J., Takenoto K., Wada C.,
Yamamoto Y., Horiuchi T.;
Takeda J., Takenoto K., Wada C.,
Yamamoto Y., Horiuchi T.;
Takeda J., Takenoto K., Wada C.,
Yamamoto Y., Horiuchi T.;
Takeda J., Takenoto K., Wada C.,
Yamamoto Y., Horiuchi T.;
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                                                                                                                                                                                                                       use by non-profit institutions as long as modified and this statement is not removed. U entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ML 308-225;
Henderson I.R., Owen
Submitted (JAN-1997)
                                                                                                                                       EMBL; AE000291; AAC75061.1;
EMBL; D90838; BAA15825.1; AI
EMBL; D90839; BAA15832.1; AI
EMBL; U24429; AAB47869.1; -
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEMS Microbiol. Lett. 149:115-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97257509; PubMed-9103983;
Henderson I.R., Meehan M., Owen P.;
*Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia
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SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA CHAIN).
SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.
SIMILARITY: TO ADHESIN ALDI-I AND TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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ANTIGEN 43 ALPHA CHAIN.
ANTIGEN 43 BETA CHAIN.
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SL -> FF (IN STRAIN ML 308-225).
T -> K (IN STRAIN ML 308-225).
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23 301	GAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPK 71	
72 352	-TGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTA-SGAAI-GSEAANKTVTLS 126       : :        :	
127 409	GFSALSFLKSPASTYTNGLGAINVKGNLSLLDNDKVLIQDNFSTGDGGAINCAGSL 182	
183 453	KIANNKSLSFIGNSSSTRGGAIHTKNLTLSSGGETLFQGNTAPTAAGKGGAIAIADSGTL 242:	
243 501	SISGDSGDIIFEGNTIGATGTVSHSAIDLGTSAKITALRAAQGHTIYFYD 292 ::  :  :  :  :  :    :    :    :      :	
293 552	PITVTGSTSVADALNINSPDTGDNKEYTGTIVFSGEKLTEAEAKDEKNRTSKL- 345	
346 596	LONVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDLGTSLVANTESIELTNLEIN 400 :: : :  :   :    PATLKVKNLNGQNGTISLRVRPDMAQNNADRLVIDGGRATGKTILNL-VN 644	
401 645	IDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDESEYQNGFLNEDHSYDGILELDAGKDI 460 : a:	
461 685	VISADSRSINAVQSPYGYQGKWTINWSTDDKKATVSWAKQSENPTAEQEAPLVPNLLWGS 520 :	
521 718	FIDVRPFQNFIELGTEGAPYEKRFWVAGISNVLHRSGRENQRKFRHVS	
570 760	GAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNTNFAKTYAGSLRLQHDASLYSVVSILL 629	

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RESULT 15
SLAP_CAUCR
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                                                                                                                                                                                                                                                                                                                                               secreted by an ABC transporter (type I) secretion apparatus.";
J. Bacteriol. 180:3062-3069(1998).
-I. FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
-I. SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMTERY.
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P35828; Q46015;
01-JUN-1994 (Rel. 29, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
S-LAYER PROTEIN (PARACRYSTALLINE SURFACE LAYER PROTEIN).
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilchrist A., Fisher J.A., Smit J.K.;
"Nucleotide sequence analysis of the gene encoding the Caulobacter crescentus paracrystalline surface layer protein.";
Can. J. Microbiol. 38:193-202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89008089; PubMed-3049545; Fisher J.A., Smit J.K., Agabian N.; "Transcriptional analysis of the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 19089
MEDLINE-93007489;
                                                 Pfam; PF00353; hemolysinCabind; 1. PRINTS; PR00313; CABNDNGRPT.
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STRAIN-ATCC 19089 / CB15;
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    J. Bacteriol.

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                  CNIT_MET
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                               wall; S-layer;
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                               Calcium-binding
98209 MW; AFC8B519820B1A5F CRC64;
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                                                                        AGAAAQGSHNANGFTALQLGATAGATTFTNVAVNVGLTVLAAPTGTTTVTLANATGTSDV 762
FNLTLSSSAALAAGTVALAGVETVNIAATDTNTTAHVDTL-----TLQATSAKSI 812
                                  FSQDANSKLIMDLGTSLVANTESIEL----TNLEINIDSLRNGKKIKLSAATAQKDI 421
                                                                                                                                                    GD------DTVTVSSATLGAGGSVNGGDGTDVLVANVNGSSFSADPAFGG---FETLRV 702
                                                                                                                                                                                        AQGHTIYFYDPITVTGSTSVA------DAL--NINSPDTGDNKEYTGTIVFSGEKL 330
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1 MKIPLRFLLISLVPTLSMSN.....FEWRGSSRSYNVDAGSKIKF 841
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sp_unclassified:*
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sp_rodent:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	17	16	15	14	13	12	11	10	9	8	7	6	U	4	w	2	1	Result
1006	1090	1277.5	1328.5	1329.5	1353.5	1364.5	1376.5	1381.5	1400.5	1413.5	1413.5	1429.5	1429.5	1482	1495	3394	4278	Score
23.4	25.4	29.7	30.9	30.9	31.5		32.0		32.6	32.9	32.9	33.3	33.3	34.5	34.8	79.0	99.5	Query Match I
1276	973	926	936	936	914	772	928	846	928	930	930	949	928	847	839	712	841	Length
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Q9JRW2	Q9Z896	P71135	Q9JS42	Q9Z898	086163	Q9RB71	Q9Z398	P71133	Q9RB65	Q9RB66	Q9Z393	Q9K299	086164	P71132	P77792	Q9RB73	Q9Z3A1	ID
Q9k2al Q9jrw2	092896	P71135	Q9js42	868z6Ö	086163	Q9rb71	86£z6Ö	P71133	Q9rb65	Q9rb66	Q9z393	Q9k299	086164	P71132	P77792	Q9rb73	Q9z3a1	Description
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## ALIGNMENTS

Ol-MAY-1999 (TrEMBLrel 10, Created) Ol-MAY-1999 (TrEMBLrel 10, Last sequ Ol-MAY-1999 (TrEMBLrel 10, Last anno OMPT OR PMP_2 OR CPO761. Chlamydia pneumoniae (Chlamydophila p Bacteria; Chlamydiales; Chlamydiaceae CBL_TaxID=8358; ESQUENCE FROM N.A. STRAIN=CW1029; MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., L Olinger L., Grimwood J., Davis R.W., "Comparative genomes of Chlamydia pne Nat. Genet. 21:385-389(1999). [2] SEQUENCE FROM N.A. STRAIN=VR1310; Hjernoe K., Boesen T., Daugaard L., K Christiansen G., Birkelund S.; "Chlamydia proteins containing the GG of autotransporting pathogenicity fac Submitted (JAN-1999) to the EMBL/GenB SEQUENCE FROM N.A. STRAIN=AR39; MEDLINE=20150255; PubMed=10684935; MEDLINE=2015025;	Q923A1 PRELIMINARY; PRT; 841 AA. Q923A1; Q923A1; Q923A1; Q1-MAY-1999 (TrEMBLrel. 10, Created) Q1-MAY-1999 (TREMBLrel. 16, Last sequence update) Q1-MAY-1999 (TREMBLrel. 16, Last annotation update) Q1-MAY-2001 (TREMBLrel. 17, Last annotation update) Q1-MAY-2001 (TREMBLrel. 17, CPC-MAY-2001 (MAY-2014) Q1-MAY-2010 (Chlamyddaphila pneumoniae) Q1-MAY-2010 (Chlamyddaphila pneumoniae) Q1-MAY-2010 (Chlamyddaphila pneumoniae and C. trachomatis.* Q1-MAY-2013 (MAY-2014) Q1-MAY-2014
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DUF145; 1.
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Pred. No. 1.3e-244;
3; Mismatches 1;
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C STRAIN-U138; PubMed=10871362;

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Chlamydia pneumoni
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PROTEIN G FAMILY.
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Pred. No. 1.6e-192;
1; Mismatches 1;
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Longbottom D., Russell M., Jones G.E., Lainson F.A.,
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databas
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                                 FFYDPITGGGS----DELNINKKETVD---YTGKIVFSGEKLSDEEKARAENLASTFNQP
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MEDLINE-96406378; PubMed-8810531;
Longbottom D., Russell M., Jones G.E., Lainson F.A., He
"Identification of a multigene family coding for the 90
of the ovine abortion subtype of Chlamydia psittaci.";
FEMS Microbiol. Lett. 142:277-281(1996).
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    pneumoniae
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DR EMBL; AJ001311; CAA04672.1; -.
DR EMBL; AJ001311; CAA04672.1; -.
DR EMBL; AD133034; CAB37072.1; -.
DR EMBL; AD101628; AND18593.1; -.
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                                                LSNNKFLYFEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHAKKLA
                                                                                                                                               FLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSI
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TICR: CP0302: -.
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Bacteria; Chlamydiales;
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InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
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(TTEMBLrel. 16, Last annotation update)
MEMBRANE PROTEIN G FAMILY.
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                                                                                                                                                                                                                                                        (Chlamydophila pneumoniae).
es; Chlamydiaceae; Chlamydophila
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                                                                                                                                                                                                                                                                                                                                                                                           TAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHMFSHDQL
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              LARQAGIVQASGFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF 841
                                                                              DSHLYNLAIPLGIK-LEKRFAEQY-YHVVAMYSPDVCRSNPKCTTTLLSNQGSWKTKGSN
                                                                                                                                         TDHTSWGGYVWAGELGTRVAVENTSGRGFFREYTPFVKVQAVYSRQDSFVELGAISRDFS
                                                                                                                                                                                                       ASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGQLSYGHTDHRMKTE--SLPPPPPTLS
                                                                                                                                                                                                                                                ENRKGFRHTSGGYVIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNNSRTYGGTLFFKHS
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LSRQAFILRGSNNYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF
                                                                                                                         ESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGFS
                                                                                                                                                                                     HTLQPQNYLRLGRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLP----
                                                                                                                                                                                                                                                                               ENORKFRHVSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNTNFAKTYAGSLRLQHD
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                                                            IGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGN
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35.8%; Pred.
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Pred. No. 3e-76;
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Matches 355
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Q9Z393;
Q1-MAY-1999
Q1-MAY-1999
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update
01-MAR-2001 (TrEMBLrel. 16, Last annotation upda
00TER MEMBRANE PROTEIN 11 PRECURSOR.
0MP11 OR PMP_8.
Chlamydia pneumoniae (Chlamydophila pneumoniae)
Chlamydia; Chlamydiales; Chlamydiaceae; Chlamydop
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Christiansen G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                         GAIHTKNLTLSSGGETLFQGN-TAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGA
                                                                                                                                                                                                                                    TADKALTFTGFSNLSFIAAPGTTVASGKSTLSSAGALNLTDNGTILFSQNVSNEANNNGG
                         TSAPTSTRNAIYLGSSAKITNLRAAQGQSIYFYDPI-ASNTTGASDVLTINQPDSNSPLD
                                       TG--TVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKE
                                                                            GAICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIAIADSGSLSLSANQGDITFLGNTLTS
                                                                                                                              FEASSSITQNSSLFFSGNTATDAAGKGGAIYCEKTGETPTLTISGNKSLTFAENSSVTQG
                                                                                                                                                                                   AITTKTLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQLVFMNNKGETGGGALG
                                                                                                                                                                                                                                                  AANKTYTLSGFSALSFLKSPASTYTNGLGAINVKGNLSLLDNDKYLIQDNFS------
                                                                                                                                                                                                                                                                                                                                                           MKIPLRFLLISLVPTLSMSNLLGAAT---TEELSASNSFDGTTTSTTSFSSKTSSATDGTN
YTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLI
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                                                                                                                                                                                                                                                                                                                  YVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSE 117
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Pred. No. 2.5
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Umayam L.A., Utterba Berry K., Bass S., Linher K., Weidman J., Khouri H., Cra Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kol McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
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Shirai M., Hirakawa H., Kimoto M., Tabu
Shiba T., Ishii K., Hattori M., Kuhara
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EMBL; AP002546; BAA98654.1;
EMBL; AE002193; AAF38164.1;
TIGR; CP0307; -
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01-MAY-2000 (TrEMBLrel. 13,
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01-MAR-2001 (TrEMBLrel. 16,
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                                                                                  "Genome sequences of Chlamydia trachon pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
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Bacteria; Chlamydiales;
NCBI_TaxID=83558;
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55; Conservative
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DAA; 97639
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Q9RB65; Q9RB84; Q9S6P2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
POLYMORPHIC QUTER MEMBRANE PROTEIN G FAMILY (OUTER MEMBRANE PROTEIN 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hjerno K., Boesen T., Daugaard L., Knudsen K., Christlansen G., Birkelund S.; "Chlamydia proteins containing the GGAI-repeat of autotransporting pathogenicity factors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ
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Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumc
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae (Chlamydophila pneumoniae). Bacteria; Chlamydiales; Chlamydiaceae; Chlamydop. NCBI_TaxID=83558;
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PMP_10 OR OMP5 OR CP0303.
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InterPro; IPR
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161; Mismatches 315
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POMP91B PRECURSOR.
                                                                                     Chlamydia psittaci (Chlamydophila psittaci). Bacteria; Chlamydiales; Chlamydiaceae; Chlam NCBI_TaxID=83554;
Longbottom D., Russell M., Jones G.E., Lainson F.A., "Identification of a multigene family coding for the of the ovine abortion subtype of Chlamydia psittaci."
                                      STRAIN-OVINE ENZOOTIC ABORTION ISOLATE S26/3; MEDLINE-96406378; PubMed-8810511;
                                                                SEQUENCE FROM N.A.
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                                            EILLPYVSKTL----PCSFYGQLSYGHTDHRMK---TESLPPPPPTLSTDHTSWGGYVWA 688
                                                                                              YAQTPSDDVCSAAFCQLFGKDKDYFVSKNSSTIYAGSIYYQH-ISYWNTWNTLL-----
                                                                                                                     TLWGAFSDTRAIQNLMDISVNGADYSRGFWVSSLANFLNKSGSDTKRKFRHHSAGYALGV
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Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAR-2001 (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                MEDLINE-20330349; PubMed-10871362; Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumo from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
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Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OUTER MEMBRANE PROTEIN PRECURSOR (POLYMORPHIC MEMBR
                                                               EMBL;
EMBL;
EMBL;
EMBL;
TIGR;
                                                                                                                                                     MEDLINE=20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heid White O., Hickey E.K., Peterson J., Umayam L.A., Berry K., Bass S., Linher K., Weidman J., Khouri Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy McClarty G., Salzberg S.L., Eisen J., Fraser C.M. "Genome sequences of Chlamydia trachomatis MoPn a
                                                                                                                                                                                                                                                                                                                                                                                                               Hjerno K., Boesen T., Daugaard L., Knudsen Christiansen G., Birkelund S.; "Chlamydia proteins containing the GGAI-re of autotransporting pathogenicity factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat.
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                                     InterPro;
                                                                                                                            Nucleic
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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AJ133034; CAB37069.1;
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WKTTGTNLSRQAGIGRAGIFYAFSPNLEVTSNLSMEIRGSSRSYNADLGGKFQF
                  WKTKGSNLARQAGIVQASGFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF
                                                                          AISRDFSDSHLYNLAIPLGIKLEK--RFAEQYYHVVAMYSPDVCRSNPKCTTTLLSNQGS
                                                                                                                                               PPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGFFREYTPFVKVQAVYSRQDSFVELG-
                                                                                                                                                                                            GSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGQLSYGHTDHRMKTESLPP
                                                                                                                                                                                                                                                        NVLHRSGRENQRKFRHVSGGAVVGASTRNPGGDTLSLGFAQLFARDKDYFMNTNFAKTYA
                                                                                                                                                                                                                                                                                                                 KKATVSWAKQSENPTAEQEAPLVPNLLWGSFIDVRPFQNFIELGTEGAPYEKRFWVAGIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTKNLTLSSGGETLFQGNTA-PTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTI--GAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKIPLRELLI--SLYPTLSMSNLLGAATTE-ELSASNSFDGTTSTTSFSSKTSSATDGTN
                                                         TLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTS
                                                                                                                   P----KGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIKVEASYIHQDSFKERNT
                                                                                                                                                                           ASLHLQHLATL-SSPSLLR-----YLPGSESEQPVLFDAQISYIYSKNTMKTYYTQA
                                                                                                                                                                                                                                      NFFHKDSTKINKGFRHISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKNRASAYA
                                                                                                                                                                                                                                                                                                KAATLTWTKTGYNPNPERRGTLVANTLWGSFVDVRSIQQLVATKVRQSQETRGIWCEGIS
                                                                                                                                                                                                                                                                                                                                                            DVSWNNPQVFSCLTLTADDPANIHITDLAADPLEKNPIH--WGYQGNWALSWQEDTATKS
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Pred. No. 3.9e
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01-MAY-2000
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Bacteria;
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Pfam; PF02415; DUF145; 1.
SEQUENCE 772 AA; 82931 MW;
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FWCAGLSNFFHKDSTKTRRGFRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAK · 544
                                            FWVAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNT
                                                                                                                                             NWSTD-DKKATVSWAKQSFNPTAEQEAPLVPNLLWGSFIDVRPFQNFIELGTEGAPYEKR
                                                                                                                                                                                                                                                                                                           AFTQQADSRLEMDVGTTLEPADTSTI--NNLVINISSIDGAKKAKIETKATSKNLTLSGT
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                                                                                                 VWGTGASTTATFNWTKTGYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRA
                                                                                                                                                                                                       ITLLDPTGTFYENHSLRNPQSYD-ILELKASGTVTSTAVTPDPIMGEKFHYGYQGTWGPI
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Chlamydiales; Chlamydiaceae; Chlamydophila.
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Best Local S
Matches 321
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001311; CAA04671.1; -.
InterPro; IPR003357; -.
InterPro; IPR003358; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02385; OMP; 1.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence upda:
01-MAR-2001 (TrEMBLrel. 16, Last annotation up
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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ISTKNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPTLFSNNIAEAAGGA
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Pfam; PF02415; DUF145; 1. SEQUENCE 936 AA; 100079 MW;

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Q1-MAY-1999 (TrEMBLrel. 10, Cr
f 01-MAY-1999 (TrEMBLrel. 16, Lr
T 01-MAR-2001 (TrEMBLrel. 16, L
       MEDLINE-99206606; PubMed-10192388;

Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

"Comparative genomes of Chlamydia pneumoniae and C. trachomat Nat. Genet. 21:385-389(1999).

EMBL; AE001627; AAD1389(1999).

InterPro; IPR003357; -.

InterPro; IPR003357; -.
                                                                                                                                                POLYMORPHIC OUTER MEMBRANE PROTEIN FAMILY.

PMP_7.

Chlamydia pneumoniae (Chlamydophila pneumoniae).

Bacteria; Chlamydiales; Chlamydiaceae; Chlamydop

NCBI_TaxID-83558;
                                                                                                               STRAIN-CWL029
                                                                                                                          SEQUENCE FROM N.A.
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                   GSNLARQAGIVQASGFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF
                                                        AFNKSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMAY
                                                                                  DFSDSHLYNLAIPLGIKLEK--RFAEQYYHVVAMYSPDVCRSNPKCTTTLLSNQGSWKTK
                                                                                                                  DNSIIKGSWRNDAFCADLGASLPFV-ISVPYLLKEVEPFVKVQYIYAHQQDFYERHAEGR
                                                                                                                                 DHT----SWGGYVWAGELGTRVAVENTSGRGFFREYTPFVKVQAVYSRQDSFVELGAISR
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                                                                                                                                                                                       DASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGQLSYGHTDHRMKTESLPPPPPTLST
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Matches 309
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EMBL; AP002546; BAA98653.1; -
EMBL; AE002193; AAF38165.1; -
TIGR; CP0308; -
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Q9JS42;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
POLYMORPHIC OUTER MEMBRANE PROTEIN G FAMILY (POLYMORPHIC PROTEIN G FAMILY).
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Pfam; PF02315; OMP; 1.
Pfam; PF02415; DEP145; 1.
ProDom; PD004952; -; 1.
SEQUENCE 936 AA; 100105 MW;
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
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                             TKNLTLSSGGETLFQGNTAPTAAGK--GGAIAIADSGTLSISGDSGDIIFEGNTIGATGT
GLKVSISAGGPTLFQSNISGSSAGQGGGGAINIASAGELALSATSGDITFNNNQVTNGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1328.5; DB 2; Length 936;
Pred. No. 2.7e-70;
B; Mismatches 360; Indels 123;
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                      GSNLARQAGIVQASGFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF
                                                                       DASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGQLSYGHTDHRMKTESLPPPPPTLST
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                                                                                                                DNSIIKGSWRNDAFCADLGASLPFV-ISVPYLLKEVEPFVKVQYIYAHQQDFYERYAEGR
                                                                                                                                         DHT----SWGGYVWAGELGTRVAVENTSGRGFFREYTPFVKVQAVYSRQDSFVELGAISR
                                                                                                                                                                     TEGLFDIANFLWGKATRAPWVLSEISQIIPLSFDAKFSYLHTDNHMK------TYYT
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                                                         ATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCA 862
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NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
PATENT: WO 9858953-A 13 30-DEC-1998;

MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)

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1979 GCTTTCGCCATTTCAGTGGCGGTTATGTCAFAGGAGGAACCCTACATACTTCTTCAGATA 2038 	Db Qy
19 CTTTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCG 197 	Оу Дъ
1859 ATATTAGCTCTCCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTG 1918	Оy
1799 TTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAG 1858	Qy
1745 GGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATA 1798	Оу
1685 ATCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCCAATTGTTT 1744	рь Оу
1631 ACATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAG 1684	Qу
1571 TATTGGACCCGACGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACG 1630	Оy
1511 AGGCAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTT 1570	ОУ
1451 CTGATACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGA 1510	Qy Db
1391 CATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGAACGTAGGAACTACTCTAGAACCTG 1450	Qу
1331 CTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAGG 1390	Qу
1271 AAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGC 1330	Оy
1211 TTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGAG 1270	Qу
1151 TCTACTTCTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAAG 1210	Оу
1094 TCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGCTGGTAGAGCCA 1150	Db Oy
1043 TITTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTA 1093 	Qy Qy
983 CCATAGCTATCGAAGATAGTGGGGAATTGAGTTTTATCCGCCGATAGTGGTGACATTGTCT 1042 	Оу

1925	CTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCCGTGCTTTTTG	1866	Qy
1865 199213	TCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGII	1806 199154	g Q
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1745 199093 1805	THE THE PROPERTY OF THE PROPER	1585 199034 1746	S B 3
(a) (b)	CTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAGA	63 97	, B 6
1634 198973	GGACCCGACGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACGACAT	1575 198914	D Qy
157 <b>4</b> 198913	AAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTTTATT	1515 198854	Оу
1514 198853	TACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGC	1455 198794	당 성
1454 198793	TCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCTGA	1398 198734	ду 40
1397 198733	TCTTTCAGGAGGTACTCTATATTTAAAACATGGAGTGACTCTGCAGACTCAGGCATTCAC	1338 198674	g 8
1337 198673	ATCAGAGACAGAGGCCGCAGAITCTAAAAAATCTTACTTCGAAGCTACTACAGCCTGTAAC	1278 198614	g Qy
1277 198613	GACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGGAAAAAGTT	1218 198554	g dg
1217 198553	CTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAAGTTAATGA 	1158 198497	ρ Q
1157 198 <b>4</b> 96	CTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGGTAGAGCCATCTACTT	1098 198437	B 8
1097 198436	CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATCGA	1041 198377	Db dg
1040 198376	AGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT	981 198317	dg VQ
980 198316	CGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGG	921 198257	D Q
920 198256	CAACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAAGCTCGAACTGGCTTC	861 198197	ρ γ
860 198196	TTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAG	801 198137	ОУ

RESULT 15
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2787 bp DNA Sequence 13 from Patent W09858953. A81839 A81839.1 GI:6731077

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SOURCE ORGANISM

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                                                                                     200051 AGAACTCTCTGGGGAAGCTGCTTATGAGCTTCGTGGCTCAGCACACATCTACAATGTAGA 200110
                                                                                                                                                                                                                                                                                                                                                                                                                                              199811 TGATGGAGACCTAGTGGAACTGCTCTATCCCTGTCGGCATTCGGTTAGAAAAAATCTCCCGA 199870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1986 CCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAGATTCT 2045
                                                                                                                                                                                                                                                                                                                                                         AGATGAAAAAAATAATTTCGAGATTTCTCTAGCCTACATTGGTGATGTGTATCGTAAAAA 199930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCCCAGCTAAGCTACAGCTACACTAAAAATGATATGGATACTCGCTATACTTCCTATCC 19963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCATCAGGAACTGCGAATTTCTTCCATAAGGATAAATCAGGAACTAACCAAGCATTCCG 199333
                                                                                                               TGAAGCCTTTAGCCAATTTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGA 2762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTCATAACTATTTAGCGTCGCTATACCTGCAACATCGAGCATTCCTAGGAGGACTTCC 199513
                                         CTTAGGAGCAAAATACCAATTCTA 2786
                                                                                                                                                                                                    TTTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAATTT 2702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTAGCCGTCTTGTGAATCTTGCCTTTACCTATCGGGATCCGATTTGATAAGGAATCAGA 2522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGAAGCTCGTGAATTTGG 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGA---AGAGC 2342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACCC
                                                                                                                                                                                                                                                                   TCCCCGTTCGCGTACTTCTCTAATGGTCAGTGGAGCCTCTTGGACTTCGCTATGTAAAAA 199990
                                                                                                                                                                                                                                                                                            CCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAA 2642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTATATCTCCCTAAAGAAGCACCGTTCTTCCAGGGATATTTCCCCTTCTTAAAGTTCCA 199750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCTTCC 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATAAAAGCTACGGCTATATTGTTGGAGGAAGTGCTGAAGATTTTTCTGAAAATATCTT 199393
                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAA 2582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAGTCTACAGCCGCCAACAAAACTTTAAAGAGAGTGGCGCTGAAGCCCGTGCTTTTGA 199810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCA 2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAAACACGACGCGGGTTTCG 1985
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SKFPNLLCNGSSGIAVGMATNIPPHNLGELIEATLLLLANPQASVDEILQVMPGPDFP
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complement(5871. .8375)
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                                                                                                                                                                                                                                                                                                 complement(8391.
                                                                                                                                                                                                                                                                                                                                                                   complement(8391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MFIVIEGGEGSCKSSLAKALGDQLVAQDRKVLLTREPGGCLIGE
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GIABGLGADFVADLCSKVVGFTPFLPMFVLLLDIPADIGLQRKHRQKVFDKFEKKPLS
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/db_xref="GI:8978649"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GVRSILINERNGNVLGAIPVTDHDSILLMSSQGQAIRINMQDVRVMGRSTQGVRLVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMGRTARGVRGVSLKNEEDKVVSCQIVTENQSVLIVCDQGFGKRSLVEDFRETNRGGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLNLGLKASALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="WHLEEENOGWEALLRKYYHOEVPPAILLHGFTLPYLODKAEOLA
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ILCSKETFSYLFRYAQCEIPVTEVSQIIKESSETDKQVLRDKVORFMEVLLELYRDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4359. .5255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4359. .5255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHEIPSVVFQKMQVTVPNWIDPARG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="WTDYSFFRRKIGNIEAIECPGNPQDPIIIICHGYGSLADNLTFF
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                                                                                                                                                                                                   transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="thymidylate kinase"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="dnax_2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="lysophospholipase esterase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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Matches 1406;
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Best Local
198095 CACTGCAACAGATGCTGCAGGCAAG--
                                                                                                                                                                                                                                                                                                                                                          197915 CACTAGTAATAGCGCAAAAAATTAGGTGGAGCGATCTATAGCTCTGCGGCTGCAAGTAT 197974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197795 TCTTACCGATAATGGAACGATTCTCTTTAGCCAAAACGTCTCCAATGAAGCTAATAACAA 197854
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                                                       741 TAAGGTCACAGGAGCGCGCTCCTCAACAACGGGGGGATATGTCAGGAGGTGCTATCTGTGC 800
                                                                                                                                                       681 AATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTTCCTTTATTGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 TGGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGGCAC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501
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                                                                                                                                                                                                                                                                                                                                                                                                               561 TTCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCAT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCAATCACAAAAAGCTGTTTTAACAACACTAAGGGCGATTTGACTTTCACAGGTAACGG 269
                                                                                                                                                                                                                                        TTCAGGAAACACCGGCCAGTTAGTCTTTATGAATAATAAAGGAGAAACTGGGGGTGGGGC
                                                                                                                                                                                                                                                                                               TACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCGGAGCGATCACCGCAAAAACTCTTTCTATTTCTGGGAATACCTCTTCTATAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTGGAACTACAGTTGCTTCAGGAAAAAGTACTTTAA---GTTCTGCAGGAGCCTTAAA 197794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTATTGCGTC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATACTCATTTCATTCAACACGGTAGATGCGGGTTCGAATGCAGGAGCTGCGG----CAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAACGAACTATGTCTTATCAGGAAATGTCTATAT---AAACGATGCTGGGAAAGGCAC 197560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGG-----ATAA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTTGAA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACAACTGCTGATAAAGCCCTAACATTCACAGGATTTTCTAACCTTTCCTTCATTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTTAACAG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCATTAACAGGCTGCTTTACAGAAACTACGGGTGATCTGACATTTACTGGAAAGGG
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SYLLMLGTNESSILFKSTERELRGEALESFINVILDVESFINILEKKAIPFSEFLEMY
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LGEMNADQLMDTTMNPEQRTLIHVSLKDAVEADHIFTMLMGEEVPPRREFIESHALSI
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SFDKVTFFYEGGIQSFVSYLNQNKESLFSEPTYICFTWGDDGEIEFEAALQWISGYS
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RRFQAILPIRGKILNVEKARLQKIFQNQEIGTIIAALGCGIGADNFNLSKLRYRRIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHVQIREIQFLLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mflkrkkrggggqvqnkrtaspikhakhylhnylqblqkimaarp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(10812.
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REPLINE 2030349  REPERENCE 2 (bases 1 to 300650)  AUTHORS Shiral, M.  TITLE Direct Submitssion  Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.  Mutsunori Shiral, Yamaguchi University School of Medicine,  Department of Microbiology: 1-1-1 Minamikogushi, Ube, Yamaguchi 75-8505, Japan (E-mail:mshiral@po.cc.yamaguchi-u-ac.jp,  Tel:81-836-22-227, Fax:81-836-22-2415)  On Sep 15, 2000 this sequence version replaced gi:6172390  gi:617232 gi:6172334 gi:6172336 gi:6172338 gi:6172382 gi:6172384	SOURCE Chlamydophila pneumoniae J138 (strain:J138) DNA.  ORGANISM Chlamydophila pneumoniae J138  Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.  REFERENCE 1 (sites)  AUTHORS Shiral, M., Hirakawa, H., Kimoto, M., Tabuchi, M., Kishi, F., Ouchi, K.,  Shiba, T., Ishii, K., Hattori, M., Kuhara, S. and Nakazawa, T.  Comparison of whole genome sequences of Chlamydia pneumoniae J138  from Japan and CWLO29 from USA.  INCLEAN ALGE DOE 20 (12) 2311-231 (2000)	RESULT 14 AP002546 AP002546 300650 bp DNA BCT 08-DEC-2000 DEFINITION Chlamydophila pneumoniae J138 genomic DNA, complete sequence, section 2/4. ACCESSION AP002546 AB033782 AB033783 AB033784 AB033785 AB033800 AB033801 AB03802 AB033803 AB033804 AB033805 AB033807 AB033808 AB033802 AB033811 AB033812 AB033813 AB033814 AB033815 AB0336079 AB033810 AB033811 AB033812 AB033813 AB033814 AB033815 AB036079 AB036079 AB036081 AB036082 AB038348 AB038349 BA000008 VERSION AP002546.2 GI:10176692	76	Qy 2703 TGAAGCCTTTAGCCAATTTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGA 2762	QY 2643 TTTGGCAAGACCATTTAGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAATTT 2702	2583 CCCCGACTGTACGACACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAA	2523 CTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAA	QY 2463 AAGTAGCCGTCTTGTGAAICTTGGCCTTACCTATCGGGATCCGATTTGATAAGGAATCAGA 2522	Qy 2403 GTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGGAAGCTCGTGAATTTGG 2462	Qy 2343 TCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCA 2402	Qy 2286 TACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGC 2342	QY 2226 AGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCC 2285
/protein_id= baAs9400.1 /db_xref==0i= baAs9400.1 /db_xref==0i= baAs9400.1 /db_xref==0i= baAs9400.1 /translation="MPDKKAQITFSLPEVMSAIHQGKIVALPTDTVYGFVLSLYASEA /translation="MPDKKAQITFSLPEVMSAIHQGKIVALPTDTVYGFVLSLYASEA /translation="MPDKKAQITFSLPEVMSAIHQGKIVALQLIFQAITLVYKHRNP EERLYALKDREPSKAFALYVNSIEDLIGTSANLSEEPSALTAQEIFADFADHDLCIF DGPCSHGLESTVDHSVYCEHPKDGTLLGTSANLSEEPSALTAQEIFADFADHDLCIF DGPCSHGLESTVVASDPLYIYEELLGTSAVIENIAGTEAKIFHTTSHAFSKHIKIYTV KNQEQLVSFLSGSLDFKGVVCEHPKPKNFYTRLREALKKKTPSIVFIYDINTSDYPEL FPFLSPYIE" gene	gene AEAHPVLNQLIBRIFSKOKAESILSSRAEKFLKQVIVEQVNPKITDVKL"  gene 'yene"ywlC"  complement(24873347)  CDS complement(24873347)  /gene="ywlC" /codon_start=1 /transl_table=11 /transl_table=11 /transl_table=11	/gene="Cpj0269" /codon_start=1 /transl_table=11 /transl_table=11 /transl_table=11 /transl_table=11 /product="dipeptidase" /product="dipeptidase" /protein_id="BAA98479.1" /db_xref="GI:8978643" /db_xref="GI:8978643" /translation="MYIDMHCDILSHPHFCRKDPAVRCSPEQILSGGVRQOVCAIFVP /translation="MYIDMHCDILSHPHFCRKDPAVRCSPEQILSGGVRQOVCAIFVP /translation="MYIDMHCDILSHPHFCRKDPAVRCSPEQILSGGVRQOVCAIFVP /translation="MYIDMHCDILSHPHFCRKDPAVRCSPEQILSGGVRQOVCAIFVP /translation="MYIDMHCDILSHPHFCRKDDAVRCSSCQKKSLSLIRSIENASALGD DTAPLGTILAKLIHLTKOGPLAYIGIVKGDNRFGGGTEAPKRLINDGKVLLDIMYEL GVPIDLSHCSNKLABGILDYTADKLPNLAVIASHSNERSVLDHRRILVDAHAKEIVRR	FULPKIDPENAQANPPOTST PAVENGI DIDLNPLIGQPNEQNNANNPGTSGSNPTSLPA PERLPETEENSQEEEOGSQNNEDLIG"  gene complement (14952472)  CDS complement (14952472)	/transl_table=11 /product="hypothetical protein" /protein_id="BAA98478.1" /db_xref="GI:8978642" /db_xref="GI:8978642"	/gene="CPj0268"  /gene="CPj0268"  /codon_start=1	QYGKYFQEVYGYKEPSIPKNDNYHKLTSCLPSPLDIESPSPEASTPVSKLRIAGCSG VALVLGYVTLLIGAVVSVEFCTGYLQLALCVGFACLGTALFVGGLAGLRTHSLIAQGIM YLYLTYYLSSALEERNETVKDQRNEINTYLTEECRQQKREKALLE"  9571343	/protein_id="BAA98477.1" /db_xref="GI:8978641" //translation="MSIMSINKTWALLNQPEPAVCLNAWDPKYINQDRKTFACTVTLL /translation="MSIMSINKTWALLNQPEPAVCLNAWDPKYINQDRKTFACTVTLL VTATLWITTMATTTYTTILAMCSDGISVINGTITGTGTGTGTGTGTGTTTTTTTTTTTTTTTLTTTTTTTT	/gene="crjuzor" /codon_start=1 /transl_table=11 /product="hypothetical protein"	gene 144. 935  CDS 144. 935	/organism="Chlamydophila pneumoniae J138" /strain="J138" /db_xref="taxon: 138677"		gi:6172386 gi:6172388 gi:6172390 gi:6172392 gi:6172394 gi:6174666 gi:6635174 gi:6635176 gi:6635178 gi:6635180 gi:8547433 gi:8547438 gi:8547448 gi:8547448 gi:8547448 gi:8547448 gi:8547448 gi:8547448 gi:8547448 gi:8547448 gi:854748 g

57	GTTCTGCTGCTGGTAGAGCCATCTACTT 115 	1098 CTTAGGAACGAGTGCAAAGATGACAGCTTTGC	Оу
97	TACTACTCCTGGGACGAATAGAAGTAGTATCGA 109 	1041 CTTTTTAGGGAATACAGTCACTTC	Оу
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0	GTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGG 980 	921 CGGAGGACTTACCCTATTCA 	Db Db
84	CGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTC 920 	861 CAACAATACATCGACAACAGO	Qy Db
0	GATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAG 860	801 TTATAAACTAGTACAGA             2103 TGAAAAAACAGGAGAGAC	Qy Db
04	TCCTCAACAACGGGGATATGTCAGGAGGTGCTATCTGTGC 800 	741 TAAGGTCACAGGAGCGAGC	Db Qy
46	TCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAA 740 	681 AATTTTTACAGAAGCCTC           2205 TCTGGGCTTTGAAGCCAG	Db
06 0	AAGTCTCTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGC 680	621 TACTGGAAACCAAGGGGA 	Оу
66 0	CTCCTCAAAGAAAGGCGAGCCATTCAGACTTCCGATGCCCTTACCAT 620 	561 TTCTGAAAATACCTCCTC	Qу
0	TATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTT 560 	501 TGGCGGTGCTATCACCGC                    2385 TGGCGGAGCGATCACCGC	рь
86	TIGCTCITCAGCAAAAACTTITCAACGGATAA 500 	450 GTTTGACAAAAATGTCAGT	Db 04
9 46	GGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTTGAA 449 	390 TCCTGGAAGTTCGATAACTACO                        2502 TCCTGGAACTACAGTTGCTTCJ	DP QA
9	CCACGTTTATAGGGTTTTCTTCGCTATCTTTTATTGCGTC 389 	330 CAGCGTGGTAGATAAATCTI	Qу
63	TCTATTGTTCCAAACGGTGGATGCAGGGGGCTGTAACAG 329	270 GAACTCTCTATTGTTCCA                  2619 ATACTCATTTTCATTCAA	рь
20	ACAAAAAGCTGTTTTAACAACACTAAGGGCGATTTGACTTTCACAGGTAACGG 269 	210 AGCAATCACAAAAAGCTG	Фр
9	GGAAATGTCACTCTAGAAAATATTCCTGGAACAGGCAC 209 	150 TGGAACTACCTACCTATTTAAG                        2736 TGGAACGAACTATGTCTTATCA	Оy
11;	6%; Score 517.2; DB 1; Length 10026; 8%; Pred. No. 8.2e-117; 0; Mismatches 1198; Indels 60; Gaps	uery Match Sest Local Similarity 52. Matches 1406; Conservative	¥ m̂ O

6 TTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTTTC 2225	Qy 2166 Db 726	п о
CTCTCA	Db 786	-
6	Qy 210	~
6 CAGTGTAGCTTTCTGCCAGCTCTTCGGTAAAGATAAAGACCTGTTTATAGTTGAAAATAC 787	Db 84	-
6 TAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCA 2105	Qy 204	^
⊳	Db 906	_
6	Qy 198	_
6 GGCATCAGGAACTGCGAATTTCCTTCCATAAGGATAAATCAGGAACTAACCAAGCATTCCG 907	96	_
6	Qy 192	_
6 CACTCTACAGCAGATCATGACATCTCAAGCGAATAGTATCTATC	Db 102	_
6 CTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTTG 1925		~
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	Qу 1806	_
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	Qy 1746	_
6 TCCAGTACAAACTCCAGAACCTCATTACGGGTATCAGGGACATTGGGAAGCCACTTGGGC 1147	Db 1206	_
6	Qy 168	_
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5 CTTAGAGCTCAA	Qy 163	_
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5 GGACCCGACGGCACGTTTTATGAAAATC	Qy 157	_
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➣	Qy 1515	_
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8	Оу 139	_
6	Db 156	_
8 TCTTTC	Qу 133	
6 CTCTGCAGATGAAGCGAAAGCTGCTGATAACTTCACATCTATATTAAAGCAACCATTGGC 1567	Db 162	
æ	Qy 127	_
6 ACCGGATAGCAACTCGCCTTTAGATTATTCAGGAACGATTGTATTTTCTGGGGAAAAGCT 1627	Db 1686	
	Qy 1218	_
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Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., White, O., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.

Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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Chlamydophila pneumoniae AR39.
Bactteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 10026)
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Nucleic Acids Res. 28 (6), 1397-1406 (2000)
20150255
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AE002193.2 GI:81
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1, 2000 this sequence version replaced gi:7189234.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="synonym: Chlamydia complement(105..2897)
/gene="CP0307"
                                                                                                                          /translation="mkiplhkllisstlvtpillsiatygadaslsptdsfdgaggst
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                                                                                                                                                                                                                                                                                                                                                                                  complement(105. .2897)
/gene="CP0307"
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                                                                        SQNVSNEANNNGGAITAKTLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQL
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                                                                                                                                                                                                                                                                                                                                  similarity;
                                                                                                                                                                                                                                                                                                                                /note="similar to GP:4376729;
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="AR39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Chlamydophila
                                                                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                                        codon_start=1
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BASE COUNT
ORIGIN
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gene CDS

2726

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GNSSLTGNTHILF SCHKATGENNSSANQEGCGGALLSFLESASYSTKKGLWIEDHENV

SLSGNTATVSGGALYATKCALHGNTTLIF DGNTAETAGGALYTETEDFTLTGSTGTVT

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SINQLLETKSSGEFFERELWLSGIANFYRDSHTRHGFRHIGGYALGITATFPAED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQKNTSEKDGAAVSAYSIDLAKTTTAALLDQNTSTKNGGALCSTANTTVQGNSGTVTF
SSNTATDKGGGIYSKEKDSTLDANTGVVTFKSNTAKTGGAWSSDDNLALTGNTQVLFQ
ENKTTGSAAQANNPEGCGGAICCYLATATDKTGLAISQNQEMSFTSNTTTANGGAIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAKETSDASGTTYTLTSDVSITNVSAITPADKSCFTNTGGALSFVGADHSLVLQTIAL
THDGAAINNTNTALSFSGFSSLLIDSAPATGTSGGKGAICVTNTEGGTATFTDNASVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity;
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/gene="CP0309"
complement(6013. .9843)
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LTLMYILDAYRRNPKCQTSLIASDANWMAYGTNLARQGFSVRAANHFQVNPHMEIFGQ
FAFEVRSSSRNYNTNLGSKFCF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFSTTDAAAGTTYSLLSDVSFQNAGALGIPLASGCFLEAGGDLTFQGNQHALKFAFIN
AGSSAGTVASTSAADKNLLFNDFSRLSIISCPSLLLSPTGQCALKSVGNLSLTGNSQI
IFTQNFSSDNGGVINVKNFLLSGTSQFASFSRNQAFYCKQGGVVYATGTITIENSPGI
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/gene="CP0308"
complement(2941. .5751)
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/protein_id="AAF38166.1"
/db_xref="Gi:7189237"
/translation="MKYSLPWLLTSSALVFSLHPLMAANTDLSSSDNYENGSSGSAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="polymorphic membrane protein
/protein_id="AAF38165.1"
/db_xref="GI:7189236"
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FLKFQAVYSRQQNFKESGAEARAFDDGDLVNCSIPVGIRLEKISEDEKNNFEISLAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTPEPHYGYQGHWEATWADTSTAKSGTMTWVTTGYNPNPERRASVVPDSLWASFTDIR
TLQQIMTSQANSIYQQRGLWASGTANFFHKDKSGTNQAFRHKSYGYIVGGSAEDFSEN
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AGANKTITLTSPLVFQDSSGNFYESHTINQAFTQPLVVFTAATAASDIYIDALLTSPV
                                                                                                                LVLHGQVSYGRNHHNMTTKLANNTQGKSD\DSHSFAVEVGGSLPVDLNYRYLTSYSPY
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similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="CP0309"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
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1453 GATACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAG 1512 	ОУ
1396 ACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCT 1452 	Фр
1336 ACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAGGCATTC 139	Оy
1276 TTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTA 1335 	Qy Db
1216 GAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGAGAAAAG 127 	Ор
1156 TTCTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAAGTTAAT 1215	Оу
1096 GACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGGTGAGGCCATCTAC 1155	DP QA
1042 TTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATC 1095	Дy
982 GCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTC 104	Оy
922 GGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGA 981	Оу Оъ
862 AACAATACATCGACAACAGCGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCC 921	Оy
802 TATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGC 861	Дb
742 AAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCT 801	Оy
682 ATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAAT 741	QУ
622 ACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCA 681	Оу
562 TCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATT 621	Qу рь
502 GGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTT 561 	dp Qy
442 AGCTTGAAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAAT 501 	Qу Дъ

2640	AACCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACG	2581	Qy
2550	TTCTCCGATAAGTCTACGTATGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTAAT	2491	ДD
2580	GACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTGGTAGT	2521	Qy
2490	CAAAGTGAAGACCTCTTCAATCTAGCGGTTCCTGTAGGGATAAAATTTGAGAAA	2437	рb
2520	GGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATAAGGAATCA	2461	Qy
2460 2436	CAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGAACAGAAGCTCGTGAATTT	2401 2377	Qy Vo
2376	CCGGTAGTTGCTTCAGGACGTCGGTCTTGGGTGGATACCCACACGCCATTTCTAAACCTA		Дb
2400	CCGA TTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTG	2344	γQ
w (		2257	B K
ω 4	OCTACTTRAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGTC	2284	Q
2283 2256	TCAGGAAACCTTAGCTACACCATACGACAAACATATTACAACAAGTATACAACAAGTATACAACAAGTATACAACAAGTACACAAGTACACAAGTACACAAGTACACAAGTACACAAGTACACAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACCAAAAGTACACAAAAGTACACCAAAAGTACACAAAAGTACAACAACAACAACAACAACAACAACAACAACAACAAAAGTACAACAAAAGTACAACAAAAAGTACAACAAAAAGTACAAAAAAGTACAAAAAAAA	2224	Оу
	GCTAAGATTTTGTCAGGAAATTCTGACTCCCTACCTTTTGTCTTC	2152	DЬ
2223	CCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTT	2164	Qy
2151	CATACCCATGTATATGCAGGGGCAATGAGTTACCGACACCTCGGAGAGTCTAAGACCCTC	2092	Db
2163	CAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCTCTT	2104	Qy
2091	TTTAATTTTGCTTTTTGTCAGCTTTTTGGCTACGACAAGGACCATCTTGTGGCTAAGAAC	2032	dα
2103	CTTAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAAT	2044	QУ
2031	CGTCATTCTAGCGCGGGTTATGCATTAGGAGGAGGATTCTTCACGGCTTCTGAAAATTTC	1972	Db
2043	CGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAGATT	1984	Qy
S		9	ρb
1983	TGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGCGGGGTTT	1924	у
1911		1852	מם
1923	AGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTT	1864	ур
1851	ATTCCAGAACGTCAGGGACCTTTGGTTCCTAATAGCCTGTGGGGTTCTTTTGTCGATGTC	1792	qa
1863	ARTCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATT	1804	Qy
7	GATGCAACTGCAAAAACAAAAAATGCTACCTTAACTTGGACTAAAACAGGATACAAGCCG	7	dd #
80	GGGGCTTTTTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATTTCCT	1753	0
73		1675	Db #
1752	ATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGGCCCAATTGTTTGGGGGACA	6	0ν
1674		1615	ДD
1692	ATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAGATCCTATA	1633	Qy
1614	GTAGATGCTCAGGGGAACTATTATGAGCATCATAATCTCAGTCAACAGCAGGTCTTTCCT	1555	Db
1632	TIGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACGAC	1573	Qy
1554		1495	Db .
1572	GCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTTTA	1513	_ 0v

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10056
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                                                                                                                                           GAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGAAGCTCG
                                                     TGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCAT
                                                                                        AGCTAAGAATCAAGGTACAGTCTAACGGAGGAACTCTCTATTACCAGCACAACGAAACCTA
                                                                                                                                                                                                                                                                                                     TATAGATATTAGCTCTCCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGA 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTATATTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GG------GGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGG
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                                        AGCTTCTTCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATGCTCCATACAT
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Query Match
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Matches 1428; Conserv
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                                                                                                                                                                                                                                                                                                                   GAAGATGCTGGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGA 201
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                                     ATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGT 441
                                                                                                             GTTAACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTT 381
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Sequence 11 :
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A81837.1 GI
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1 (bases 1 to 2757)

1 (bases 1 to 2757)

Madsen,A. and Birkelund,S.

NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
PATENT: WO 9858953-A 11 30-DEC-1998;

MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)

Location/Qualifiers
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Score 528.6; DB 9;
Pred. No. 1.2e-119;
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Matches 1418;
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Best Local
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CACAGCAATCACAAAAAGCTGTTTTAACAACACTAAGGGCGATTTGACTTTCACAGGTAA 266
                                                                  TACTGGAATAGACTATACTCTGACAGGAGATATAACTCTGCAAAACCTTGGGGATTCGG-
                                                                                                                                     TGCTGGAACTACCTACTTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGG
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14579. .1617~
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GAAASTTANKHLTFSGFSLLSFDSSBSTTVTTGGGTLSSAGGVHLENIRKLVVAGNFS
TADGGAIKGAEFLLTGTSGDALFSNNSSSTKGAIATIANNTGYNFFLSNIA
TSGGAIDDGTS ILSNNKFLYFEGNAAKTTGGAIATIANNTGYNFFLSNIA
TSGGAIDDGTS ILSNNKFLYFEGNAAKTTGGAIATIANSGELSLSAETGNITF
VARTSGGAIHAKKLALSGGFTEFLRNNVSSATPKGQAISIDASGELSLSAETGNITF
VRNTLITTGSTDTPKNAINIGSSKKFTELRAAKNHTIFFYDPITSEGTSSDYLKINN
GSAGALNPYQGTILFSGTSCHLKVADNLKSSFTQPVSLSGKKLLLQKGVTLESTS
FSQEAGSLLCHDSGTTLSTTAGSITTTNLGINVDSLGLKQPVSLSGKKLLLQKGVTLESTS
FSQEAGSLLCHDSGTTLSTTAGSITTTNLGINVDSLGLKQPVSTAKGASNEYGFQG
QMNVNNTTDTAANNTKEATATWTKTGFVPSPERKSALVCNTLNGVFTDIRSLQOLVEIG
GNIVNNTTDTAANNTKEATATWTKTGFVPSPERKSALVCNTLNGVFTDIRSLQOLVEIG
ATGMERKQGFNVSSWINFLHKTGGDENNKGFRHTSGGTVIGGSATATWDLFTFAFCHL
TRANSPERKGALVNNFLHKTGGDENNKGFRHTSGGTVIGGSATATWDLFTFAFCHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTILRNFLITCSALFLALPAAAQVVYLHESDGYNGAINKSLEPK
ITCYPEGTSYIFLDDVRISNVKHDQEDAGVFIKRSGKLFFMGHRCNFTPHNLMTEGFG
ATSKRVGDTTLTLSNGSYLAFTSAFDLPQGGGAIYSLGSVMIENSEEVFTCGNYSSW
AAISKRVGDTTLTLSRGSYLAFTSAFDLPQGGGAIYSLGSVMIENSEEVTTRGPSCFE
SGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYGGAISTHNLTLTTRGPSCFE
NNHAYHDVNSNGGAIAIAPGGSISISVKSGDLIFKGNTASQDGNTIHNSIHLQSGAQF
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HYGYQGTWGMTWVDDTASTPKTKTATLAWTNTGYLPNBERQGPLDVPNSLWGSFSDIQA
IQGVLERSALTLCSDGFWAAGVARFLDKDKKGEKRXTRHKSGGYAIGGAAQTCSENL
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LEGQLAYSHYSNDLKTKYTAYPEVKGSWNNAFNMLGASSHSYEYLHCFDTYAPYI
                                                                                                                                                                                                                                                                                                                                                                                                           NLTSTILQDVTLAGGTLSLSDGVTLQLHSFKQEASSTLTMSPGTTLLCSGDARVQNLH
ILIEDTDNFVPVRIRAEDKDALVSLEKLKVAFEAYWSVYDFPQFKEAFTIPLLELLGP
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DVQVSFSHSUNRMETHYTSLEBSEGSWSINECIAGGIGLDLFYLGDSYTYDLSGFFYSD
KVEMYYVSQMSFFESSSBGRGFSIGRLLNLSFUNGAKFVGDIGDSYTYDLSGFFYSD
VYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
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14579. .16123
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11535. .1432
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11535. .1158
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/translation="MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTF
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/protein_id="CAB37072.1"
/db_xref="GI:4455887"
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/gene="omp4"
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                                                                                                                                                      AGTTAATGAGACTCCGGCAGATTCTGCACTACAATATATACAGGGAACATCATCTTCACAGG
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Submitted (21-JAN-1999) Boesen T., Department of Medical
Microbiology and Immunology, University of Aarhus, The B
Building, DK-8000 Aarhus, DENMARK
Location/Qualifiers
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hypothetical protein; c
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2 (bases 1
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                        SQNVSNEANNNGGAITTKTLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQL
VFMNNKGETGGGALGFEASSSITQNSSLFFSGNTATDAAGKGGAIYCEKTGETPTLTI
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NHMKTYYTDNSIIKGSWRNDAFCADLGASLPFYISVPYLLKEVEPFYKVQYIYAHQQD
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outer membrane
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CDS

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db\_xref="GI:4455885"

/transl\_table=11 /codon\_start=1 /note="ORF1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="omp10"
3827. .6613
                                        SRSYNADLGGKFQF"
                                                                                                                   AQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIK
VEASYIHQDSFKERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVAD
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NFSNDNGGALQGSSISLSLNPNLTFAKNKATQKGGALYSTGGITINNTLNSASFSENT
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3827. .6613
complement(6954. .8060)
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IFSVAFCQLFGKDKDLFIVENTSHNYLASLYLQHRAFLGGLPWPSFGSITDMLKDIPL
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                                                                                    VYRKNPDCTTALLINNTSWKTTGTNLSRQAG I GRAG I FYAFSPNLEVTSNLSME I RGS
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CDS gene sig\_peptide

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CDS gene

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1685 1676	CTACGACATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAGA	1626 1617
1625 1616	CACTTTATTGGACCCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAGTC	1566 1557
1565 1556	AAAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCAT	1506 1497
1505 1496	TGCTGATACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGC	1449 1437
1448 1436	GGCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACC	1389 1377
1388 1376	GCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCA	1329 1317
1328 1316	AGAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACA	1269 1257
1268 1256	AGTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGG	1209 1197
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1031 1016	TAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGG	972 957
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917 896	CAGCAACAATACATCGACAACAGCGGGAGGAGCTATCTAT	858 837
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797 802	CAATAAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTG	738 750
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677 689	CATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGC	618 630

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                                                                                                                                                                                 TCTTTTGATGACAGCAACCTCTTCAATTTATCTTTGCCTATAGGGGTGAAGTTTGAGAAG
                                                                                                                                                                                                                                    GAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATAAG
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CGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTC
                                                                             TTCTCTGATTGTAATGACTTTTCTTATGATCTGACTTTATCCTATGTTCCTGATCTTATC
                                                                                                                           GAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTGTT
                                                                                                                                                                                                                                                                                       GCTTCTTCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATGCTCCATACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATG
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TITLE
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                                                                                                      TACATTTGATAACAATGGAACTATTTTATTTAAACAAGATTACTGTGAGGAAAATGGCGG
                                                                                                                                                         ATCATCGGTAATCACAACCCCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATC---T
                                                                                                                                                                        GTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTT
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A81829
A81829.1 GI:6731865
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Madsen, A. and Birkelund,S.
NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
Patent: WO 9858953-A 3 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
LOCATION,QUALIFIETS
1. 2815
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/db_xref="taxon:32644"
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ATCATCGGTAATCACAACCCCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATC---T
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                                           GTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTT
                                                                                               TACAACTGATAAAAATCTGTCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCC
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GSAGALMPYQGTLEFSCETLTADELKYADNLKSSFTOPVSLSGGKLLLQKGVTLESTS
FSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKPVSLTAKGASNKVIVSGK
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QMNVNWTTDTATNTKEATATWTKTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIG
ATGMEHKQGFWYSSMTWFLHKTGDENRKGFRHTSGGVYIGGSAHTPKDDLFTFAFCHL
FARDKDCFIAHNNSRTYGGTLFFKHSHTLOPDNYLRLGFAKFSESAIEKFFREIPLAL
VQVSFSHSDNIMETHYTSLPESEGSWSNECIAGIGLDLPFVLSNPHFLFKTFIPQM
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TSGGAIDDEGTSILSNNKFLYFEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASN
VAETSGGAIHAKKLALSSGGTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITF
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TPKTSATTYSLTGDVFFYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHA
GAAASTTANKNLTFSGFSLLSFDSSPSTTVTTQQGTLSSAGGVNLENIRKLVVAGNFS
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/gene="pmp_10.2"
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RVVEDAAIRNLIKKQTEAGLIFFTDGEFRRYSWDFDFWWGFHGVDRRRDSNDPEIGVY
LKDKISVSKHPFIEHFEFVKTFEKGNAKAKQTIPSPSQFFHEMIFAPNLKNTRKFYPT
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/product="Polymorphic Outer Membrane
/protein_id="AAD18593.1"
/db_xref="GI:4376733"
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/note="CPn0451"
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/db_xref="GI:4376732"
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AAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATC 1566
                                    AGTACAGAGGAGGTCACTTTAACAGGTCTTTCCATTCCTGTAGACTCTTTAGGCGAGGGT
                                                                   -- TGCTGATACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCA 1506
                                                                                                        GGCTTTACTCAGACCGCGGGTTCCTCTGTTATTATGGATGCGGGCACAACGTTAAAAGCA
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5 (c) (bases 1 to 10757)
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8 (c) (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydophila pneumoniae CWL029.
Chlamydophila pneumoniae CWL029
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE001628 10757 bp
Chlamydia pneumoniae se
AE001628 AE001363
AE001628.1 GI:4376730
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Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J.,
Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.
Comparative genomes of Chlamydia pneumoniae and C. track
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .0192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRSYNADLGGKFQF"
                                                                                                                                                                                                                                                                                                                                                                                                                            AQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIK
VEASYIHQDSFKERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Polymorphic Outer Membrane Protein G/I Family"
/protein_id="AAD18591.1"
/db_xref="GI:4376731"
                                                                                                                                                                                        /gene="yxjG_2"
/note="CPn0448"
                                                                                                                                                                                                                                                                                                                                                                                     VYRKNPDCTTALLINNTSWKTTGTNLSRQAGIGRAGIFYAFSPNLEVTSNLSMEIRGS
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/note="CPn0447"
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/strain="CWL029"
                                                                                                 /gene="yxjG
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"Hypothetical Protein"

gene

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Db 207616 --CAGCTTTAACGAAGGGTTGTTTTTCTGACACTACGGAATCTTTAAGCTTTGCCGGTAA 207559
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Best Local Similarity 53.:
Matches 1419; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207675 TACTGGAATAGACTATACTCTGACAGGAGATATAACTCTGCAAAAACCTTGGGGATTCGG - 207615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 TGCTGGAACTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAAGCAGGGGCTGCTTAA 326
TGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTTTCTGA 566
                                                                                                        TACATTTGATAACAATGGAACTATTTTATTTAAACAAGATTACTGTGAGGAAAATGGCGG
                                                                                                                                                                                                                                                                                                                        ATCATCGGTAATCACAACCCCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATC---T
                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAACTGATAAAAATCTGTCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGTACTCACTTTCTTTTTAAATATTAAGTCTAGTGCTGAAGGCGCAGCACTTTCTGT 207499
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                                                                                                                                                                                                          GAAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGCGG
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vDnstdeamagycsridvrerpguividngrgipievesakogrevsalevv 
LTVLHAGGKFDKDSYKYSGGLHGVGVSCVNALSEKLVATVFKDKKCYQMEFSRGIPV 
PLQYVSYSDROGTEIVFYPDFKIFSTCTFDRSILMKRLRELAFUNRGITIVFEDDRDV 
SFDKVTFFYEGGIQSFVSYLNQNKESLFSEPIYICGTRVGDDGEIEFEAALQMNSGYS 
SELVYSYANNIFTRGGTHLTGFSTALTRVINTYIKAHRLAKNKKLALTGEDIRBGLTA 
VISKYVPNDGEQOTFKOKLGNSDVSSVAQQVVGBALTIFEENPQIARMIUNKFVAA 
QAREAAKKARELTLRKSALDSARLPGKLIDCLEKDPEKCEMYIVEGDSAGGSAKQGRD 
RRFQAALLPIRGKILNVEKAKLOKIFONGEIGTIAALGCGIGADNFNLSKLAYRRIII 
QAREAAKKARELTLRKSALDSARLPGKLIDCLEKDPEKCEMYIVEGDSAGGSAKQGRD 
RRFQAALLPIRGKILNVEKAKLOKIFONGEIGTIAALGCGIGADNFNLSKLAYRRIII 
RRFQAALLPIRGKILNVEKAKLOKIFONGEIGTIAALGCGIGADNFNLSKLAYRIII 
RRFQAALLPIRGKILNVEKAKLOKIFONGEIGTIAALGCGIGADNFNLSKLAYRIII 
RRFQAALLPIRGKILNVEKAKLOKIFONGEIGTIAALGCGIGADNFNLSKLAYRII 
RRFQAALLPIRGKILNVEKAKLOKIFONGEIGTIAALGCGIGADNFNLSKLAYRII 
RRFQAALLPIRGKILNVEKAKLOKIFONGEIGTIAALGCGIGADNFNLSKLAYRIII 
RRFQAALLPIRGKILNVEKAKLOKIFONGEIGTIAALGCGIGADNFNLSKLAYRII 
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TISGDDYVKRWPVKVFKEQRRGGHGVTGFDMKKGAGFLKAVSATKDYLLIFTWFGQ
CYWLKVWQLDEGERRAKKPIINFLEGIRFGEELAAILNIKNFDNAGFLFLAYTKRGV
KKVSLDAFSNPRKKGIRALEIDEGDELIAACHIVSDEEKVMLFTHLGMAVRFPHEKVR
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/gene="CPj0276"
complement(10812. .11159)
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SYLLMLGTNESSILFKSTERELRGEALESFINVILDVESFINTLEKKAIPFSEFLEMY
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GYRSILINERNGNYLGAIPYTDHDSILLMSSQGQAIRINMQDYRYMGRSTQGYRLYHL
KEGDALVSMEKLSSNENDDEYLSGSEEECSDTYSLR"
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HDAIDAWNQVFRDKYKGMSQAIGFRDHILLVKVYNSSLYALLKQTPQNDLIMSLYQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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/product="CT191 hypothetical protein"
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Pred. No. 1.7e-121;
0; Mismatches 1179;
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S CACTTTATTGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAGTC 16	1566	Qy
S AAAGAAGCAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCAT 	1506 206334	Дy
TGCTGATACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGC	1449 206394	₽ 80
GGCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACC 	1389 206454	Qy Db
) GCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCA 	1329 206514	ОУ
AGAAAAGTTATCAGAGACAGAGGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACACACAC	1269 206574	р Оу
AGTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGG	1209 206634	Qy Db
3 CATCTACTTCTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAA 	1149 206694	D D
TAGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTAGGAGC	1089 206754	g Q
2 TGACATTGTCTTTTTAGGGAATACAGTCACTTCTACTCCTGGGACGAATAGAAG 	1032 206814	ρ δ
Z TAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGG	97 <i>2</i> 206874	g Qy
3 TTCCGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCC	918 206934	da Vo
3 CAGCAACAATACATCGACAACAGCGGGAGGAGCTATCTAT	858 206994	B 8
TGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTT	798 207028	gy VQ
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AAATACCTCCTCAAAGAAAGGAAGCGGAGCCATTCAGACTTCCGATGCCCTTAC	567 207261	gy Qy
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TITLE
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Mutsunori Shirai, Yamaguchi University School of Medicine,
Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
755-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-227, Fax:81-836-22-2415)
On Sep 15, 2000 this sequence version replaced gi.617238 gi:617239
gi:617229 gi:6172294 gi:6172296 gi:6172326 gi:6172328 gi:6172384
gi:6172332 gi:6172334 gi:6172336 gi:6172338 gi:6172389 gi:6172389 gi:6172389 gi:6172389 gi:617238 gi:6172389 gi:6172380 gi:6172380 gi:6172380 gi:6172380 gi:6172380 gi:6172390 gi:6172390 gi:6174668 gi:635174 gi:6635176 gi:6635178 gi:6635180 gi:8547433 gi:8547438 gi:8978640.

AB033782-AB033785, AB033800-AB033815: Submitted (14-Feb-2000).

AB036079-AB036083: Submitted (18-Dec-2000).
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Direct Submission
Submitted (04-JUL
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957. ∴
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144. .
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complement(4359.
/gene="dnaX_2"
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3656. .4387
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/gene="tdk"
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TLNLGLKASALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQ
LVSLQYKEKELVSVSPGQDLSN"
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SEILLSSSPGSEHKVSQKIHPDIYQFFPEGKGRLHSIDLPRGIKKQIYISPFEANYKI
YIIHEADRWTLAAISAFLKVFEEPPKHAVIILTTAKVQRLPKTIISRSLSIFIERGEK
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PSICSFSKLRPTWIFPNGILPLENDFRGSRACFPLNVLLLQELSRLYANGVGNLQEKY
DELFDVDLETPKEALEELILNLNRPYNEIIIGGFSQGAILATHLVLTSQNPYAGALIF
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EERLYALKDREPSKAFALYVNSIEDIENISGYPLSPTAKKLAQLFPGAITLVYKHRNP
RFYKETLAFRYUDHSVYEETVPHCGTLIGTSAKHLSEPSSALTAQEIFADFADHDLCIF
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IANLYNEKTLAGISDVRDESDKDKIKVLEIKKGESSEIIINELKKFTDVQVTFGANM
LALDKNLPRTMASIHANISAWIRHKEVIRRRTYELMKAETRAHVLEGS'LKALSCLDA
LVKTIRESGNKEHAKERIIESFGFTEDQALAILELRLYQLTGLEAEKIQKEYEELLNK
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/db_xref="GI:8978646"
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CCGTGCTTTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACG
                                                                                                                                                                  CTATATTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATT
                                                                                                                                                                                                                                                                                   GG-----
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                                                                                         TATAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGA
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                                                                                                                                         CTACCTTCCGAATCCTGAGCGTCAAGGACCTTTAGTTCCTAATAGCCTTTGGGGGATCTTT
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              2754 CAATGTAGACTTAGGAGCAAAATACCAATTCTA
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AP002546/c LOCUS DEFINITION VERSION

AP002546 300650 bp DNA BCT 08-E Chlamydophila pneumoniae J138 genomic DNA, complete se section 2/4. AP002546 AB033782 AB033783 AB033784 AB033785 AB033800 AB033802 AB033803 AB033804 AB033805 AB033805 AB033802 AB033811 AB033812 AB033813 AB033814 AB035079 AB036080 AB035081 AB033812 AB033814 AB033814 AB036079 AB036080 AB035081 AB036082 AB038348 AB038349 AP002546.2 GI:10176692 (strain:J138) r 08-DEC-2000 complete sequence, AB033801 AB033815 AB033815

KEYWORDS SOURCE ORGANISM

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LIRNDPKCTTALVISGASWETYANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGS
SRIYNVDLGGKFQF"
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ASKNVALISGPILLDNOGNAYENHDLGKTQDFSFVQLSALGTATTDVPAVPTVATPT
HYGYQGTWGMTWVDDTASTPKTKTATLAWTNTGYLPNERQGPLVPNSLWGGSFSDIQA
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LEGQLAYSHYSNDLKTKYTAYEEVKGSWGNNAFNMALGASSHSYPEYLHCFDTYAPYI
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LDLPFVLSNPHPLFKFF1POMKVEMVYVSONSFFESSSDGRGFSIGRLLNLSIPVGAK
FVQGDIGDSYTYDLGGFFVSDYYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSN
NYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF"
                                                                                                                                                                                                                                                                             complement(9785. .12571)
/gene="CP0306"
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EQFLWIHNLVMKDRPEDLFVSLHVCRGDYQAEFFSRRAYDSIEBPLFAKTDVDSYHYY
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DSTDTLNLNKADAGNSTDYSGSIVFSGEKLSEDEAKVADNLTSTLKQPVTLTAGNLVL
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SAEGAALSVTTDKNLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILF
KQDYCEENGGAISTKNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPT
/product="polymorphic membrane protein G family"
/protein_id="AAF38163.1"
/db_xref="GI:7189233"
                                                                                                                                                    similarity; putative"
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/protein_id="AAF38162.1"
/db_xref="GI:7189232"
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/gene="CP0304"
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VTFSGNQAVANGGAIYAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSL
                                                                                                                                                                                                                                                                                                                                                                      WALDDKYSGGAEPLAYVSGEKHVCLGLISSNHSCIEDRDAVVSRIYEAASYIPLERLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAF38161.1"
/db_xref="GI:7189231"
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                                                                                        transl_table=11
                                                                                                                                                                                     note="similar to GP:4376731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MEMMSPFQQPEQCHFDVVGSFLRPESLTRARSDFEEGRIVYEQM"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="polymorphic
/protein_id="AAF38160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene≖'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "translation="MDLSSRWLNKLKTRKQLDQNIKYDCKSYCLRGISQILGWV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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ASQTVTLSGSLSLVDESGNVZEDVSWNUPQVESCLTLTADDPARMHITDLAADPLEKN
PIHRGYGGNAALSWGEDFDATKSKAATLTWTKTGYNPRERRGTLVANTLWGSSFVDVRS
IQQLVATKVRQSQETRGIWCEGISNFFHKDSTKINKGFRHISAGYVVGATTTLASDNL
                                                                                                                                                                                                                                                                                                                                                                                                    LNFIGNTAITSGGAIYTDNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLSA
LGGDITFEGNTVVKGASSSQTTTRNSINIGNTNAKIVQLRASQGNTIYEYDPITTSIT
AALSDALNLNGPDLAGNPAYQGTIVFSGEKLSEAEAAEADNLKSTIQQPLTLAGGQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAGANCTFTNTAANKLLSFSGFSYLSLIQTINATTGTGAIKSTGACŠIQSNYSCYFGQ
NFSNDNGGALQGSSISLSLNPNLTFAKNKATQKGGALYSTGGITINNTLNSASFSENT
AANNGGAIYTEASSFISSNKAISFINNSVTATSATGGAIYCSSTSAPKPYLTLSDNGE
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YTPPAQTTNADGTIYNLTGDVSITNAGSPTALTASCFKETTGNLSFQGHGYQFLLQNI
                                                                                                                                                              ITAAFCQLFGKDRDHFINKNRASAYAASLHLQHLATLSSPSLLRYLPGSESEQPVLFD
AQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIK
                                                                               VYRKNPDCTTALLINNTSWKTTGTNLSRQAGIGRAGIFYAFSPNLEVTSNLSMEIRGS
                                                                                                                         VEASYIHQDSFKERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVAD
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ORIGIN BASE COUNT

Query Match

Length 12676;

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                                                                                                                                                                                         Chlamydophila pneumoniae AR39.
Chlamydophila pneumoniae AR39.
Chlamydophila pneumoniae AR39.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 12676)
Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F.,
                                                                                White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weldman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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AE002192.
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Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Wediman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-MAR-2000) The Institute for Genomic Research,
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DISSLIPVJAEDDPNSEYGFQCGNNVNNTTDTATNTKEATATWTKTGFYBSPERKSALV
CNTLWGVFTDIRSLQQLVEIGATGMEHKQGFFWSSMTNPLHKTGDENRKGFRHTSGGY
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1, 2000 this sequence version replaced gi:7189226
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GP:/similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2077. .4926)
/gene="CP0302"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="polymorphic membrane protein G family"
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AAISNRYGDTTLTLSNFSYLAFTSAPLLPQGGGAIYSLGSVMLENSEEVTFCGNYSSW
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similarity; putative"
/codon start
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2077. .4926)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EITSTP"
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ILIEDTDNFVPVRIRAEDKDALVSLEKLKVAFEAYWSVYDFPQFKEAFTIPLLELLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYGGAISTHNLTLTTRGPSCFE
NNHAYHDVNSNGGAIAIAPGGSISISVKSGDLIFKGNTASQDGNTIHNSIHLQSGAQF
KNLRAVSESGVYFYDPISHSESHKITDLVINAPEGKETYEGTISFSGLCLDDHEVCAE
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LLTLNKAEGDKTYNGRIIFSGEKLTEEQAAVADNLKTTFTQPITLAAGELVLRSGVEV
EAKTVVQTAGSLILMDAGTKLSAKTEDATLTNLAINFHYLDGKKFAVVDAVAAGKNVT
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BASE COUNT ORIGIN stem\_loop 1472 മ /note="potential 9-base terminator 1033 c 1031 g 1390 t sequence'

Query Match Best Local Sim Matches 1391;

Similarity

19.7%; 53.8%;

Conservative

0;

Score 548.2; DB 2; Pred. No. 1.8e-124; D; Mismatches 1133;

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Gaps

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4926; 63;

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GTTAGGAGCCACAACAATACCTCGAGAGAGGATTCTCTTAGTGTGGCTTTCTGTCAGTT CATAGGAGGAAACCTACATACTTGTTCAGATAAGATTCTTAGTGCTGCATTTTGTCAGCT

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TACTATAAGAGATAACAAAGTCTTGATTTTTGAGGAAAATACTTCTTCAGCAAAAGGTGG CACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGGAGG

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GACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTAATACTGTGGATCTTGTTCGTAGT
                                                                                                               TATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGA
                                                                                                                                                                                                                                                                                                        AACCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACG
                                                                                                                                                                                          GCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTG
                                                                                                                                                                                                   GCTCCGATTTGCTTAGAAGTGCAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTG
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Chlamydophila abortus.
Chlamydophila abortus.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Longbottom, D., Russell, M., Dunbar, S.M., Jones, G.E. an
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Query Match
Best Local Similarity
Matches 2784; Conserv
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AAAAACTTTTCAACGGATAATGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGG 540
                                                              GCCGTTAGCTGCTCTACGGGTAGCTTGAAGTTTGACAAAAATGTCAGTTTGCTCTTCAGC 480
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                                       GCCGTTAGCTGCTCTACGGGTAGCTTG-AGTTTGACAAAAATGTCAGTTTGCTCTTCAGC 21548
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1620	ACCATCACTTTATTGGACCCGACGGCACGTTTTATGAAAATCATAGTTTAAGAAAATCCT	156	Qy
22628	9 GGTGCAAAGAAGGCAAAAATAGAAACCAAAAGCTACGTCAAAAAATCTGACTTTATCTGGA	2256	Дb
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1500	TAGAACCTGCTGATACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGA	144	Qy
1440 22508	.CAGGCAGATTCTCGTCTCGA                          .CAGGCAGATTCTCGTCTCGA	138 2244	P 04
22448		2238	Вβ
1380	TACTACAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCT	132	Qy
1320 22388	ATCAGAGACAGAGGCCGCAGATTC: 	126 2232	B , 정
1260 22328	TTAATGAGACTCCGGCAGATTCTGCACTACAATAI 	120 2226	Db Qy
22268	GTAGAGCCATCTACTATGATCCCATAACTACAGGATCATCCACAAACAGTTACAG	2220	В
1200	GGTAGAGCCATCTACTTCTATGATCCCATAACTACAGGATCTTCCACAAACAGTTACAGAT	114	Qy
22208	GAACGAGTGCAAAGATGACAGCTTTGCGTTCTG	2214	В
1140	ATAGAAGTAGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGC	108	Qy
1080 22148	TTTAGGGAATACAGTCACTTC 	102 2208	Qy Db
22088	CTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTT	2202	рь
1020	GTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATC	96	Qy
22028	TCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAATAGTGT	2196	В
960	AAAAGCTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGG	90	Qy
900 21968	ICTTCAGCAACAATACATC	84 2190	Db Qy
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840	GTGCTATCTGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCT	78	Qy
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21788	CAGAAGCCTCGGTGACTATTTCTAAT	2172	Дb
720	CTTCGGATTCTGGAGCTGCAATTTTTTACAGAAGCCTCGGTGACTATTTCTAATAATAC	66	Qy
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660	CTTCCGATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATA	60	Qy
21668	ACTACAATGTCAGCTCTGTTTTCTGAAAATACCTCCTCAAAGAAAG	2160	B 2
; <u>;</u>	AAAACTTTTCAACGGTTAATGGGGTGCTATCACCGCAAAAACTCTTTCAACAGG	- 4.	Дb

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FEATURES
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Mutsunori Shirai, Yamaguchi University School of Medicine,
Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
755-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-227, Fax:81-836-22-2415)
On Aug 31, 2000 this sequence version replaced gi:6172286
gi:6172288 gi:6172310 gi:6172312 gi:6172314 gi:6172316 gi:6635162
gi:6172320 gi:6172322 gi:6172324 gi:6635158 gi:6635160 gi:6635162
gi:635164 gi:6635166 gi:6635168 gi:6635170 gi:6635172 gi:8547422
gi:8547426 gi:8547430 gi:8978373.
AB033780-AB033781, AB033792-AB033792: Submitted (14-Peb-2000).
AB036071-AB036078: Submitted (14-Peb-2000).
Ioccation/Qualifiers
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onirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T. Comparison of whole genome sequences of Chlamydia pneumon from Japan and CWHO29 from USA Nucleic Acids Res. 28 (12), 2311....
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COMMENT FEATURES

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White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.

Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Submitted (11-MAR-2000) The Institute for Genomic Research, 9712
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EAPILVPULLMGSFIDVRSFQNFIELGTEGAPYEKRFWVAGISNVLHRSGRENQRKFRH
VSGGAVVGASTRAPGGDTLSLGFAQLERADKDYFMITNBRKTXAGSLRLGHDASLYSV
VSILLGEGGLREILLPYVSKTLPCSFYGQLSVCHTDHRMKTESLPPPPFLSTDHTSG
GGYVMAGELGTRVAVENTSGRGFFQEYTPFVKVQAVYARQDSFVELGAISRDFSDSHL
                                                                                                              AKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDLGTSLVANTESI
ELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDESFYQNGFLNEDHSYDG
ILELDAGKDIVISADSRSIDAVQSPYGYQGKWTINWSTDDKKATVSWAKQSFNPTAEQ
                                                                                                                                                                                              NIDATTASGAAIGSEAANKTYTLSGESALSFLKSBASTYTNGLGAINVKGNLSLLDND
KVLIQDNESTGDGGAINCAGSLKIANNKSLSETIGNSSSTRGGAIHTKNLTLSSGGETL
FQGNTAPTAAGKGGALAIADSGTLSISGDSGDIIFEGNYIGATGTVSHSAIDLGTSAK
ITALRAAQGHTIYFYDPITYTGSTSVADALNINSPDTGDNKEYTGTIVESGEKLTEAE
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/codon_start=1
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/gene="CP0761"
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/gene="CP0761"
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/gene="CP0758"
/note="hypothetical pro"
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complement(150. .2987)
/gene="CP0757"
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/product="hypothetical protein"
/protein_id="AAF38560.1"
                                                                                                                                                                                                                                                                                                                  FSSKTSSATDGTNYVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFS
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/protein_id="AAF38561.1"
/db_xref="GI:7189674"
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/translation="MRLLLSCPMLFIAACASFFGFQEEMQGRNIQSLDANASSLGELF
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                                                           TCAGGAGGTGCTATCTGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGA
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                                                ACTTCCGATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACT
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Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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/note="putative"
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GGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGGAATTGAGTTTATCC
                    GGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGGAATTGAGTTTATCC
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                                                                                             AAAGTTTCCTTTATTGACAATAAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGATATG
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Chlamydia
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QSKTRGGAIGGANVTIVGNYDSVSFYQNAATFGGAIHSSGPLQIAVNQAEIRFAQNTA
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AUTGTGNKVOEFFWDKINYKPRPEKEGNLVPNILMGNAVNVRSLMQVOETHASSLOTD
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'note="hypothetical"

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Best Local Similarity
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      GGGTTTTCTTCGCTATCTTTTATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGA 420
                                                                      GGGACTGTAGCAGGGGCTGCTGTTAACAGCAGCGTGGTAGATAAATCTACCACGTTTATA 360
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LQEFTDAIGMELGEIEEIIGEENGYRADSEAEELLTGIGIPNEMEDKKMAMIPIDLQF
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SOVQSRLFEIKKLQPQELKKSNIQRFYIRFPLSDKSSGKVVLSLEAITWOYGOHOVIL
PFSLEIYQGDKLGIIGNNGLGKTTLMKLLAGVEAPSSGSIKLGHQAICSYFPQNHSDV
LADCGQETLFEWLRNRKTGINDQEIRSVLGKMLFGGDDAFKQIQALSGGETARLLMAG
                                                                                                                                                                                                     SGLRISEIVAVNKQDFDLSTHLIRIRGKGKKERIIPVTSNAIQMIQIYLNHPDRKRLE
KDPQAIFLNRFGRRISTRSIDRSFQEYLRRSGLSGHITPHTIRHTIATHMLESGMDLK
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VIQKILLENDAETIHGPRLPKELPSPMTYAQYEVLMATPDISKYHGLADRCLMELFYS
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Kalman,S., Mitchell,W., M
Grimwood,J., Davis,R.W. a
Direct Submission
Submitted (01-DEC-1998) P
of California, 235 Earl W
                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAAT
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Chlamydia pneumoniae section
AE001587 AE001363
AE001587.1 GI:4376271
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(bases 1 to 16448)

Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R
Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
                                                                                                                                                                                                                                                                                               Chlamydophila pneumoniae CWL029.
Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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172. .2957
                        /note="Polymorphic contains frame shi1 172...705
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/note="CPn0014"
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2E 1 (bases i to 2787)

2E 1 (bases i to 2787)

RS Madsen, A. and Birkelund, S.

RS Madsen, A. and Birkelund, S.

NOVEL SURPACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE

NOVEL SURPACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE

1AL Patent: WO 9858953-A 9 30-DEC-1998;

MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)

ES Location/Qualifiers

Ource //Organism="unidentified"
//Organism="unidentified"
//db_xref="taxon:32644"

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              ATGAAGTCTTCTTTCCCCAAGTTTGTATTTTCTACATTTGCTATTTTCCCTTTGTCTATG
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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AP002546 Chlamydop	AE002192 Chlamydop	U72499 Chlamydophi	AP002545 Chlamydop	AE002235 Chlamydop	AJ133035 Chlamydia	AE001587 Chlamydia	A81835 Sequence 9	Description

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It is described as a subsequence of a claimed nucleic acid fragment (see AAX06817) encoding omp5 (see AAX08418). The invention provides a new species specific test for identifying mammals (including humans) infected with C. pneumoniae. The test comprises detecting antibodies specific for surface exposed proteins Omp4-Omp15 (see AAX088147-28) or detecting nucleic acid fragments encoding them (see AAX06816-27), especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly
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Best Local Similarity
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01-DEC-1998;
This sequence encodes a Chlamydia antigen of the invention, designated CPN100639. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they not be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to down regulate nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The
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1514	NTAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGC	1455	Qy
1451	  aagcagatactga	392	Дb
1454	AGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCTGA	1398	Qy
1391	totagcototggaacottagcactcaaaggaaatgtogagttagatgtoaatggtttcac	1332	DЪ
1397	JAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAGGCATTCAC	1338	Qy
(4)		1272	Дb
1337		1278	Qγ
1271	accygatagcaactcgcctttagattattcaggaacgattgtattttctggggaaaagct	1212	Db
1277		1218	Qy
1211	ctatgatccgattgcatctaacaccacaggagcttcagacgttctgaccatcaacca	1155	рЬ
1217	SATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAAGTTAATGA	1158	Qy
1154		1095	Db
1157	TGCTGGTAGAGCCATCTACTT	1098	Qy
1094		1035	DЬ
1097	GGACGAATAGAAGTAGTATCGA	1041	Qy
1034	ogctattgcaattgccgactctggatctttaagtctctctgcaaatcaaggagacatcac	975	В
1040	CATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT	981	Qy
974	tgctggccctaccctattttcaaataatagatgcgggaacacagctgcaggcaagggcgg	915	Д
980	GAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGG	921	Qy
914	gagaactcttcagtaactcaaggcggagcaatctgtgcccatggtctagatctttccgc	855	Дb
920	ACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTC	861	Qy
854	tgaaaaaacaggagagactcctactcttactatctctggaaataaaagtctgaccttcgc	795	ДЬ
860		801	Qy
794	cactgcaacagatgctgcaggcaagggcgggggccatttattg	753	В
800	AGGTCACAGGAGCGAGCTCCTCAACAACGGGGGGATATGTCAGGAGGTGCTATCTGTGC	741	ργ
752	totgggctttgaagccagctcctcgattactcaaaatagctcccttttcttctctctgaaa	693	Db
740	AATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTTCCTTTATTGACAA	681	Qy
692	ttcaggaaacaccggccagttagtctttatgaataataaaggagaaactgggggggg	633	рь
680		621	Qy
632	cactagtaatagcgcaaaaaattaggtggagcgatctatagctctgcggctgcaagtat	573	DЬ
620	TTCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCAT	561	Qy
572	tggcggagcgatcaccacaaaaactctttctatttctgggaatacctcttctataacctt	513	당 .
560		501	Ωy
512	tottacogataatggaacgattototttagccaaaacgtotocaatgaagctaataacaa	453	₽

CCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGA 	Qy 2583 Db 2589	
CTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACC	Qy 2523 Db 2529	
AAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGGATTTGATAAGGAATCAGA 2522	Qy 2463 Db 2469	
GTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGAAGCTCGTGAATTTGG 2462	Qy 2403 Db 2409	
TCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCA 2402	Qy 2343 Db 2349	
TACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGC 2342 	Qy 2286 Db 2289	
AGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCC 2285 	Oy 2226 Db 2229	
TIGCAAACTACGGCCTTGTTCGTTGTCTTATGTTTCCTACAGAGATTCCTGTTCTCTTTTC 2225	Qy 2166 Db 2172	
AGGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCTCTTCC 2165	Qy 2106 Db 2112	
TAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCA 2105 	Qy 2046 Db 2052	
CCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAGATTCT 2045	Qy 1986 Db 1992	
GIGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGGTTTCG 1985 	Qy 1926 Db 1932	
CTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTTG 1925	Qy 1866 Db 1872	
TCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAG 1865	Qy 1806 Db 1812	
GGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATTCCTAA 1805 	Qy 1746 Db 1752	
CCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTG 1745	Qy 1686 Db 1692	
CTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAGA 1685	Qy 1635 Db 1632	
GGACCCGACGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACGACAT 1634	Qy 1575 Db 1572	

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                                             Chlamydia pneumoniae
                                                                             Omp11; outer membrane protein 11; surface exposed protein; infection; diagnosis; vaccine; atherosclerosis; asthma; ss
                                                                                                                           Chlamydia pneumoniae surface exposed protein Omp11 DNA.
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               GTTTGACAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding Omp4-Omp15 proteins (see AAW08417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89.6-100.3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises defecting antibodies specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This DNA sequence codes for the novel 97.6 kDa surface exposed protein Ompl1 (see AAW88424) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outer membrane proteins of C. pneumoniae or nucleic acids encoding these proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for
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                                                        CAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTTATTGCGTC
                                                                                                                                    GAACTCTCTATTGTTCCAAACGGTGGATGCAGGGGACTGTAGCAGGGGCTGCTGTTAACAG
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TCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTTGAA
                                      cacaactgctgataaagccctaacattcacaggattttctaacctttccttcattgcagc
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CHRISTIANSEN
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upper respiratory tract disease; bronchitis; sinusitis;
c bronchitis; adult-onset asthma; acute exacerbations of asthm
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This sequence encodes a Chlamydia antigen of the invention, design CPN100638. The nucleic acids (and their complementary sequences) used as diagnostic agents for detecting the presence of nucleic encoding Chlamydia antigens in samples according to standard meti

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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This invention describes a novel nucleic acid (N1) encoding a Chlamydia CC pneumoniae protein (P1), given in the specification. The isolated nucleic acid is useful for diagnostic and analytical methods, such as, CC hybridization-based assays or amplification-based assays. The protein may CC be used for diagnostic purposes, for their enzymatic or structural CC activity, or as a vaccine. The invention also describes (1) a probe CC comprising a hybridizing fragment of N1; (2) an isolated nucleic acid CC (N2) that hybridizes under stringent conditions to N1; (3) an expression CC cassette comprising N1 under the transcriptional regulation of a CC transcriptional initiation region functional in an expression bost, and a CC transcriptional itermination region; (4) a cell comprising an expression CC cassette of (3) as part of an extrachromosomal element or integrated into CC cassette into the host cell, and the cellular progeny of the host cell; C (5) a method for producing a P1 comprising growing a cell of (4) where CC the protein is expressed and isolating the protein free of other comprising of P1; and (7) a monoclonal antibody binding specifically to the
                                                                                                                                                                                                                                                                                                                           Query Match 18.6%;
Best Local Similarity 53.1%;
                                                                                                                                                                                                                                                                                                             Matches 1420;
 105410
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 128-320; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1998;
08-APR-1999;
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                       323 TTAACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTTCTTCGCTATCTTTTA 382
                                                                                                                                                                                                                                                   143 AAGATGCTGGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid for use in diagnostic and analytical methods
TTACCAATACAGCTGCAAATAAGCTTCTCTCCTTTTCAGGATTCTCCTATTTGTCACTAA 105351
                                                                             GCCACGGCTACCAATTTCTCCTACAAAATATCGATGCGGG
                                                                                                               GTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTG 322
                                                                                                                                                                                           CAGGCACAGCAATCACAAAAAGCTGTTTTAACAACACTAAGGGCGATTTGACTTTCACAG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic sequence of Chlamydia pneumoniae
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Pred. No. 2.3e-139;
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1510	1451 CTGATACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGA	Qy
1450 104298	1391 CATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTG	D 04
1390 104358	1331 CTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAGG	Db Qy
1330 104418	1271 AAAAGTTATCAGAGACAGAGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGC	Оy
1270 104478	1211 TTAATGAGACTCCGGCAGATTTCTGCACTACAATATACAGGGAACATCATCTTCACAGGAG	Оy
1210 104538	1151 TOTACTTCTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAAG	Оу
1150 104598	1094 TCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGCTGGTAGAGCCA	pb 04
1093 104658	1043 TTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTA	pb 04
1042 104718	983 CCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTCT	Qy Db
982 104778	923 GAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGAG	Оу
922 104838	863 ACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAAGCTCGAACTGGCTTCCG	Db Qy
862 104898	803 ATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCA	ρ <sub>ο</sub> ο
802 104958	743 AGGTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCTT	Db 04
742 105003	683 TTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATA	Qу
682 105063	623 CTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCAA	о Оу
622 105123	563 CTGAAAATACCTCCTCAAAGAAAGCGGGGGGCCATTCAGACTTCCGATGCCCTTACCATTA	DB 98
562 105183	503 GCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTTT	Qy Db
502 105240		9y 0b
442 105300	383 TIGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTA	Фр

1798 1801	TCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATA 	Дb
1744 1741	AAATTCCATTACGGCTATCAGGGAACTTGGGGGCCCAATTGTTT	Db Qy
1684 1681	1631 ACATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAG	Db Oy
1630 1621	TTATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACG 	B 6
1570 1561	1511 AGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTT	g Q
1510 1501		Db Qy
1450 1441	1391 CATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGAACGTAGGAACTACTCTAGAACCTG	Db 04
1390 1381		D Q
1330 1321		Db
1270 1261	1211 TTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGAG	Дb
1210 1201	1151 TCTACTTCTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAAG	Db Qy
1150 1141	1094 TCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGCTGGTAGAGCCA	P 44
1093 1081	GTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTA	B 6
1042 1021	CGCCGATAGTGGTGACATTGTCT                     ggctcttggtggagacatcactt	DP 6A
982 961	GAG     gag	D Qy
922 901	863 ACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAAGCTCGAACTGGCTTCCG 	Db Qy
862 841	803 ATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCA	B 64
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                                                   ctccaaatcttgaggtcacaagtaacctatctatggaaattcgtggatcttcacgcagct
                                                               ACTCAAATTTTGAAGCCTTTAGCCAATTTTCTTTTGAATTGCGTGGGTCATCTCGCAATT
                                                                                                                 TCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTTGCTTTA 2692
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RESULT 11 AAC81914/C ID AAC81914 standard; DNA; 273254 BP. XX

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RESULT 10

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Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific
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Mygind P;
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This DNA sequence codes for the novel 98.4 kba surface exposed protein Omp10 (see AAW88423) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polycional antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding Omp4-Omp15 proteins (see AAW88417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: omp12,11,10,5,4,13 and 14 in one cluster and omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89.6-100.3 kba and about 56.1 kba. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae The test Commission of Abroting antibodies of antibodies of the constant of the c
                                                                    pneumoniae. The test comprises detecting antibodies specific for Omp4-omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
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748 T; 0 other
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Sequence 2787 BP; 815 A; 689 C; 535 G;

18.6%; 53.1%;

Length 2787;

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tttacacggaagctagcagttttattagcagcaacaaagcaattagctttataaacaata

433 tocaccipatacanaatciptogotaacaggattittoggatcitticttottoggagoccc 387 GTCTCCTGGAAGTTCGATAACTACCGCTAAGGAGGCGTTACGTCTTACGGGTAGGTA	Query Match  Best Local Similarity 52.6%; Pred. No. 1.7e-140;  Best Local Similarity 52.6%; Pred. No. 1.7e-140;  Matches 1407; Conservative 0; Mismatches 1191; Indels 75; Gaps 10;  Qy 147 TGCTGGAACTACCTACTATTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGG 206
Db 1477 aggetttactcagacoggoggttcoctciggtattattggatgggggacottcagacgcggggatggttatattattggatgggggatggttaaaaggc1336  Oy 1449GGTGATACTACACCANACATTTGGTCATTACATCAGTTGTATACAGGGTCC 1505  Oy 1567 AAGAAGGAAAATTAGAACCANAGGTAGGTCAAAAAACCATTACGTTGTATACATCAGTTGTATACAGGGTCC 1505  Db 1537 aagtacagagggaggtcatttaacaggtctttccattcctgtagacctcttaggggaggg 1596  Oy 1566 CACTTTATTGGACCCGAAGGGCACCTTTTGGAACCATTAAAAACCAAAAACCATTAAGACTCAAATCATTAGAATCCTAATCCTAGAACCAAAAACCAAAAACCAAAAACCAAAAACCAAAAACCAAAA	Db 1237 catctttttctacgatccgattactgctaatacggctgcggattcttcaagatactttaaa 1296  Qy 1209 AGTTAATGAGACTCCGGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGG 1268  Qy 1209 AGTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGG 1268  Qy 1209 AGAAAGTTATCAGAGAGCAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACTACA 1356  Qy 1269 AGAAAAGTTATCAGAGAGCAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACA 1328

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                                                                                                                                                                                                                                                                                            gattctcgagaaacgagcgtgcgtcttacgaagctactgtcatctacgttgccgatgtct
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RESULT

Sequence 2950 BP; 836 A; 593 C;

652 G;

869 T; 0 other;

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                                                                                                                                          This sequence encodes a Chlamydia antigen of the invention, designated CPN100635. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of the community acquired nonemonia unper respiratory tract
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01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquired pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia antigen; diagnosis; infection; community acquired pneumonia; therapy; upper respiratory tract disease; bronchitis; sinusitis;
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                                                        (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD.
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DB; AAY90237, AAY90238.
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Query Match
Best Local Similarity
Matches 1421; Conserv
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                                                                                                                        CTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTA 622
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acaatacgttaaactcagcatcattttctgaaaataccgcggcgaacaatggcggagcca
                                              CTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCAA
                                                                                               gaggcgccctccaaggcagctctatcagtctatcgctaaaccccaacctaac---gtttg
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and treating diseases such as community acquired
sinusitis and asthmatic bronchitis, adult-onset
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98US-0110438
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98US-0110427.
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Best Local
                                                                                                                  AAZ61502-09 encode Chlamydia pneumoniae polypeptides. The polypeptides are present in the bacterial membrane structure, in the external vicinity of the membrane structure, in the inclusion membrane structure, in the external vicinity of the inclusion membrane structure, and in the cytoplasm of the infected cell. The polypeptides may be used to prevent, treat and detect the presence of Chlamydia infection and/or the presence of Chlamydia in a sample. The polypeptides may also be used to induce an immune response in a mammal. The vaccine vector comprising the polynucleotides is used to induce an immune response in a mammal. Antibodies directed against the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia infection.
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                                                                                                                                                                                                                                                                                                                                                                                    Novel antigens and corresponding DNA molecules that can prevent, treat and diagnose disease caused by Chlamydia mammals, especially humans -
                                                                        Sequence 2957
                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 15-E; 201pp; English.
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1452 1434	1396 ACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCT	Qy Db
1395 1374	1336 ACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAGGCATTC	DP 6A
1335 1314	1276 TTATCAGAGACAGAGCCGCAGATTCTAAAAATCTTACTTCGAAGCCTACTACAGCCTGTA	Db Qy
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1215 1194	1156 TTCTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAAGTTAAT	ОУ
1155 1143	1096 GACTTAGGAACGAGTGCAAAGATGACAGCTTTTGCGTTGCTGCTGGTAGAGCCATCTAC	Qу
1095	1042 TTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATC	DP QA
1041 1023	982 GCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTC	Db Qy
981 963	922 GGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGA	ОУ
921 903	862 AACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCC	당 성
861 843	802 TATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGC	DP 6A
801 790	742 AAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCT	Qу ДЪ
741 744	682 ATTITACAGAAGCCTCGGTGACTATITCTAATAATGCTAAAGTTTCCTTTATTGACAAT	Фр
681 684	622 ACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCA	р У
621 624	562 TCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATT 	Db Qy

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23-JUN-1997;
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                                                                                                                                            Omp9; outer membrane protein 9; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
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97DK-0000744
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protein Omp9 (see AAW88422) or the number comparison of Chlamydia pneumoniae. By generating antibodies against C. Chlamydia pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding Cmp4-Cmp15 proteins (see AAW88417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89.6-100.3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for
                                     omp4-omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antiquens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
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Mygind P;
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Sequence 2757 BP; 770 A; 564 C; 642 G; 781 T; 0 other;

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Best Local Similarity 53.0%;
Matches 1418; Conservative
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Pred. No. 1.2e-145;
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     This DNA sequence codes for the novel 97.2 kDa surface exposed protein Omp5 (see AAW88418) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against c. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding Omp4-Omp15 proteins (see AAW88417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89,6-100.3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia
                                                                                                                                                                                                                                   Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encoc
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(CHRI/) CHRISTIANSEN
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tion; diagnosis; vaccine; atherosclerosis; asthma; ;
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pneumoniae

test

comprises detecting antibodies

specific

Chlamydia

pneumoniae genome

DNA

diagnosis;

vaccine;

27-FEB-2001

(first entry)

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel nucleic acid (N1) encoding a Chlamydia pneumoniae protein (P1), given in the specification. The isolated nucleic acid is useful for diagnostic and analytical methods, such as, hybridization-based assays or amplification-based assays. The protein may be used for diagnostic purposes, for their enzymatic or structural activity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizing fragment of N1; (2) an isolated nucleic acid (N2) that hybridizes under stringent conditions to N1; (3) an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cassette comprising N1 under the transcriptional regulation of a transcriptional initiation region functional in an expression host, and a transcriptional termination region; (4) a cell comprising an expression cassette of (3) as part of an extrachromosomal element or integrated into the genome of a host cell as a result of induction of the expression cassette into the host cell, and the cellular progeny of the host cell; (5) a method for producing a P1 comprising growing a cell of (4) where the protein is expressed and isolating the protein free of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid for use in diagnostic and analytical methods encodes genomic sequence of Chlamydia pneumoniae \cdot
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08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins; (6) a purified polypeptide composition comprising at least 50 weight % of P1; and (7) a monocional antibody binding specifically to the
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                                                             04-NOV-1998;
21-NOV-1997;
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                                                                                                                                                                           Chlamydia pneumoniae
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TCTTCGGATTCTGGAGCTGCAATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCT
                                              acttccgatgcccttaccattactggaaaccaaggggaagtctctttttctgacaatact
                                                               ACTTCCGATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACT
                                                                                                              aaaaacttttcaacggataatggcggtgctatcaccgcaaaaactctttcattaacaggg
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                                                                                                                                                                                                                                                                                                      gggttttcttcgctatcttttattgcgtctcctggaagttcgataactaccggcaaagga
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1180	agtca	1121	В
1080	CCGATAGTGGTGACATTGTCTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGAC	1021	Qy
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1020	GCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATC	961	ργ
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960	CTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGG	901	Qy
1000	tcttcagcaacaatacatcgacaa	941	뮍
900	ATCAGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGGGGGGG	841	Qy
940	tctgtgcttataaaactagtaca	881	Дb
840	CAGGAGGTGCTATCTGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGG		Qy
880	ttgacaataaggtcacaggagcgagctcct	821	Db
780	AAGTTTCCTTTATTGACAATAAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGAII	N	οy
820	attctggagctgcaattttacagaagcctcggtgactatttctaat	761	망
720	CTTCGGATTCTGGAGCTGCAATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGC	661	Qy
760	ttaccattactggaaaccaaggggaagtctcttttctgac	701	Db
660	CTTCCGATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATAC	601	Qy
700	ctctgttttctgaaaatacctcctcaaagaaaggcggagcc	641	망
600	CTACAATGTCAGCTCTGTTTTCTGAAAATACCTCCTCAAAGAAAG	541	Qγ
640	aaaaacttttcaacggataatggcggtgctatcaccgcaaaaactctttcattaacaggg	581	рь
540	AAAACTTTTCAACGGATAATGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGG	m	Qy
86		521	밁
	CCGTTAGCTGCTCTACGGGTAGCTTGAAAATTGTCAGATTTGCTCTTCAG	421	o <b>v</b>
520		461	Дb
	TTTTCTTCGCTATCTTTTATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGG	361	Qγ
460	actgtagcaggggctgctgttaacagcagcgtggtagataaatctaccacgttta	401	Дb
360	ACTGTAGCAGGGGCTGCTGTTAACAGCAGCGTGGTAGATAAATCTACCACGTTTAT	301	Qy
	cgatttgactttcacaggtaacgggaactctctattgttccaaacggtggatg	341	Db
300	GGCGATTTGACTTTCACAGGTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGC	241	φ
340	acagcaa	281	망
240	CTCTAGAAAATATTCCTGGAACAGGCACAGCAATCACAAAAAAGCTGTTTTAACAACAC	181	Qy
280	tgagagtcaggaagatgctggaactacctacctatttaaggg	221	Db
180	TTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACTACCTAC	121	Qy
220	gtttggattcaagtgcgagtttcgatgggaataaaaa	161	망
120	GCTACCGAGACAGTTTTGGATTCAAGTGCGAGTTTCGATGGGAATAAAAATGGTAA	61	Qy
160	atgaagtcttctttccccaagtttgtattttctacatttgctattttccctttgtctatg	101	Db
60	AAGTCTTCTTTCCCCAAGTTTGTATTTTCTACATTTTGCTATTTTTCCCTTTTGTCTT	<sub>L</sub>	Qy

1361 CTRACTRACACCTGTRACTCTTTCAGGAGGTACTCTATCTTATAAAACATGGAGTACTCTATCTTATCTATC					
CTACTACAGCCTGTAACTCTTTCAGGAGGTACTCTATCAAAAAAAA	198 208 204 214 210 210 210 210	18 19 18 19 19 20	16 16 17 17 17 17 17	138 148 144 150 150	4 3 3 3 3 3 1 1 0
	TTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGAAACCTACATACTTGTTCAGATAAG 2	CCTAATCCCGAAGGGTATCGGCTCTTTAGGTCCCTAATAGCTTATGGAATGCATTTATAGAT 1	accatcactttattggaccgacggcacgtttatgaaaatcatagtttaagaaatcct accatcactttattggaccgacgggcacgtttatgaaaatcatagtttaagaaatcct accatcactttattggaccgacgggcacgtttatgaaaatcatagtttaagaaatcct acagacctacacacacacacacacacacacacacacacac	CAGACTCAGGCATTCACTCAACAGGCAGATTCTCGTCTTCGAAATGGACGTAGGAACTACT	ATAGAAGTAGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCT 1

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                                                                                                         TTTGAAGCCTTTAGCCAATTTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTA
                                                                                                                                                     aatttggcaagacaagctttagtccttcgtgcagggaaccatttttgctttaactcaaat
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                                                      CC from Chlamydia pneumoniae. The genomic sequence was amplified using two CC pCR primers. The 5' primer contains a NotI restriction site, a ribosome CC pCR primers. The 5' primer contains a NotI restriction site, a ribosome CC the 98kDa putative outer membrane protein coding sequence close to the 5' end of CC the 98kDa putative outer membrane protein coding sequence of the putative contains the sequence encoding the C-terminal sequence of the putative contains the sequence encoding the C-terminal sequence of the putative conter membrane protein and a BsrGl restriction site. The stop codon was cervaluded and an additional nucleotide was inserted to obtain an in-frame CC terminal fusion with the Histidine tag. The PCR product was cloned conto a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with NotI and BamHl and performing a CC ligation reaction. This expression vector was injected intramuscularly cand intramasally into mice, which were subsequently inoculated with CC were lower than those of the controls. Thus the 98kDa putative outer membrane protein can be used as a vaccine to provide protection against CC chlamydia infections, especially Chlamydia pneumoniae infections. CC The polypeptide may also be administered orally to treat Chlamydia CC infection. The present sequence may also be used in the construction of attenuated Chlamydia strains that can over-express the cCC gene or express it in a non-toxic form.
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01-MAR-1999;
27-OCT-1999;
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CC pneumoniae by generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see AAX06816-27) encoding
CC Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
CC pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12,11.10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other, and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific test
CC omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with C. pneumoniae.
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Result
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Listing first 45 summaries
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AAF58255	82	AAF58259	AAF58257	AAF58254	AAF58252	AAX06829	AAX60539	AAX60547	AAA64752	AAX60557	AAA64758	AAX60556	AAX06824	AAX06830	AAA27342	AAA50035	AAX06818	AAX06819	AAA28690	AAA28691	AAX06827	AAZ61508	AAA30848	AAX06816	AAA30847	AAA48839	AAA30850	AAA30854	AAA48838	AAX06828	AAA30853	AAX06823	AAA30852
Oligonucleotide Dl	Oligonucleotide D2				Oligonucleotide D1	Chlamydia pneumoni	C. trachomatis LGV		C. trachomatis pmp	ID No: 24 c	C. trachomatis pmp	••			Chlamydia POMP91B	-		Chlamydia pneumoni	C. pneumoniae CPN1	3	Chlamydia pneumoni	μ.					Chlamydia antigen	_	_	_	_	_	Chlamydia antigen

## ALIGNMENTS

AAX06820

AAX06820 standard; DNA; 2787 BP

AAX06820;

26-APR-1999 (first entry)

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Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for
                                                                                                                                                                                                           Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                Chlamydia pneumoniae surface exposed protein Omp8 DNA.
                                WPI; 1999-105610/09.
P-PSDB; AAW88421.
                                                               Birkelund S, Christiansen Mygind P;
                                                                                                                                                                                          W09858953-A2.
                                                                                                                                                                                                                                 Omp8; outer membrane protein 8; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
                                                                                           (BIRK/) BIRKELUND S. (CHRI/) CHRISTIANSEN G.
                                                                                                                            23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LAWRENCE C. B. Chan
TITLE OF INVENTION: HUMAN AND MOUSE VERY LOW
TITLE OF INVENTION: DENSITY LIPOPROTEIN RECEPTORS
TITLE OF INVENTION: AND METHODS FOR USE OF SUCH
TITLE OF INVENTION: RECEPTORS.
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                               STREET: 611 West SCITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 90017
                                                                  FILING DATE:
                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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611 West Sixth Street
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                                                                                                   including application described below:
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US-08-149-103-1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3330 base pairs
                                                                                                                                                                                                                                                                                                                                             Query Match 1.2%;
Best Local Similarity 50.0%;
Matches 108; Conservative
  1409
                                                                                      1469
                                                                                                                                                                     1529 CACAGTGTTTCTTAGCTGTTCAACTAGTTGGATATATTCTTTCCTCTCTAAGCCAATCTT 1470
                                                                                                                                                                                                                                                           1589 AGCCTTTTGGCTTAGATCGGCCCAGAATAGTTTCTGGGCAGCAATGTCAGCATCGAGAGC 1530
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                                                                                                                                                                                                                2122 GGAACTCTCTATTACCAGCACAACGAAACCTATATCTCTTTCCTTGCAAACTACGGCCT 2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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GCCAGTAGCAAGATCCATTTGATAGCCACGACTACA 1374
                        ACCCATACGGATAACGATCTGAAAACCAAGTATACA 2277
                                                                                      CCTGATGTCTCTTCGATTAGTGAAGATCAGACTTGGCTCTTTGCCTACTGCCTTGCACAC 1410
                                                                                                               TGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTTTTCAGGAAAACCTTAGCTAC 2241
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Search completed: October Job time: 51500 sec 2, 2001, 03:48:27

; TOPOLOGY: lir; MOLECULE TYPE: US-08-945-994-2

STRANDEDNESS:

double

linear

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                                                   TELEX:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5340 base pairs
nucleic acid
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Patent No. 6194166
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Best Local Similarity 45.7%;
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APPLICANT: Takash
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                                                                                                                                                                                               NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 3,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                     FILING DATE: September CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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  MOLECULE TYPE:
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                    LENGTH: 5340 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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/ENTION: GENE REGULATING AUREOBASIDIN SENSITIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                             202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette,
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genomic DNA
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Pred. No. 6.6;
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US-08-232-463-14/c
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Best Local Similarity
Matches 117; Conserv
                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                          REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                              FILING DATE:

APPLICATION NUMBER: EP 9:

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

ENTER SENT CHARACTORY
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3752 GGGTGGGATGGATACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3572 TAATATTGTAGGTGTTTGCGTCATGTGTATTGTTTACTTGCCGTGGTTTGCTATCGCAAT 363:
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                                                                                       TELLEFAX: TELEFAX: 899149
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                                                                                                                                                                                                  NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                   STRANDEDNESS:
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FOPOLOGY:
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                              nucleic acid
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                                                   7218 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                         (703)683-4109
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 linear
             single
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Pred. No. 6.6;
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US-08-423-752-9
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Best Local Similarity 45.7%;
Matches 117; Conservative
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APPLICANT: Takash
INFORMATION FOR
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                                                                                                      APPLICATION NUMBER: 08/24:
FILING DATE: May 16, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,36
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APPLICATION NUMBER: US/08/4

FILING DATE: April 18, 1995
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                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3632 TCCGTTTCTTTTGGTCATCTTTGTTCTGATTGCTGATCATTATCAGAGTTCTGGTAGAGA 369:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3572 TAATATTGTAGGTGTTTGCGTCATGTGTATTGTTTACTTGCCGTGGTTTGCTATCGCAAT 3631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 TACGGGTAGCTTGAAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTTCAAC 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615 TACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGG 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 805 Fifte
CITY: Washington
                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 20005
                                  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                           D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              805 Fifteenth Street, N.W., #700
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VENTION: A GENE CODING FOR A PROTEIN REGULATING

VENTION: AUREOBASIDIN SENSITIVITY
                                                                                                                                                                                                                                                                                             Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                             IBM Compatible SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wenderoth,
SEQ ID
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NO:
                                                                                                                                                                                 08/243,403
                                                                                                                                                                                                                                                         US/08/423,752
                                                                                                      33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                   5.25 inch, 500 kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08945994 Patent No. 6043051 GENERAL INFORMATION:
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Best Local Similarity
Matches 117; Conserv
              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                              REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-721-8200
                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                      FILING DATE: NO. 604:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3692 AATTAAAAGACTTGAAGCTGTGCAACGGTCTTTTGTTTACAATAATTTAAATGAAGTTTT 3751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 TACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGG 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 GGATAATGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGC 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 TACGGGTAGCTTGAAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAAC 494
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2033 K SUCITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                         TELEX:
                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCGTTTCTTTTGGTCATCTTTGTTCTGATTGCTGATCATTATCAGAGTTCTGGTAGAGA 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takashi OKADO et al
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                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                Diskette,
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45.78;
                                                                                                                                                                                                                                                                                               6043051ember 6, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROMOTER
                                                                                                                                                                                                                                                                                                                  us/08/945,994
                                                                                                                                                        33,367
                                                                                                                                                                            Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                  3.5 inch, 1.44 mb
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Pred. No. 6.6;
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STREET: 1001
CITY: WASHINGTON

CORRESPONDENCE ADDRESS TITLE OF INVENTION: NUMBER OF SEQUENCES:

MUTATIONS IN THE APC GENE

ADDRESSEE:

E: BANNER & 1001 G STREI

WITCOFF, LTD

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                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                               Sequence 10, Application US/09157210B Patent No. 6204003
APPLICANT: Steele, J. Kevin
APPLICANT: Telford, David L.
APPLICANT: Telford, David L.
APPLICANT: Cutting, John A.
APPLICANT: Cutting, John A.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF FELINE
TITLE OF INVENTION: INFECTIOUS ANEMIA
FILE REFERENCE: SYNBIO.100A
CURRENT APPLICATION NUMBER: US/09/157,210B
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 60/059,551
EARLIER FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               1897 GAAGGGTTGCAGGGAGACCGTGCTTTTTTGGTGTGCTGGATTATCTAACTTCTTC 1950
                                                                                                                                                                                                                                                                                                                                                                                                                                      1837 AGCTTATGGAATGCATTTATAGATATTTAGCTCTCTCCATTATCTTATGGAGACTGCAAAC 1896
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POSITION IN GENOME:
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TELEPHONE: 202 508 9100
TELEFAX: 202 508 9299
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
                                                                                                                                                                                                                                                                                                                           733 GCTGTCGTATACGAAGTATGTCCTTTTCGATTTGCTGAATTCTGGCTATTCTTC 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                    793 AGCCGGTTTCATGCTTCTTGAGATGACCTCTCTGCTTCTGTTGCTTGGGACTGTAAAA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01:
ILECOMMUNICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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Pred. No. 2.3;
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; NAME/KEY: misc_feature; CATION: 186, 816, 860, 885, 9; OTHER INFORMATION: n = A, T, C US-09-157-210-10
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Best Local Similarity 51.0%;
Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Haemobartonella
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                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/24:
FILING DATE: May 16, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr
                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: June 20, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: RENUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2329 TTCGGTGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCC 2388
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                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2389 TTCATGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGAA 2448
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IAME/KEY: CDS
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 20005
                     REFERENCE/DOCKET NUMBER:
                                     NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,36
                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                              Washington
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                           U.S.A.
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                                 33,367
                                                                                                                                                                                                                                                                                       3.5 inch,
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C or G
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Pred. No. 2.4;
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US-08-452-654-1/c
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                                                                                                                         Sequence 1, Application US/08452654
Patent No. 5691454
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                            GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                      APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                     1897 GAAGGGTTGCAGGGAGACCGTGCTTTTTGGTGTGCTGGATTATCTAACTTCTTC 1950
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ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
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                                         APPLICANT:
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.46943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 12-AUG-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 65; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
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ALBERTSEN, HANS
ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
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1001 G Street, NW
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MARKHAM, ALEXANDER F.
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JOSLYN, GEOFF
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Pred. No. 2.3;
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RESULT 8
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                                                                                            Sequence 1, Application US/08370235A Patent No. 5910418
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Best Local Similarity 57.0
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PRIOR APPLICATION NUMBER: US 07/741,940
APPLICATION NUMBER: US 07/741,940
FILLING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.03557.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                GENERAL INFORMATION:
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                                              APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: JOHNSON, TITLE OF INVENTION:
                 APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                793
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LOCATION:
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                                                                                                                                                                                                                                                                                               AGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAAC 1896
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                              VOGELSTEIN, BERT
KINZLER, KENNETH W.
HILL, DAVID E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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SYSTEM: PC-DOS/MS-DOS
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KAREN A.
ANTIBODIES AND ASSAYS FOR DERMINING
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Pred. No. 2.3;
0; Mismatches 49;
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JOSLYN, GEOFF

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                              Sequence 1, Application US/07741940 Patent No. 5352775 GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
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               APPLICANT:
                                                                                                                                                                                                                                                                     1837 AGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAAC 1896
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CLONE: DP2.5(APC)
APPLICANT:
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ORIGINAL SOURCE:
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NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Relicorrent Application Number: US
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
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                                                                                                                                                                                                                                                                                                                            Match 1.3%;
Local Similarity 57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kagan, Sarah A
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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ANAND, RAKESH
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                  ALBERTSEN, HANS
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                                                                                                                                                                                                                                                                                                                                             Length 8532;
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                                                                                                                                                                                                                                                                                                           Gaps
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US-08-289-548A-1/c

Sequence 1, Application US/08289548A Patent No. 5648212

GENERAL INFORMATION:

APPLICANT:

ALBERTSEN, HANS ANAND, RAKESH CARLSON, MARY

APPLICANT:

GRODEN, JOANNA

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                                                                                                                                  Matches
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TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9606 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/741,940 FILING DATE: 19920109 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CORIGINAL SOURCE:
ORGANISM: Homo
                                                                                  1837 AGCTTATGGAATGCATTTATAGATATTAGCTCTCTCTCCATTATCTTATGGAGACTGCAAAC 1896
                               1897 GAAGGGTTGCAGGGAGACCGTGCTTTTTTGGTGCTGCATTATCTAACTTCTTC 1950
                                                                                                                                                                                                                                                                    FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
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733 GCTGTCGTATACGAAGTATGTCCTTTTCGATTTGCTGAATTCTGGCTATTCTTC 680
                                                               793 AGCCGGTTTCATGCTTCTGAGATGACCTCTCTGCTTCTGTTGCTTGGGACTGTAAAA 734
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LOCATION:
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                                                                                                                                                                                                                                                                                    CLONE:
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TOPOLOGY: li
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65; Conserv
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THLIVERIS, ANDREW
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HEDGE, PHILIP J.
                                                                                                                                  Conservative
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                                                                                                                                              Score 35.6;
Pred. No. 2.
                                                                                                                                  Mismatches
                                                                                                                                                                  DB 1;
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US-09-107-858-11
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Best Local Similarity
Matches 98; Conserv
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SEQ ID NO 11
LENGTH: 1269
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                                                                                                                    Sequence 1, Application US/08452655B Patent No. 5783666
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TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR FILE REFERENCE: DCI-099CPDV
CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT FILING DATE: 1998-06-30
EARLIER APPLICATION NUMBER: 08/758,621
EARLIER APPLICATION NUMBER: 09/758,621
EARLIER FILING DATE: 1996-11-27
NUMBER OF TEXT TO THE TRANSPORT
                                                                                                 GENERAL INFORMATION:
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                                              APPLICANT:
APPLICANT:
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APPLICANT:
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           ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
                                                                                   ALBERTSEN, HANS
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Pred. No. 0.3;
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RESULT 4
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                                                        Sequence 1, Application US/08450582 Patent No. 6114124
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Best Local Similarity
Matches 65; Conserv
                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 8532 base pair:
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APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: DP2.5(A
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APPLICATION NUMBER: UFILING DATE: 12-AUG-1
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                   APPLICANT:
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                                                                                                                                                                                                                                          760
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 8532 base pairs TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/452,655B FILING DATE: 25-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Banner & Witcoff, Ltd STREET: 1001 G Street, NW
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                                                                                                                                                                                                                                          AGCCGGTTTCATGCTTGTTCTGAGATGACCTCTCTGCTTCTGTTGCTTGGGACTGTAAAA 701
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MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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ilarity 57.0%;
Conservative
ALBERTSEN, HANS
ANAND, RAKESH
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.2;
0; Mismatches
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CARLSON, MARY GRODEN, JOANNA HEDGE, PHILIP J

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Listing first 45 summaries
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1: /cgn2_6/ptodata/2/
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2787
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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      Length
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(c) 1993 - 2000 Comp
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US-08-422-6558-11
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US-08-452-654-1
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US-08-452-459-94-2
US-08-716-873-23
US-08-716-873-31
US-08-716-873-31
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US-08-858-830-7
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7586 Lou, Regu ble /MS- Se # 8/75 18,5	US-08-336-345-1 US-08-336-345-2 US-08-647-655-1 US-08-647-655-2 US-08-894-489-3 US-08-894-795-5 US-09-249-200-1 US-07-992-865D-2 US-08-994-795-703-5 US-08-975-703-5
Uses Therefor	Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 23, Appli Sequence 23, Appli Sequence 24, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli

Query Match
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Matches 98; Conserv

Conservative

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Mismatches 102;

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1.3%;

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Search completed: October Job time: 51677 sec
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JOURNAL
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Best Local Similarity 51.2%;
Matches 82; Conservative
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                                                                                  139 CAGGAAGATGCTGGAACTACCTACCTATTTAAGGGAAATG 178
                                                                                                                                                         179 TTGGGGTCAAGTGGCATTGCAGAAGAAAATNAGACGGCTTAGATTTTAGGTCAGGTGAGA 120
                                                                                                                                                                                                                             239 AGGGTGGAAAAATTTGAANGTGCCATTTTCTGGCTATTTNGAACTACTGTTNAGTTTGTA 180
                                                                                                                                                                             79 TTGGATTCAAGTGCGAGTTTCGATGGGAATAAAAATGGTAATTTTTTCAGTTCGTGAGAGT 138
                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
Washington Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2349 Std.Error: 0.00
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 130.
Location/Qualifiers
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="GDB:5215514"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                         1407 AGATTCTCGTCTCGAAATGGACGTAGGAACTTACTAGAACCTGCTGATACTAGCACCAT 1466
1587 CACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAGT 1624
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                                                                                             CAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTTTATTGGACCCGACGGG 1586
                                                CACCGCACCCTCAATAAGCCACCCATTAACCTACTACACCATTTAAATTAACACCCCTTG
                                                                                                                                                TAAAAATTGTATAATAAAGATTGAAGATATAAACACTATATTGCGAACAACAATTCCTAC
                                                                                                                                                                                                                                              AAACGCTCGGTTATAAGTATAGATGGAAGCGATAATAAGAAGTAATAATACTAAGATAAC 506
                                                                                                                                                                                                                                                                                                                                                106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duke University
Durham, NC 27708-1000
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963087D05.x1 C. reinhardtii CC-1690, Stress condition I, normalized
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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919 613 8177
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone_lib="C. reinhardtii CC-1690, Stress condition I, normalized, Lambda Zap II"
/note="vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP-N (30 min, lhr, 4hr), TAP-S (30 min, lhr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, lhr, 4hr) and NH4 to NO3 (30min, lhr, 4hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites.
pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with EXASSIST (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Pred. No. 8.6;
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Best Local Similarity
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                                              2338 AGAGCTCCGATTTGCTTAGATGAA 2361
                                                                                                                                                 2278 ACATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGA 2337
                                                                                                                                                                                                                                                    2218 CTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACA 2277
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GCAGACACTCCTTTCTAGGAACAA 432
                                                                                                                                                                                                     CTCTGTTTCAAAAATAATAATAATAATAATAATAATAATCTGTCAAATAATTATCAA 516
                                                                                                GCAGATTCTAATGGTTGGGGATGATGTTAAAATCAGAGCTTCACTAGAAAATTATATAAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1055)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start: 27 High quality sequence stop: 738.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_*IMAGE:3839828"
/clone_tib=*NMEL.S7"
/tissue_type=*glioblastoma*
/lab_host=*DH10B (T1 phage-resistant)*
/lab_host=*DH10B (T1 phage-resistant)*
/note=*Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
/note=*Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccattaftggcc);
Site_2: SfiI (ggccattaftggcc);
Site_2: SfiI (ggccattaftggcc);
Site_1: SfiI (ggccattaftggcc);
Site_2: SfiI (ggccattaftggcc);
And 3: adaptors were used in cloning as follows: 5'
adaptors sequence: 5'-CACGGCCATTATCGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCAGGCGCGAATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratorles (Palo Alto, CA)."
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Pred. No. 13;
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               Query Match
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les 113; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCTGATAC 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATC 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-CCTTTCTCAACACACTTTTGAATTACATGATTTCCATTTTGGTCTTGAAACATGCAAT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAAATGCTAATACTCTTCCTTTAAATGCAAAAATAATTGAATCAATAATTTTTAAGTC 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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wh51g06.xl NCI_CGAP_Kidll Homo
                                                                                                                                                                                                                                                                                                                                                                  www-bio.llni.gov/bbrp/image/image.html
Insert Length: 393 Std Error: 0.00
Seq primer: -40Up from Gibco.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 372)
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL
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                                                                                                  /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECC RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                 Fatima Bonaldo.
1 74 c 55
                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2384314"
                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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1.4%;
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Primates;
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38.8; DI
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               102;
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C23720/c
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Best Local Similarity 44.4%;
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GAGTGACTCTGCAGACTCAGGCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACG 1429
                                                                                                                                                                                                                                                                                                        GTGTTGCTCCTTGTTTAATTGCCCATTCTTTCATACCATTAGCTACCATATCTGCAATCT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAACAAACCCTGAGGGTTTTTGCTGTGATGTGAAGGCAGGGTGCTTTTGTCCCCAGTTG 109
                                                                                                                                 GTAATGTCTCCCTCATTGCATTTAATCCATATGTATCACTATCATAAATATCTGTTAAATC 225
                                                                                                                                                                                                                     CTGGATCTAATGCACTACCTGTTTGCATTACTTCACGAATTTTCTTATAACAATGTGATG 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACTGT 2291
                                             TATCTGCTTTATCACTAATATCAATATCTGCTTCAACTGGTTCTCTACTATCAATATATT 165
                                                                                      TTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATG 1369
                                                                                                                                                                     GGAACATCATCTTCACAGGAGAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATC 1309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sexual cDNA in CSM
Unpublished (1997)
Contact: Hideko Urushihara
Institute of Biological Sciences
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Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: d402hu@sakura.cc.tsukuba.ac.jp.
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3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
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Shimizu, H. and Urushihara, H
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/clone="FC-AB21"
/clone_lib="Dictyostelium discoideum
/clone_11b="Dictyostelium discoideum
80 c 128 g 203 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dulon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                        Yarrowia lipolytica.

Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence are the sequence of the other extremity of this insert.
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail sequence cns.fr - Web: www.genoscope.cns.fr)
This BAC end sequence is part of a random genomic sequencing program of thirteen yeast species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zygosaccharomyces rouxii
FEBS Lett. 487 (1), 52-55 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de Montigny, J., Straub, M., Potier, S., Tekaia, F., Dujon, B., Wincker, P., Artiguenave, F. and Souciet, J. Genomic exploration of the hemiascomycetous yeasts: 8.
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GSS; clone AR0AA009D07;
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T7 end of clone AR0AA009D07 of library AR0AA from strain CBS
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Candida tropicalis and
                                                                                                                                                                                                                                                                                                                                                                                   Debaryomyces hansenii var.
                                                                                                                                                                                                                                                                                                                                                                                                                Pichia angusta,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus
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                                                                        /strain="CBS 732"
/db_xref="taxon:4956"
/clone="AR0AA009D07"
                                                  /clone_lib="AR0AA"
                                                                                                                                                  /organism="Zygosaccharomyces
                                                                                                                                                                                                     Location/Qualifiers
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1 (bases 1 to 929)

Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bjloftus@tigr.org
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
/note: Bst I; Constructed at Constructed at Clark,
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

13 a 146 c 102 g 368 t
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                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:5759"
                                                                                                                                                                                                                                                                                                                                                                             /strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Entamoeba histolytica"
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Pred. No. 7
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM863 row: c_column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF105345 952 bp mRN7
601822058R1 NIH_MGC_75 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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/clone="IMAGE:4043310"
/clone_lib="NIH_MGC_75"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: fil (ggcgcttattatgcc); S' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCACTTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGCGGCCGACATG-GT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones
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/lab_bost="DHIOB (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
a 159 c 118 g 341 t 2 others
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/clone="IMAGE:3912241"
/clone_lib="NIH_MGC_71"
                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 5.9;
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                                                                   Query Match 1.4%; Score 39.4; EBest Local Similarity 42.8%; Pred. No. 6.7; Matches 74; Conservative 21; Mismatches
      1453 GATACTAGCACCATAAACAATTTTGGTCATTAAACATCAGTTCTATAGACGGTGCAAAGAAG 1512
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DB

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1064; 0;

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Gaps

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                                                                                                                                                                                                                           - Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and the DNA was prepared from the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN12/16 of DrosBAC library from Drosophila melanogaster (frufly), qenomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                    pBeloBAC11.
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                  /clone_lib="DrosBAC"
/clone="BACN12J16"
/note="end : T7"
a 222 c 216 g
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222 c 231 g 252 t 2 others
                                                                                                        /organism="Drosophila
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                             CTACWACTACWGCTACTGCTACTCCAACTGCTACWACTGCTACWACTGCWACTG
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Anopheles gambiae BAC end sequence T7 end of clone
Notrebamel library from strain PEST of Anopheles ga
malaria mosquito), genomic survey sequence.
                        African malaria mosquito.
Anopheles gambiae
Eukaryota; Metazoa; Arthr
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          Pterygota;
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/db_xref="taxon:99883"
/clone="199C24"
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/note="Genoscope sequence
265 c 69 g 184
        Metazoa; Arthropoda; Tracheata; Hexapoda; Neoptera; Endopterygota; Diptera; Nematoco
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                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9730 row: h column: 02
High quality sequence stop: 564.
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 775)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE885056 775 bp mRNA EST 601510804F1 NIH_MGC_71 Homo sapiens cDNA clone mRNA sequence.
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High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 904)
Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J.
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/clone="31C01"
/clone_11b="NotreDame1"
/note="end : T7"
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Tex: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ881488 467 bp DNA
HS_5162_A1_F07_T7A RPCI-11 Human
genomic clone Plate=8930 Col=13 F
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                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence scanning the human genome
                                                                                                                                                                                                                                                                                Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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/db_xref="taxon:99883"
/clone="123M05"
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                                                                           (bases 1 to 773)

(bases 1 to 773)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,

Saurin,W. and Weissenbach,J.

Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using

Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                               Weissenbach, J.

Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
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                  Direct
                                        Genoscope.
                                                                                                                                                                                                                                                                                          Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot,
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1 (bases 1 to 773)
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/db_xref="taxon:9606"
/clone="plate=8930 Col=13 Row=K"
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/sex="male"
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1 (bases 1 to 596)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S.
                                                            Takifugu rubripes.
Takifugu rubripes
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A1483617 EST249481
A1878146 fc58a05.y
AW037541 EST278868
AL130699 Fugu rubr
AL393296 T7 end of
AL444958 Fugu rubr
AZ444958 Fugu rubr
AZ645421 EW1DU53TF
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AL077673 Drosoph11

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Human gene number estimate provided by Tetracdon nigroviridis DNA sequence Unpublished 3 (bases 1 to 735)
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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                                                                                          2 (bases 1 to 735)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bound
Bernot, A., Fizames, C., Wincker, P., Brottier, P.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                               Tetraodontidae; Tetraodor
1 (bases 1 to 735)
Roest-Crollius,H., Jaillo
Bouneau,L., Billault,A.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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01-DEC-1998;

98US-0110438

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This sequence is a Chlamydia antigen of the invention, designated CC CPN100639. The nucleic acids (and their complementary sequences) may be CC used as diagnostic agents for detecting the presence of nucleic acids CC encoding Chlamydia antigens in samples according to standard methods, CC and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction CC (PCR) assays. Antisense sequences may be used to down regulate CC expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they CC encode according to standard recombinant DNA methodologies. The CC (i.e. as vaccines) for preventing infection by Chlamydia. The CC infections. Chlamydia is a pathogen implicated in the development of CC (for example) community acquired pneumonia, upper respiratory tract CC disease (especially bronchitis and sinusitis, asthmatic bronchitis, cut of adult-onset asthma and acute exacerbations of asthma in adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 412;
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tslcknlarqaflasagshltlsphvelsgeaayelrgsahiynvdcglrysf 930
                                                   earafddgdlvncsipvgirlekisedeknnfeislayigdvyrknprsrtslmvsgasw
                                                                  EAREFGSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGDSW
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Search completed: October Job time: 30245 sec 2001, 03:26:53

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RESULT 14
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Best Local Similarity
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                                                                                                                                The present sequence is the mature, processed form of CPN100640, the 98 kDa outer membrane protein from Chlamydia pneumoniae. Chlamydia pneumoniae is a common cause of community acquired pneumonia and upper respiratory tract symptoms and diseases, including bronchitis and sinusitis. It also has an association with atherosclerosis and asthma.
nucleotide sequence encoding the protein or the protein itself may administered as a vaccine to prevent or treat infection and they may also be used to diagnose infection. The gene encoding CPN100640 was
                                                                              The 98 kDa outer membrane protein is a C. pneumoniae-specific antigen which can confer immune protection against chlamydial infection. The
                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is CPN100640, the 98 kDa outer membrane protein from Chlamydia pneumoniae. Chlamydia pneumoniae is a common cause of community acquired pneumonia and upper respiratory tract symptoms and diseases, including bronchitis and sinusitis. It also has an association with atherosclerosis and asthma. The 98 kDa outer membrane protein is a C. pneumoniae-specific antigen which can confer immune protection against chlamydial infection. The nucleotide sequence encoding the protein or the protein itself may be administered as a vaccine to prevent or treat infection and they may also be used to diagnose infection. The gene encoding CPN100640 was amplified from Chlamydia pneumoniae genomic DNA by PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                             vtngstst-rnainiidtakvtsiraatgqsiyfydpitnpgtaastdtlnlnladanse
                                                                                                                                                                                                                                                                                                  GGAIYVKKLELASGGLTLFSRNSVNGGTAPK--GGAIAIEDSGELSLSADSGDIVFLGNT
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yenhnlksastypllelttagangtitlgalstltlqepethygyqgnw-qlswanatss
                    YENHSLRNPQSYDILELK---ASGTVTSTAVTPDPIMGEKFHYGYQGTWGPIVWGTGAST
                                                                  LEMDVGTTLEPADTS-TINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTF 531
                                                                                                                                       ieyggaiv fsgekl sp tekaiaan v tstir qp av larg dlvlrdgv tv tfkdlt qsp gsr
                                                                                                                                                       LQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGGTLSLKHGVTLQTQAFTQQADSR 472
                                                                                                                                                                                                                                                VTSTTPGTNRSSIDLGTSAKMTALRSAAGRAIYFYDPITTGSSTTVTDVLKVNETPADSA 412
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                                    Chlamydia antigen; diagnosis; infection; community acquired pneumonia; therapy; upper respiratory tract disease; bronchitis; sinusitis; asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthm
            Chlamydia
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                                                                                                                                                                                                                                          GTNLARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGLSNFFHKDSTKTRRGFRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQG
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CC PNIJO638. The nucleic acids (and their complementary sequences) may be cused as diagnostic agents for detecting the presence of nucleic acids cand their complementary sequences) may be cused as diagnostic agents for detecting the presence of nucleic acids cand therefore, for diagnosing chlamydia infections. For example, they may come therefore, for diagnosing chlamydia infections. For example, they may come sequences and probes for diagnostic polymerase chain reaction complex. Antisense sequences may be used to down regulate compression of the proteins and may be used to treat infections. The concleic acids may also be used to produce the protein antigens they compressed according to standard recombinant DNA methodologies. The concode according to standard recombinant DNA methodologies. The contents may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The confictions. Chlamydia is a pathogen implicated in the development of confictions. Chlamydia is a pathogen implicated in the development of confictions community acquired pneumonia, upper respiratory tract constants as the concentration of asthmatic bronchitis, as dult-onset asthma and acute exacerbations of asthmatic bronchitis.
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01-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquire pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onse
Sequence
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                                              sfissnkaisfinnsvtatsa-----tggaiycsstsapkpvltlsdngelnfigntai
                                                                                                                                                                                                    DKSTTFIGFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGAITA 173
TAGGAIYYKKLELASGGLTLFSRNSVNGGTAPKGGAIAIEDSGELSLSADSGDIVFLGNT
                                                                                                                                    KTLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFTEAS
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                                                                               VTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKV-TLTGNQMLLFSNNTST
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                                                                                                                ssisls-lnpnltfaknkatqkggalystggitinntlnsasfsentaannggaiyteas
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44.98;
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                    SWKTFGTNLARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF 928
                                                                                                    GTEAREFGSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGD
                                                                                                                                                                                                               LKTKYTTYPTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFMKLQFVYAHQEGFKEQ
                                                                                                                                                                                                                                                          lvaknhtdtyagafyiqh----itecsgfigclldklpgswshkplvlegqlayshvsnd
                                                                                                                                                                                                                                                                                                    FVAKNOGTVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDND
                                                                                                                                                                                                                                                                                                                                             sdrgfwaagvanfldkdkkgekrkyrhksggyaiggaagtcsenlisfafcglfgsdkdf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtegrsfddsnlfnlslpigvkfekfsdcndfsydltlsyvpdlirndpkcttalvisga
                                                                                                                                                                     lktkytaypevkgswgnnafnmmlgasshsypeylhcfdtyapyiklnltyirgdsfsek
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Pred. No. 2.6
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.6e-123;
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S S 
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YLFKGNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVV 113

ynltgdvsitn-agsptaltascfkettgnlsfqghgyqfllqn1dag--anctftntaa

MKSSFPKFVFSTFAIFPLSM-----IATETVLDSSASFDGNKNGNFSVRESQEDA-GTT

mksslhwfvissslalplslnfsafaavveinlgptnsfsg--pgtytppaqttnadgti

58

54 59 Dy Qy

Query Match Best Local : Matches 42

Local Similarity nes 429; Conserv

41.5%; Score 1981; DB 20; ilarity 45.2%; Pred. No. 3.9e-122; Conservative 148; Mismatches 329;

Length Indels

44;

Gaps

19;

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RESULT 10
AAW88423
ID AAW884
XX AAW884
XX Omp10;
KW OMP1;
PN WO9858
XX (BIRK/PA (CHRI/X)
PA (CHRI/X)
PA (BIRK/PA (CHRI/X)
PA (CHRI/X)

                                                         This polypeptide comprises the novel 98.4 kDa surface exposed protein Ompl0 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAX06822) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Omp4-Ompl5 (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Ompl5 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals. The nucleic acids and proteins can also be used in the immunization of waccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 60-62; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
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outer membrane proteins of C. pneumoniae or nucleic acids encoding

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Query Match
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                                                                                                                                                                                                                                                                                                                                         WCAGLSNFFHKDSTKTRRGFRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFYAKN
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                                                                    astpktktatlawtntgylpnpgrqgplvpnslwgsfsdiqaiqgviersaltlcsdrgf
                                                                                                                                                         nqgnayenhdlgktqdfsfvqlsalgtatttdvpavptvatpthygyqgtwg-\texttt{mtwv}ddt
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                                                                                          -GTGASTTATENWTKTGYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRAF
                                                                                                                                                                                                      PTGTFYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEKFHYGYQGTWGPIVW----
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Pred. No. 1.2e-123;
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This sequence is a Chlamydia antigen of the invention, designated CPN10635. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The

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                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding preventing, diagnosing pneumonia, bronchitis,
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and treating diseases such as community acquired
sinusitis and asthmatic bronchitis, adult-onset
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide comprises the novel 96.7 kDa surface exposed ein Omp9 of the human respiratory pathogen Chlamydia
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CHRISTIANSEN
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 Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies speci
                                          N-PSDB; AAX06828
                                                       WPI; 1999-105610/09
                                                                                             Birkelund S,
                                                                                                                                                              23-JUN-1997;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 mammals,
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27-AUG-1998;
17-AUG-1999;
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20-AUG-1998;
20-AUG-1998;
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                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ61509.
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20-AUG-1998;
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                                       LFKGNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVD 114
                                                                           mrssfslllissslafpllmsvsadaadltigsrdsyngdtstteftpkaatsdasgtty 60
                                                                                                      MKSSFPKFVFSTFAIFPLSMI----ATETVLDSSASFDGN-KNGNFSVRESQEDA-GTTY 54
KSTTFIGFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGAITAK 174
                          ildgdvsisq-agkqtslttscfsntagnltflgngfslhfdniisstvagvvvsntaas 119
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45.7%;
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%; Pred. No. 2.2e-124;
151; Mismatches 314;
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GSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGDSWKTFGT
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                                                                                           spvkgswgndafgiecggaipvvasgrrswvdthtpflnlemiyahqndfkengtegrsf
                                                                                                                 PTVKGSWGNDSFALEFGGRAPICLD-ESALFEQYMPFMKLQFVYAHQEGFKEQGTEAREF
                                                                                                                                       vyagamsyrhlgesktlaki-----lsgnsdslpfvfnarfayghtdnnmttkytgy
                                                                                                                                                            VYGGTLYYQH----NETYISLPCKLRPCSLSYVPTEIPVLFSGNLSYTHTDNDLKTKYTTY
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AAW88422 standard; Protein; 918 A

AAW88422;

26-APR-1999 (first entry)

Chlamydia pneumoniae surface exposed protein Omp9

ARMSH42 AAWB42 XX AAWB AC AAWB XX AAWB XX Chla XX Chla XX Omp9 KW Omp9 KW infe XX Chla XX Omp9 XW WO98 Omp9; outer membrane protein 9; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma.

Chlamydia pneumoniae

exacerbations of asthma in

adults

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AAY90237
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01-DEC-1998;
01-DEC-1998;
                             (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of the production of the development of the protein of the development of the development of the productions.
                                                                                                                                                                                            CPN100635. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction
                                                                                                                                                                                                                                                                           This sequence is a Chlamydia antigen of the invention, CPN100635. The nucleic acids (and their complementary s
                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquir pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onse
                                                                                                                                                                                                                                                                                                                                           Claim
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                  example) community acquired pneumonia, upper respiratory tract
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DB; AAA30849, AA
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                   This polypeptide comprises the novel 97.2 kDa surface exposed protein Cmp5 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAX06817) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Cmp4-Cmp15 (see AAX08417-28), and nucleic acid sequences encoding them (see AAX06816-27). A new species specific test is claimed that is use
                                                                                                                                                                                                                                                                     Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encocouter membrane proteins of C.
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                                                                             LPCKLRPCSLSYVPTEIPVLFSGNLSYTHTDNDLKTKYTTYPTVKGSWGNDSFALEFGGR
                                                                                                FTGEKLSETEAADSKNUTSKLLQPVTLSGGTLSLKHGVTLQTQAFTQQADSRLEMDVGTT
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C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tide comprises the novel 90.0 kDa surface exposed of the human respiratory pathogen Chlamydia Its amino acid sequence was deduced from DNA (see
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01-MAR-1999;
27-OCT-1999;
Chlamydla pneumoniae. The genomic sequence was amplified using two PCR primers. The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence close to the 5' end of the 98kDa putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BsrG1 restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame c-terminal fusion with the Histidine tag. The PCR product was cloned into a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with NotI and BamHI and performing a ligation reaction. This expression vector was injected intramascularly and intranasally into mice, which were subsequently inoculated with Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice were lower than those of the controls. Thus the 98kDa putative outer
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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Chlamydia pneumoni
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## ALIGNMENTS

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AAW88421 standard; Protein; 928

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26-APR-1999 (first entry)

Chlamydia pneumoniae surface exposed protein Omp8

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AAW88421
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ACX A
Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for
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N-PSDB; AAX06820.
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(CHRI/) CHRISTIANSEN G.
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                                                                                                   NDSFALEFGGRAPICLDESA---LFEQYMPFMKLQFYYAHQEGFKEQGTEAREFGSSRLV 826
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Search completed: October 2, 2001, 03:29:20 Job time: 1337 sec

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R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
A;Accession: D72077
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A;Molecule type: DNA
A;Residues: 1-928 <ARN>
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A;Gene: pmp_11
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                                                                                                                               NEFHKDSTKTRRGFRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGTVYG
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                                                               GTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSL
 PESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGF
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%; Pred. No. 4.5e-93;
171; Mismatches 332;
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HSLRNPQSYDILELKASGTVTS----TAVTPDPIMGEKFHYGYQGTWGPIVWGTGASTT-DSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYES

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polymorphic membrane protein G family CP0302 [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: F81591 R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicl R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.; McClarty, G.; Salzi Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR: A;Reference number: A81500; MUID:20150255 A;Accession: F81591
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A:Molecule type: DNA
A:Residus: 1-949 <REA>
A:Cross-references: GB:AE002192; GB:AE002161;
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0302
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                                                                            TGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGGTLSLKHGVTLQTQAFTQQADSRLEM
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DVGTTLE-PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFYEN
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42.6%; Pred. No. 4.7e-93;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <STO>
A;Cross-references: GB:BA000008; NID:g8978822;
A;Experimental source: strain J138
C;Genetics:
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A;Title: Comparison of whole genome sequences of chlamydia pneum A;Reference number: A86491; MUID:20330349
A;Accession: H85546
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Similarity
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68
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No. 4.5e-93;
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polymorphic outer membrane protein g family - Chlamydophila pneu C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C; Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change C; Accession: D72077

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                  TNLARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF
GNLSRQAFILRGSNNYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF
                                                             GTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIFLALDVQVSFSHSDNRMETHYTSL
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                                                                                             GSSRLVNLALPIGIRFDKESDCQDA-TYNLTLGYTVDLVRSNPDCTTTLRISGDSWKTFG
                                                                                                                                               PTVKGSWGNDSFALEFGGRAPICL-DESALFEQYMPFMKLQFVYAHQEGFKEQGTEAREF
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                                                                                                                              PESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGF
                                                                                                                                                                                                                                                          {\tt HMFSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWN-VNWTTDTATNT}
                                                                                                                                                                                                                                                                                                                                                                                                                            HSLRNPQSYDILELKASGTVTS----TAVTPDPIMGEKFHYGYQGTWGPIVWGTGASTT-
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                                                                                                      AGGAIYVKKLELASGGITLFSRNSVNGGTAPKGGAIAIEDSGELSLSADSGDIVFLGNTV
                                                                                                                                       SITQNSSLFFSGNTATDAAG-----KGGAIYCEKTGETPTLTISGNKSLTFAENSSYT
                                                                                                                                                                                                                                  KGNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDKS 116
                                                                                                                                                                                                                                                                                                                                                          MKSSFPKFVFSTFAIFPLSM-IAT---ETVLDSSASFDGNKNGNFSVRESQEDAGTTYLF
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TSLCKNLARQAFLASAGSHLTLSPHVELSGEAAYELRGSAHIYNVDCGLRYSF 930
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                                       TSTSAPTSTRNAIYLGSSAKITNLRAAQGQSIYFYDPIASNTTGAS----DVLTINQPDS
                                                              TSTT-PGTNRSSIDLGTSAKMTALRSAAGRAIYFYDPI---TTGSSTTVTDVLKVNETPA
                                                                                      QGGAICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIAIADSGSLSLSANQGDITFLGNTL\\
                                                                                                                                                      VTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLFSNNTSTT
                                                                                                                                                                                                                                                             TTFIGFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTD---NGGAITA 173
                                                                                                                                                                                                                                                                                     SGNVYI-NDAGKGTALTGCCFTETTGDLTFTGKGYSFSFNTVDAGSNAGAAA-STTADKA 118
                                                                                                                                                                                                                                                                                                                                     MKIPLHKLLISSTLVTPILLSIATYGADASLSPTDSFDGAGGSTFTPKSTADANGTNYVL
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative 164;
                                                                                                                                                                                                                                                                                                                                                                                               40.4%; Score 1929; DB 2; 43.4%; Pred. No. 3.4e-97;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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A;Molecule type: DNA A;Rosidues: 1-930 <ARN> A;Residues: 1-930 <ARN> A;Cross-references: GB:AE001627; GB:AE001363; NID:94376721; PIDN:AAD18590.1; PID:9437 A;Experimental source: strain CWL029 C;Genetics: A;Gene: pmp_8
                                                                                                                                                                                                           polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C;Accession: D72078 R;Kalman, S; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grim Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                       RESULT
D72078
                                                                                                                         A;Title: Comparative genomes of Clamydia | A;Reference number: A72000; MUID:99206606 A;Accession: D72078 A;Status: preliminary
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Š 밁 Ω 밁 Š 밁 δÃ Query Match Best Local : Matches 174 57 Local Similarity 43.3%; Pees 413; Conservative 164; KTLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFTEAS SGNYYI-NDAGKGTALTGCCFTETTGDLTFTGKGYSFSFNTVDAGSNAGAAA-STTADKA KGNVTLENIPGTGTAITKSCENNTKGDLTETGNGNSLLEQTVDAGTVAGAAVNSSVVDKS 116 MKIPLHKLLISSTLYTPILLSIATYGADASLSPTDSFDGAGGSTFTPKSTADANGTNYVL MKSSFPKFVFSTFAIFPLSM-IAT---ETVLDSSASFDGNKNGNFSVRESQEDAGTTYLF 40.3%; Score 1925; I 43.3%; Pred. No. 5.6e 7ative 164; Mismatches ; DB 2; 5.6e-97; hes 328; Length 930; Indels 48; Gaps 233 118 60 56 17;

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A;Cross-references: GB:AE002193; GB:AE002161; NID:g7189234; PIDN:AAF38165.1; A;Experimental source: strain AR39, HL cells C;Genetics: A;Gene: CP0308
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 LARQGFSVRAANHFQVNPHMEIFGQFAFEVRSSSRNYNTNLGSKFCF
          LARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF 928
                                                                                                PTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFMKLQFVYAHQEGFKEQGTEAREFG
                                                                                                                                                                        NETYRDSMPTRHGERHISGGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGDTYG
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                                           KSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMAYGTN
                                                                                      SIIKGSWRNDAFCADLGASLPFVISVPYLLKEVEPFVKVQYIYAHQQDFYERYAEGRAFN
                                                                                                                               ASLYFHHTEGLFDIANFLWGKATRAPWVLSEISQIIPLSFDAKFSYLHTDNHMKTYYTDN
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R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae A;Reference number: A86491; MUID:20330349
A;Accession: D86546
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A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_8
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086546

polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae proteins: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: D86546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 KTLSLIGTTMSALFSENTSSKKGGALQTSDALTITGNQGEVSFSDNTSSDSGAAIFTEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 AGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAIAIEDSGELSLSADSGDIVFLGNTV 353
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                       RAFWCAGLSNFFHKDSTKTRRGFRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFV 698
                                                                                                           ATWADTSTAKSGTMTWVTTGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQ
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                                                                                                                                        PIVWGTGASTTATFNWTKTGYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGD
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RGLWASGTANFFHKDKSGTNQAFRHKSYGYIVGGSAEDFSENIFSVAFCQLFGKDKDLFI
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polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae (str C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c;pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: C86546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349
A;Accession: C86546 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-936 <STO> A;Cross-references: GB:BA000008; NID:g8978817; PIDN:BAA98653.1; GSPDB:GN00142 A;Experimental source: strain J138 C;Genetics: Apgen: pmp_7
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                 MKSSVSWLFFSSIPLFSSLSIVAAEVTLDSSNNSYDGSNGTTFTVFSTTDAAAGTTYSLL
                                                                                              MKSSFPKFVFSTFAIF-PLSMIATETVLDSS-ASFDGNKNGNFSVRESQE-DAGTTYLFK
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                                                                                                                                               40.8%;
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Pred. No. 2.5e-98;
9; Mismatches 330;
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                                                                                          KSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMAYGTN
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A;Title: Genome sequences of A;Reference number: A81500; M A;Accession: B81591 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-936 <REA> R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis A;Reference number: A81500; MUID:20150255 polymorphic membrane protein G family C (;Species: Chlamydophila pneumoniae, Ch C;Date: 31-Mar-2000 #sequence\_revision C;Accession: B81591 R;Read, T.D.; Brunham, R.C.; Shen, C.; c membrane protein G family CP0308 [imported] - Chlamydophila Chlamydophila pneumoniae, Chlamydia pneumoniae -Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-;

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Heidelberg, J.F.; Kolonay, J.; McCl

McClarty, White,

G.; 0:,

Salzbe Hicke #text\_change 11-May-2000

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polymorphic membrane protein G family CP0306 [imported] - Chlamydophila pneumoniae (stra C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae
C; Species: Chlamydophila pneumoniae
C; Species: Chlamydophila pneumoniae
C; Species: Chlamydia pneumoniae
C; Species: Chlamydia pneumoniae
R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Reference number: A72000; MUID:99206606
A; Accession: B72077
A; Molecule type: DNA
A; Residues: 1-928 < ARN>
A; Residues: 1-928 < ARN>
A; Experimental source: strain CWL029
R; Read, T. D.; Brunham, R. C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Accession: B81592
A; Accession: B81592
A; Accession: B81592
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A;Experimental source: strain AR39, HL cells
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFISSNKAISFINNSVTATSA-----TGGAIYCSSTSAPKPVLTLSDNGELNFIGNTAI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKV-TLIGNQMLLESNNTST 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFTEAS 233
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GNVYEDVSWNNPQVFSCLTLTADDPANIHITDLAADPLEKNPIHWGYQGNWA-LSWQEDT
                                                                                                                                                                                                            LAGNPAYQGTIVFSGEKLSEAEAAEADNLKSTIQQPLTLAGGQLSLKSGVTLVAKSFSQS
                                                                                                                                                                                                                                                                                                                  VVKGASSSQTTTRNSINIGNTNAKIVQLRASQGNTIYFYDPITTSITAALSDALNLNGPD
                                                                                                                                                                                                                                                                                                                                                                          V---TSTTPGTNRSSIDLG-TSAKMTALRSAAGRAIYFYDPITTGSSTTVTDVLKVNETP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKLLSFSGFSYLSLIQT--TNATTGTGAIK-STGACSIQSNYSCYFGQNFSNDNGGALQG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKSTTFIGFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGAITA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNLTGDVSITN-AGSPTALTASCEKETTGNLSFQGHGYQFLLQNIDAG--ANCTETNTAA 115
                                               GTFYENHSLRNPQSYDILELKAS -- GTVTSTAVTPDPIMGEKFHYGYQGTWGPIVWGTGA
                                                                                                      PGSTLLMDAGTTLETADGITINNLVLNVDSLKETKKATLKATQASQTVTLSGSLSLVDPS
                                                                                                                                 ADSRLEMDVGTTLEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPT
                                                                                                                                                                                                                                                              ADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGGTLSLKHGVTLQTQAFTQQ 468
                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt TSGGAIYTDNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLSALGGDITFEGNT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLFKGNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKSSLHWFLISSSLALPISLNFSAFAAVVEINLGPTNSFSG--PGTYTPPAQTTNADGTI 58
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45.1%; Pred. No. 8.3e-100;
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polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain CWL029 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C;Accession: C72078 C;Accession: C72078 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
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A;Experimental source: strain CWL029
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A; Residues: 1-936 <ARN>
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                                                                                                                                                                       180 LLSGTSQFASFSRNQAFTGKQGGVVYATGTITIENSPGIVSFSQNLAKGSGGALYSTDNC 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNDLKTKYTT 760
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GGAISGLKVSISAGGPTLFQSN-ISGSSAGQGGGGAINIASAGELALSATSGDITFNNNQ
                      GGAIYVKKLELASGGLTLFSRNSVNGGTAPK--GGAIAIEDSGELSLSADSGDIVFLGNT 352
                                                                                      SITDNFQVIFDGNSAWEAAQA-----QGGAICC--TTTDKTVTLTGNKNLSFTNNTALTY
                                                                                                                                                                                                                                                                                                                                        SDVSFQNAGALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSSAGTVASTSAADKNL
                                                                                                                                                                                                                                                                                                                                                                                                                              MKSSVSWLFFSSIPLFSSLSIVAAEVTLDSSNNSYDGSNGTTFTVFSTTDAAAGTTYSLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFDSGDLINVSVPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTSWKTT 878
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                                                                                                                                                                                               SLTGTTMSALFSENT--SSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFTEASV
                                                                                                                             TISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLFSNNTSTTA 294
                                                                                                                                                                                                                                                                                                 TFIGFSSLSFIASPGSSIT-TGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGAITAKTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 40.8%; Score 1951; DB 2; Similarity 43.1%; Pred. No. 2.2e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 179; Mismatches 330;
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polymorphic outer membrane protein G/I family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: B8546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T. Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349 A;Accession: E86546 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-928 <STO> A;Cross-references: GB:BA000008; NID:98978819; PIDN:BAA98655.1; GSPDB:GN00142
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ANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGSSRIYNVDLGGKFQF 928
                                                                                                                                                                                                                                                                                                     EFGSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGDSWKTF
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644 AGLSNFFHKDSTKTRRGFRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQG
                  EFGSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGDSWKTF
                                                                                                                    YPTVKGSWGNDSFALEFGGRAP-ICLDESALFEQYMPFMKLQFVYAHQEGFKEQGTE-AR
                                                                                                                                                                                                                                                   TYYGGTLYYQHNETYISLPCKLRPCSLSYVP----TEIPVLFSGNLSYTHTDNDLKTKYTT
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SFDSGDLINVSVPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTSWKTT
                                                                                               APKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIKVEASYIHQDSFKERNTTLVR
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                                                                                                                                                                                                 -PSLLRYLPGSESEQPVLFDAQISYIYSKNTMKTYYTQ
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9; Mismatches 329;
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349
A;Accession: G86546
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <570>
A;Residues: 1-928 <570>
                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000008; NID:g8978821; A;Experimental source: strain J138 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 02-Mar-2001 C;Accession: G86546
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          AVANGGAIYAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITF
                        STTAGGAIYVKKLELAS--GGLTLFSRNSVNGGTAPKGGAIAIEDSGELSLSADSGDIVF
                                                                                                                                                                              STTFIGFSSLSFIASPGSSITT--GKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGAITA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AREFGSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGDSWK 876
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                                                            TGNCTITGNTSLVFSENSVT----ATAG--NGGAL----SGDADVTISGNQSVTFSGNQ
                                                                                                              KNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPTLFSNNIAEAAGGAINS
                                                                                                                                                                                                                                                                      {\tt MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNT--TTGIDYT}
                                                                                                                                                                                                                                                                                                                     43.3%; Score 2069; DB 2; ilarity 46.9%; Pred. No. 8.4e-105; Conservative 141; Mismatches 319;
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                                                            SFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPDLIRNDPKCTTALVISGASWETY
                                                                         EFGSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGDSWKTF 878
                                                                                                                                     TTYPTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFMKLQFVYAHQEGFKEQGTEAR 818
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J., C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlam A;Reference number: A81500; MUID:20150255 polymorphic membrane protein G family CP0303 [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000 C;Accession: G81591 C; Genetics: A; Gene: CP0 A;Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38160.1; A;Experimental source: strain AR39, HL cells A; Molecule type: DNA A; Residues: 1-928 < REA> A; Reference number: A81500; A; Accession: G81591 A; Status: preliminary Query Match Best Local Sim Matches 446; 59 56 Local Similarity \_ 1 MKSSFPKFVF-STFAIF---PLSMIATETVLDSSASFDGNKN-GNFSVRESQEDAGTTYL CP0303 FKGNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDK 115 MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNT--TTGIDYT Conservative 46.98; 141; Score 2069; DB 2; Pred. No. 8.4e-105; 41; Mismatches 319; Length 928; Indels Chlamydia 44; .F.; White, O.
McClarty, G.; Gaps pneumoniae 55 115 58 ' 0 :: 20; PID:9718 ; Hicke Salzbe

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### ALIGNMENTS

RESULT H86492

C;Accession: H86492
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Accession: H86492
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-772 <STO>
A;Cross-references: GB:BA000008; NID:g8978389; PIDN:BAA98226.1; GSPDB:GN00142
A;Experimental source: strain J138 Pmp\_3 [imported] - Chlamydophila pneumoniae (strain J138)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001 δÃ В γQ 밁 δã Вp Š 밁 QΥ 밁 밁 밁 Qy 8 A;Gene: pmp\_3\_2 Query Match
Best Local Similarity
Matches 771; Conserv ;Genetics: 361 397 TYTDYLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPYTLSGGTLSLKH 157 LLFSKNFSTDNGGAITAKTLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSF 277 TLTGNQMLLFSNNTSTTAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAIAIEDSGE 217 SDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKV 181 LSLSADSGDIVFLGNTVTSTTPGTNRSSIDLGTSAKMTALRSAAGRAIVFYDPITTGSST 121 TLTGNQMLLFSNNTSTTAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAIAIEDSGE 61 SDNTSSDSGAAIFTEASYTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKV 1 MLFSKNFSTDNGGAITAKTLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSF LSLSADSGDIVFLGNTVTSTTPGTNRSSIDLGTSAKMTALRSAAGRAIYFYDPITTGSST ilarity 99.9 Conservative 83.5%; 99.9%; Score 3991; DB 2; Pred. No. 2.5e-209; 1; Mismatches 0; 2; Length Indels 0, Gaps 576 456 336 276 360 516 240 396 180 120 60 216 0 H.;

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D	699 ETLRVAGAAAQGSHNANGFTALQLGATAGATTFTNVAVNVGLTVLAAPTGTTTVTLANAT 758
Qy	433DSKNLTSKLLQPVTLSGGTLSLKHGVTLQTQAFT 466
đ	759 GTSDVENLTLSSSAALAAGTVALAGVETVNIAATDTNTTAHVDTLTLQATSAKSIVVT 816
Qy	467 QQADSRLEMDVGTTLEPADTSTINILVINISSIDGAKKAKIETKATSK 514
В	817 GNAGLNLTNTGNTAVTSFDASAVTGTAPAVTFVSANTTVGEVVTIRGGAGADSLTGSATA 876
Qy	515 NLTLSGTITLLDPTGTFYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEKFHY 571
뭥	IGGAGADTLVYTGGTDTFTGGTGADIFDINAIGTSTAFVTITDAA
Qγ	572 GYQGTWGPIVWGT-GASTT 589
Ъ	933 VGISTNGAIADGAFGAAVT 951
RESULT	15 142-
 g g g	Sequence /, Application US/U9142648B Patent No. 6210948 GENERAL INFORMATION:
	Smit, John Bingle, Wade H.
	TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULA FILE REFERENCE: 08106/002002
	ENT APE
	PPLICATION NUME
· · · · ·	LICATION NUMBE
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	<b>T</b> .
	TYPE: PRT ORGANISM: Caulobacter crescentus
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M B Q	Query Match 5.0%; Score 240.5; DB 4; Length 1026; Best Local Similarity 24.8%; Pred. No. 6.1e-10; Matches 183; Conservative 86; Mismatches 253; Indels 217; Gaps 35;
ð	TVI.DSSASTINANANANANANANANANANANANANANANANANANANA
ру	12 TFAIFPLSMIATETVLDSSASFDGNKNGNFSVRESQEDAGTTYLFKGNVTLENIPG 67    ::       ::
Qy	KSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVN
В	323 SGAAITLNTSSGVTG-LTALNTNTSGAAQTVTAGAGQNLTATTAAQAANNVAVD 375
Qy	121 GFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGAITAKTLSLTG 180
В	376 GRANVTVASTGVTSGTTTVGANSAASGTVSVSVANSSTTTTGAIAVTG 423
Qy	181 TTMSALFSENTSSKKGGAIQTSDÅLTITGNQGEVSFSDNTSSDSGAAIFTEASVTI 236
Db	24 GTAVTVAQTAGNAVNTTLTQADVTVTGNSSTTAVTVTQTAAATAGATVAGRVNGAVTI
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Search completed: October 2, 2001, 03:27:58 Job time: 7240 sec

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino aci
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APPLICANT: Smit, John
APPLICANT: Bingle, Wade H.
APPLICANT: Bingle, Wade H.
APPLICANT: NO. 5976864e1lini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF
TITLE OF INVENTION: HETEROLOGOUS
TITLE OF INVENTION: POLYPEPTIDES FROM CAULOBACTE
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       818 MIGKGIVAKKNITFEGG-NITFGSRKAVTE-----IEGNVTINN--NANVTLIGSDFDN 868
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLSLKHGVTLQTQAFTQQADSRLEMDVGTTLEPADTSTIN-----NLVIN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISGNTVTVTANSGALTTLAGSTIKGTESV-----TTSSQSGDIGG-----TISGG 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTMSALFSENTSSKKGGAIQTSDALTIT------GNQGEVSFSDNTSSDSGAAIFTEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HQKPLTIKKDVIINSGNL-----TAGGNIVNIAGNLTVESNANFKAITNFTFNVG- 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVEVK-----ATESLTTQSNSKIKATTGEANVTSATGTIGGTISGNTVNVTANAGDLTVG 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGSSTTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISATSGEITTKTGTTINATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAV----SN 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSADSGDIVF-LGNTVTSTTPG---TNRSSIDLG----TSAKMTALRSAAGRAIYFYDPI 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------NNTSTTAGGAIYVKKLELASGGLTLESRN-SVNGGTAPKGGAIAIEDSGELS 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTLHS 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDTEMQIGGDVSQKEGNLTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELK 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ISSIDGA-----KKAKIETKATSKNLTLSGTITLLDPTGTFYENHSLRNPQSYDIL 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703) 415-0810
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, 415-0813
- NO: 2:
                              HETEROLOGOUS
POLYPEPTIDES FROM CAULOBACTER
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Best Local Sim
Matches 183;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                     587
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                                                                                                                                                                                                                                                   424
                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                121 GFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGAITAKTLSLTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: 11
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07. FILING DATE: 09-JUNE-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0: FILING DATE: 12-MAR-1996
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STATE: Massa
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emreem: 225 Franklin Street
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TVDE: amino acid
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KMTALRSAAGRAIYFYDPITTGSSTTV----
                                   ATTLNISGDARVTITSHTAAALTGITVTNSVGATLGAELATGLVFTGGAGRDSILLGATT
                                                                                                                                         KVTLTGNQMLLFSNNTSTTAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKG-GAIAIED
                                                                                                                                                                                                   SNNA------KVSFIDNKVTGA-----SSSTTGDMSG-----GAICAYKTSTDT 274
                                                                                                                                                                                                                                                                                   TTMSALFSENTSSKKGGAIQTSDALTITGNQG--EVSFSDNTSSDSGAAIF--TEASVTI 236
                                                                                                                                                                                                                                                                                                                        GRANVTVASTGVTSGTTTVGANSAASGTV----SVSV---ANSSTTTTGAI-----AVTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                TGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAG-----TVAGAAVNSSVVDKSTTFI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFAIFPLSMIATETVLDSSASFDGNKNGNFSVRESQEDAGTTYLFKGNVTLENIP----G
                                                                      SGELSLSADSGDIV-----FLGNTVTST-----
                                                                                                        --TPTANTLTLNVNGLTTT--GAITDSEAAADDG----FTTINIAGSTASSTIASLVAAD
                                                                                                                                                                            TDSAAASATTAGKIATVTLGSFGAATIDSSALTTVNLSGTGTSLGIGRGALTA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 6.1e-10;
96; Mismatches 253
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                                                                    -----TPGTNRSSIDLGTSA
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US-08-617-697-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,51
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
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LENGTH: 1536 amino aci
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COMPUTER READABLE FORM:
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
    919
                                                                                                                                                              818
                                                                                   869
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                    20 MIATETVLDSSASFDGNKNGNFSVRESQEDAGTTYLFKGNVTLENIPGTGTAITKSCFNN 79
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
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STREET: Bldg.
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                      GSSITTGKGAVSCSTGSLKF-----DKNVSLL--FSKNFSTDNGGAITAKT--LSLT--G 180
                                                                                                                     TKGDLT-----FTGNGNSLLFQTVDAGTVAGAAVN---SSVVDKSTTFIGFSSLSFIASP 131
                                                                                                                                                            MIGKGIVAKKNITFEGG-NITFGSRKAVTE----IEGNVTINN--NANVTLIGSDFDN 868
GLFDNKGNSNISIAKGGARFKDIDNSKNLSITTNSSSTYRTIISGNITNKNGDLNITNEG
                                                                                                                                                                                                                                            138;
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Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                            1536 amino acids

    Shoemaker and Mattare, Ltd.
    2001 Jefferson Davis Hwy., 1203 Crystal Plaza

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                                                                                                                                                                                                                                                            5.1%; Score 243.5; DB 2; 22.6%; Pred. No. 6.7e-10;
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                                                                               -TAGGNIVNIAGNLTVESNANFKAITNFTFNVG- 918
                                                                                                                                                                                                                                          226;
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                                                                                                                                                                                                                                                                               Length 1536;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08719641 Patent No. 6218141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 16-SEP-1994
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                       FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barenkar TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2001 STREET: Bldg.
                                              NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
STATE: Virginia
                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDTEMQIGGDVSQKEGNLTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELK 1038
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                            GB 9205704.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-728-470-2
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08728470 Patent No. 5928651
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                               APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
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                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                    ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
                                                                          COUNTRY: U.S.A. ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 MIATETYLDSSASFDGNKNGNFSVRESQEDAGTTYLFKGNYTLENIPGTGTAITKSCFNN 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDTEMQIGGDVSQKEGNLTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELK 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NNTSTTAGGAIYVKKLELASGGLTLFSRN-SVNGGTAPKGGAIAIEDSGELS 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                  1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 16-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       1099 KVETSGSNNNTEDSSDN------NAGLTIDAKNVTVNNN-----ITSHKAVS 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1039 LTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTLHS 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
                                                                                                                                                                                                                                                                                                     339 LSADSGDIVF-LGNTVTSTTPG---TNRSSIDLG----TSAKMTALRSAAGRAIVFYDPI 390
                                                                                                                                                                                                                                                                                                                                                                                                          288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 5.1%; Score 243.5; DB 2; Length 1536;
Local Similarity 22.6%; Pred. No. 6.7e-10;
hes 138; Conservative 105; Mismatches 226; Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 TKGDLT-----FTGNGNSLLFQTVDAGTVAGAAVN---SSVVDKSTTFIGFSSLSFIASP 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                  TVEVK----ATESLTTQSNSKIKATTGEANVTSATGTIGGTISGNTVNVTANAGDLTVG 1295
                                                                                                                                                                                                   TTGSSTTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDTEMQIGGDVSQKEGNLTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELK 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSSITTGKGAVSCSTGSLKF-----DKNVSLL--FSKNFSTDNGGAITAKT--LSLT--G 180
                                                                                                                                                                                                                                                                                                                                                                                                    -----NNTSTTAGGAIYVKKLELASGGLTLFSRN-SVNGGTAPKGGAIAIEDSGELS 338
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                                                                                                 TLSLKHGVTLQTQAFTQQADSRLEMDVGTTLEPADTSTIN------NLVIN------ 495
                                                                                                                                                    ISGNTVTVTANSGALTTLAGSTIKGTESV-----TTSSQSGDIGG-----TISGG 1240
                                                                                                                                                                                                                                                   ISATSGEITTKTGTTINATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAV----SN 1195
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-KKAKIETKATSKNLTLSGTITLLDPTGTFYENHSLRNPQSYDIL 546
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547 ELKASGIVIS 556

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LENGTH: 1536 amino acid;
TYPE: amino acid;
STRANDEDNESS: single;
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-530-198-2
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US-08-530-198-2
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Best Local Similarity
Matches 138; Conserv
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,
FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 2,651
REFERENCE/DOCKET NUMBER: JMB-:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1415-0810
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APPLICANT: BARRINKAMP, STEPHEN J

APPLICANT: ST. GEME III, JOSEPH W

TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS

TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
1039 LTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTLHS 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                       234 VT----IS--NNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLFS 287
                                                                                                979
                                                                                                                         181 TIMSALFSENTSSKKGGAIQTSDALTIT------GNQGEVSFSDNTSSDSGAAIFTEAS 233
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                                                                                                                                                                                         919 GLFDNKGNSNISIAKGGARFKDIDNSKNLSITTNSSSTYRTIISGNITNKNGDLNITNEG
                                                                                                                                                                                                                                        132 GSSITTGKGAVSCSTGSLKF-----DKNVSLL--FSKNFSTDNGGAITAKT--LSLT--G 180
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                 80 TKGDLT-----FTGNGNSLLFQTVDAGTVAGAAVN---SSVVDKSTTFIGFSSLSFIASP 131
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                                                                                             SDTEMOIGGDVSQKEGNLTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELK 1038
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                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08302832 Patent No. 5603938 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5603938-Typeable Haemophilus
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                               CITY: Arlington
STATE: Virginia
                                                                                                                                                          STREET: 2001 Je:
STREET: Bldg. 1
                                                                     COUNTRY: U.S.A. ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISATSGEITTKTGTTINATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAV ---- SN 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ISSIDGA-----KKAKIETKATSKNLTLSGTITLLDPTGTFYENHSLRNPQSYDIL 546
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    Shoemaker and Mattare, Ltd.
    2001 Jefferson Davis Hwy., 1203 Crystal Plaza

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Floppy disk
3M PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.1%; Score 243.5; DB 1 22.6%; Pred. No. 6.7e-10;
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Best Local Sim
Matches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                          1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BETKSTIESSE, JETTY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
                                                                                                                                                                                                                                          1140
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                                                                                                                                                                                                                                                                                                                                                                                                   1039
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LENGTH: 1536 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: GB 9
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  979
                                                                                                                                                                                                                                                                                                                                                                                                                                        234 VT----IS--NNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVTLTGNOMLLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 MIATETVLDSSASFDGNKNGNFSVRESQEDAGTTYLFKGNVTLENIPGTGTAITKSCFNN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 16-MAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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NGAEINATEGAATLTTSSGKLTTEASSHITSAKGQVNLSAQDGSVAGSINAAN-----
                                   ----ISSIDGA-----KKAKIETKATSKNLTLSGTITLLDPTGTFYENHSLRNPQSYDIL 546
                                                                             TVEVK-----ATESLTTQSNSKIKATTGEANVTSATGTIGGTISGNTVNVTANAGDLTVG
                                                                                                                   TLSLKHGVTLQTQAFTQQADSRLEMDVGTTLEPADTSTIN-----NLVIN-----
                                                                                                                                                          ISGNTVTVTANSGALTTLAGSTIKGTESV-----TTSSQSGDIGG-----TISGG
                                                                                                                                                                                                TTGSSTTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGG
                                                                                                                                                                                                                                                                             LSADSGDIVF-LGNTVTSTTPG---TNRSSIDLG----TSAKMTALRSAAGRAIYFYDPI 390
                                                                                                                                                                                                                                                                                                                       KVETSGSNNNTEDSSDN-----NAGLTIDAKNVTVNNN-----ITSHKAVS 1139
                                                                                                                                                                                                                                                                                                                                                                                                LTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTLHS 1098
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                                                                                                                                                                                                                                        ISATSGEITTKTGTTINATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAV----SN 1195
                                                                                                                                                                                                                                                                                                                                                           ----SVNGGTAPKGGAIYVKKLELASGGLTLFSRN-SVNGGTAPKGGAIAIEDSGELS 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDTEMQIGGDVSQKEGNLTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELK 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 5.1%; Score 243.5; DB 1; Similarity 22.6%; Pred. No. 6.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 105; Mismatches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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415-0813
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-CCT-1994
PRIOR APPLICATION NUMBER: US PCT/US93/02166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08617697 Patent No. 5977336
                                                                                                                                                                                                                                                       Matches
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  1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1382 TVVNATNASGSGNV---TAKTSSSVNITGDLNTINGLNIISEN 1421
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TELECOMMUNICATION INFORMATION:
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NAME: Berkstresser, Jerr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1322 QTTLTAKDSSIAGNINAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAASGDR 1381
                                                                                                                                                                   908
                                        113 VDKSTT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492 LVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFYEN 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 --TLSLKH------GVTLQTQ-AFTQQADSRLEMDVGT-TLEPAD-----TSTINN 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          78
                                                                                                                                                                                                          31 ASFDGNKNGNFSVRESQEDAGTTYL-FKGNVTL-----ENIPGTGTAITKSCF 77
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
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STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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ENANLTIQTKELKLAGDLNISGFNKAEITAKNGSDLTIGNASGGNADAKKVTFDKVKDSK 1087
                                                                                                                          NNTKGDLTFT---
                                                                                                                                                                   STFKGEASDNLNITGTFTNNGTANINIKGVVKLGDINNKGGLNITTNASGTQKTIINGNI 967
                                                                               TNEKGDLNIKNIKADAEIQIGGNISQKEGNLTISSDKVNITNQITIKAGVEGGRSDSSEA 1027
                                                                                                                                                                                                                                                     147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1600 amino acids
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 415-0813
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/ENTION: High Molecular Weight Surface Proteins
/ENTION: of No. 5977336-Typeable Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                              linear
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16-MAR-1993
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                                                                                                                                                                                                                                                 5.7%; Score 272; DB 2; Length 1600; 22.7%; Pred. No. 4.7e-12; tive 76; Mismatches 218; Indels 20
                                    ---FIGESSLSFIASPGSSITTGKGA-VSCSTGSLKFDK----- 153
                                                                                                                          ----GN-----GNSLLFQ-----TVDAGTVAGAAVNSSV 112
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                                                                                                                                                                                                                 Sequence 2, Application US/08038682 Patent No. 5549897
                                                                                                                                                                                                GENERAL INFORMATION:
                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                               1448 SGDRTVVNATNASGSGNV---TAKTSSSVNITGDLNTINGLNIISEN 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1388 SSNGQTTLTAKDSSIAGNINAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAA 1447
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                           ADDRESSEE:
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    Shoemaker and Mattare, Ltd
    Jefferson Davis Hwy., 1203 Crystal Plaza

                                                                                                                                                                  BARENKAMP, STEPHEN J
                                                                                                                                           GEME
                                                                                            III, JOSEPH W
HIGH MOLECULAR WEIGHT SURFACE PROTEINS
OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KLELASGGLTLFSRNSVNGGTAPKGGAIAI-EDSGEL---- 337
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TELEFAX: (703) 415-081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: REFERENCE/DOCKET NUMBER: 22,651
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7707 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA: CLASSIFICATION: 424
ATTORNBY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651 STREET: 2001 Jeft STREET: Bldg 1 CITY: Arlington STATE: Virginia STRANDEDNESS: COUNTRY: U.S.A. ZIP: 22202-0286 TELEPHONE: FILING DATE: APPLICATION NUMBER: LENGTH: amino acid 1536 amino acids (703) 16-MAR-1993 415-0813 415-0810 us/08/038,682 1038-293 Version #1.25

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Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08719641 Patent No. 6218141
                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Barenk
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                                                                                                                                                                                                   TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1193 GNANITTKTGDINGKVESSSGSVTLVATGATLAVGNISGNTVTITADSGKLTSTVGSTIN 1252
  COMPUTER
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                           ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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STRANDEDNESS: sir
                                                                  CITY: Arlington
STATE: Virginia
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                                             COUNTRY:
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                       22202-0286
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READABLE FORM:
                                             U.S.A.
                                                                                                                                                                                                                                                                     Barenkamp, Stephen J
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; STRANDEDNESS: si
; TOPOLOGY: linear
US-08-719-641-10
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TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                  1193 GNANITTKTGDINGKVESSSGSVTLVATGATLAVGNISGNTVTITADSGKLTSTVGSTIN 125
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FILING DATE: 16-SEP-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1038-625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US POFILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --NVSLLFSKNFSTDNGGAITAKTLSLTGTTMSA---LFSENTSSKK------GGAIQT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDLNIKNIKADAEIQIGGNISQKEGNLTISSDKVNITNQITIKAGVEGGRSDSSEAENAN 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDLTFT-----GN-----GNSLLFQ-----TVDAGTVAGAAVNSSVVDKS 116
                                                                                                                                                                                                                                                                                                                                                                       KEGTTINATTGSVEVTAQNGTIKGN--ITSQNVTVTATENLVTTENAVINATSGTVNIST 1136
                                                                                                                                                                                                                                                                                                                                                                                                                 SDALTITGNQGEVSFSDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTGASSST----- 256
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                                                                                        GTNSVTTSSQSGDIEGTISGNTVNVT---ASTGDLTIGNSAKVEAKNGAA
                                                                                                                                                                                                                                                                        KTGDIKGG---IESTSGNVNITASGN-TLKVSNITGQDVTVTADAGALTTTAGSTISATT 1192
                                                                                                                                                                                                                                                                                                                    -TGDMSGGAICAYKTSTDTKVTLTGNQMLLFSNNT------STTAGGAIYVK- 301
                                    TTGSSTTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGG 450
                                                                                                                                                                                                                              -----KLELASGGLTLFSRNSVNGGTAPKGGAIAI-EDSGEL------
                                                                                                                                 ----SLSADSGDI--VFLGNTVTSTTPGTNRSSIDLGTSAKMTALRSAAGRAIYFYDPI 390
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US-08-617-697-9
Sequence 9, Application US/08617697
Parent No. 5977336
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EILING DATE: 01-APR-1996
CLASSIFICATION: 4.24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
EILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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APPLICANT: Barenk
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                                      1090 DGHNVTL--NSEVKTSNGSS-NAGNDNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVT 1146
                                                                                                                  1030
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                   912
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201 TSDALTITGNQGEVSFSDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTGASSST----
                                                                  154 ---NVSILFSKNFSTDNGGAITAKTLSLTGTTMSA---LFSENTSSKK-------GGAIQ 200
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                                                                                                                                                                                           970
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COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                NLTIQTKELKLAGDLNISGFNKAEITAKNGSDLTIGNASGGNADAKKVTFDKVKDSKIST 1089
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                                                                                                                                                                                       SGDLNIIDKKSDAEIQIGGNISQKEGNLTISSDKVNITNQITIKAGVEGGRSDSSEAENA 1029
                                                                                                                                                                                                                                                                 TNYTFNVAGSFDNNGASNISIARGGAKFKDINNTSSLNITTNSDTTYRTIIKGNIS--NK 969
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2001 Jefferson Davis Hwy., 12
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22.7%;
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                  TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
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                                                             REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                           NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                               APPLICATION NUMBER:
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STREET: Bldg.
                                                           TELEPHONE:
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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/ENTION: High Molecular Weight Surface Proteins
/ENTION: of No. 5928651-Typeable Haemophilus
                                         415-0813
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Patent No. 6218141
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                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Barenk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                            APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1190 RTVVNATNASGSGNV---TAKTSSSVNITGDLNTINGLNIISEN 1230
                                                                                                                                                           STREET: 2001 Jef
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                      COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G--TLSLKH------GVTLQTQ-AFTQQADSRLEMDVGT-TLEPAD-----TSTIN 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGHNVTL--NSEVKTSNGSS-NAGNDNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVT 886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQTTLTAKDSSIAGNINAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAASGD 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---NVSLLFSKNFSTDNGGAITAKTLSLTGTTMSA---LFSENTSSKK------GGAIQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGDLNIIDKKSDAEIQIGGNISQKEGNLTISSDKVNITNQITIKAGVEGGRSDSSEAENA 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KLELASGGLTLFSRNSVNGGTAPKGGAIAI-EDSGEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKEGTTINATTGSVEVTAQNGTIKGN--ITSQNVTVTATENLVTTENAVINATSGTVNIS 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STT------FIGFSSLSFIASPGSSITTGKGA-VSCSTGSLKFDK------ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITTGSSTTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGTGTAITKSC-----FUNTKGDLTFTGNGNSLLFQ-TVDAGTVAGAAVNSSVVDK 115
                                                                                                                                                                                                                E: Shoemaker and Mattare, Ltd.
2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 277.5; DB 2; ilarity 22.7%; Pred. No. 1.3e-12; Conservative 82; Mismatches 219;
                                                                                                                                                                                                                                                                                10
                        Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TLTAESGKLTTQTGSSITSSN 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 197;
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TOPOLOGY:
US-08-719-641-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 92057
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1338 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 ---NYSLLFSKNFSTDNGGAITAKTLSLTGTTMSA---LFSENTSSKK------GGAIQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            770 NLTIQTKELKLAGDLNISGFNKAEITAKNGSDLTIGNASGGNADAKKVTFDKVKDSKIST 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             652 TNYTFNVAGSFDNNGASNISIARGGAKFKDINNTSSLNITTNSDTTYRTIIKGNIS--NK 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 TETVLDSSASFDGNKNGNFSVRES------QEDAGTTY--LFKGNVTLENI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                             G--TLSLKH------GVTLQTQ-AFTQQADSRLEMDVGT-TLEPAD-----TSTIN 490
                                                                                                                                                                                                                                                                                          NGTNSVTTSSQSGDIEGTISGNTVNVT---ASTGDLTIGNSAKVEAKNGAA------ 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGHNVTL - - NSEVKTSNGSS - NAGNDNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVT 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGDLNIIDKKSDAEIQIGGNISQKEGNLTISSDKVNITNQITIKAGVEGGRSDSSEAENA 769
NLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFYEN
                                                      GQTTLTAKDSSIAGNINAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAASGD 1189
                                                                                                                                                                                                                                                                                                                                                                                                           TGNANITTKTGDINGKVESSSGSVTLVATGATLAVGNISGNTVTITADSGKLTSTVGSTI 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKTGDIKGG---IESTSGNVNITASGN-TLKVSNITGQDVTVTADAGALTTTAGSTISAT 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TGDMSGGAICAYKTSTDTKVTLTGNQMLLESNNT-----STTAGGAIYVK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKEGTTINATTGSVEVTAQNGTIKGN--ITSQNVTVTATENLVTTENAVINATSGTVNIS
                                                                                                                                                                                                                                                                                                                            -----SLSADSGDI--VFLGNTVTSTTPGTNRSSIDLGTSAKMTALRSAAGRAIYFYDP 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KLELASGGLTLFSRNSVNGGTAPKGGATAI-EDSGEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGTGTAITKSC----FNNTKGDLTFTGNGNSLLFQ-TVDAGTVAGAAVNSSVVDK 115
                                                                                                                                                                                                                             ITTGSSTTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSDALTITGNQGEVSFSDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTGASSST----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FIGFSSLSFIASPGSSITTGKGA-VSCSTGSLKFDK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415-0813
415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.8%; Score 277.5; DB 4; 22.7%; Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB 9205704.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038-625
                                                                                                                                                                          -TLTAESGKLTTQTGSSITSSN 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 197;
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Gaps

29;

GenCore version Copyright (c) 1993 - 2000

Compugen Ltd.

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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
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seq length: 20
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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       US-08-728-470-9
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US-08-719-641-10
US-08-302-832-2
US-08-302-832-2
US-08-617-697-2
US-08-719-641-2
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Sequence 10, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 4, Appli
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28 207 4.3 2353 4 US-08-968-68-68-A-10 29 199.5 4.1 674 1 US-08-913-942-4 30 195.5 4.1 674 1 US-08-317-522A-3 31 195.5 4.1 674 2 US-08-751-965-3 32 195.5 4.1 674 2 US-08-758-975-3 33 195.5 4.1 674 2 US-08-728-626-3 34 195.5 4.1 674 2 US-08-78-95-3 35 195.5 4.1 674 2 US-08-808-599A-24 37 193.5 4.1 1160 3 US-08-808-599A-24 37 193.5 4.1 1160 3 US-08-317-522A-2 39 193.5 4.0 749 1 US-08-317-522A-2 39 193.5 4.0 749 1 US-08-439-918A-2 39 193.5 4.0 749 2 US-08-731-965-2 40 193.5 4.0 749 2 US-08-738-955-2 41 193.5 4.0 749 2 US-08-78-956-2 42 193.5 4.0 749 2 US-08-808-599A-2 43 181.5 3.8 1248 2 US-08-865-965-17 44 181.5 3.8 1248 3 US-08-465-966-17																		
4.3 2353 4 US 4.1 674 1 US 4.1 674 2 US 4.1 674 2 US 4.1 674 2 US 4.1 674 3 US 4.1 1160 3 US 4.0 749 1 US 4.0 749 2 US 4.0 749 2 US 4.0 749 2 US 3.8 1248 2 US 3.8 1248 3 US	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	<u>ω</u>	30	29	28
2353 4 US 674 1 US 674 1 US 674 2 US 674 2 US 674 2 US 674 2 US 674 2 US 749 1 US 749 1 US 749 2 US 749 2 US 749 2 US 749 3 US 749 3 US 749 3 US 749 3 US	181.5	181.5	181.5	193.5	193.5	193.5	193.5	193.5	193.5	195.5	195.5	195.5	195.5	195.5	195.5	195.5	199.5	207
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4 US-08-913-942-4 4 US-08-968-695A-10 1 US-08-317-522A-3 1 US-08-739-818A-3 2 US-08-751-965-3 2 US-08-738-975-3 3 US-08-808-599A-2 4 US-08-78-626-3 3 US-08-808-599A-2 1 US-08-317-522A-2 1 US-08-731-965-2 2 US-08-751-965-2 2 US-08-751-965-2 3 US-08-808-599A-2 1 US-08-738-975-2 2 US-08-738-975-2 2 US-08-738-975-2 3 US-08-808-599A-2	1248	1248	1248	749	749	749	749	749	749	1160	674	674	674	674	674	674	2123	2353
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	Sequence 17, App	Sequence 17, Ap	Sequence 17, Ap	Sequence 2, Appl	Sequence 2, App	Sequence 2, App	Sequence 2, App	Sequence 2, App.	Sequence 2, Appl:	Sequence 24, Ap	Sequence 3, App.	Sequence 3, App	Sequence 3, App	Sequence 3, App	Sequence 3, App	Sequence 3, App	Sequence 10, App.	Sequence 4, Appl

RESULT

ALIGNMENTS

### US-08-728-470-9 US-08-728-470-9 Sequence 9, Application US/08728470 Patent No. 5928651 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION: TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: NAME: Berkstresser, Jerry W REGISTRATION NUMBER: 22,651 REFERENCE/DOCKET NUMBER: 103 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/728,47 ZIP: 22202 COMPOTER READABLE FORM: COMPOTER READABLE FORM: COMPOTER READABLE FORM: COMPOTER READABLE C APPLICANT: Barenkamp, Stephen J TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: STREET: 2001 Jeff STREET: Bldg. 1 CITY: Arlington STATE: Virginia COUNTRY: U.S.A. ZIP: 22202-0286 TYPE: amino acid STRANDEDNESS: si TOPOLOGY: linear FILING DATE: CLASSIFICATION: 424 LENGTH: ADDRESSEE: 1338 amino acids Shoemaker and Mattare, Ltd. 2001 Jefferson Davis Hwy., 1203 Crystal Plaza single Release #1.0, Version #1.30 US/08/728,470 9: 1038-633

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1 01-OCT-1994 (Rel. 30, Created)

T 01-OCT-1994 (Rel. 30, Last sequence update)

T 01-DEC-1998 (Rel. 37, Last annotation update)

T 15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                            EMBL; M73817; AAA23218.1; -.
PIR; A44140; A44140.
HSSP; Q06851; INBC.
InterPro; IPR001956; -.
InterPro; IPR002102; -.
Pfam; PF00942; CBD_3; 1.
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                                                                                                          Pfam; PF00942; CBD_3; 1.
Pfam; PF00963; Cohesin; 9.
Cellulose degradation; Cell
                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoseyov O., Takagi M., Goldstein M.A., Doi R.H.; "Primary sequence analysis of Clostridium cellulovorans binding protein A.";
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MEDLINE=92228810; PubMed=1565642;
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CELLULOSE BINDING PROTEIN A.

CELLULOSE-BINDING (BY SIMILARITY).

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                                                                    LFLDDTLGSQLISKDGVLATINFKAKTVTSTVTTPVAVSGTPVFAD--GTLAELQSKTVA 938
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 113.1 KDA PROTEIN IN PRE5-FET4 INTERGENIC
YMR317W OR YM9924.09.
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SEQUENCE 1140 AA; 113070 MW;
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Churcher C.M., Louis
Submitted (NOV-1995)
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochimie 73:1361-1374(1991)
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"Multiple IS insertion sequences
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TNRSSIDLGTSAKMTALRSAAGRAIYFYDP--
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EMBL; Z46259; CAA86371.1; EMBL; Z71603; CAA96259.1;

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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EGT2 PROTEIN PRECURSOR (EARLY G1 TRANSCRIPT 2
EGT2 OR YNL327W OR N0320.
                                                                                                                                                                                            between the Swiss Institute of Bioinformatics
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use by non-profit institutions as long as i
modified and this statement is not removed. Us
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Kovacech B., Nasmyth K., Schuster
"EGT2 gene transcription is induc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288C / FY1676;
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Maftahi M., Nicaud J.-M., Levesqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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P25653;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence u
15-DEC-1998 (Rel. 37, Last annotation
PACTOR INDUCED GENE 2.
FIG2 OR YCR089W OR YCR89W OR YCR1102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson C., Grisanti P., Frontali L.;
"The complete sequence of a 6146 bp fragment of cerevisiae chromosome III contains two new open Yeast 8:569-575(1992).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92397594; PubMed=1523889;
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$25345; $25345.
$0000685; FIG2.
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                           TGDMSGGAICA--YKTS-----
                                                                                         SLSSYPNFSSSEGSTATITNSTVTFGSTSKYPSTSVSNPTEASQHVSSSVNSLTDFTSNS
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8; Mismatches 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _ECOLI
                     MEDLINE=97251357; PubMed=9097039; Alba H., Baba T., Fujita K., Haya Kasai H., Kashimoto K., Kimura S.
                                                                                                                                                                                                                                                         Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                            STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
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                        a K., Hayashi K., Inada T., Isono
Kimura S., Kitakawa M., Kitagawa
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EMBL; M37
EMBL; AF1
EMBL; AJ2
Antigen;
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Mol. Immunol.
[5]
  CHAIN
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deficient in processing." Infect. Immun. 60:159-1650-1-1-FUNCTION: THE 120 KDA
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STRAIN-MADRID E;
MEDLINE-99039499; PubMed-9823893;
Andersson S.G.E., Zomorodipour A., Ar
Sicheritz-Ponten T., Alsmark U.C.M.,
Eriksson A.-S., Winkler H.H., Kurland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moron C.G., Yu X.J., Walker D.H.;
"Sequence analysis of ompB of Rickettsia prowazekii.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91045972; PubMed=2122457; Carl M., Dobson M.E., Ching W.M., Dasch G.A.; "Characterization of the gene encoding the protective paracrystalline-surface-layer protein of Rickettsia prowazekii: presence of a truncated identical homolog in Rickettsia typhi."; Proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).
                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92104668; PubMed=1729180;
Hackstadt T., Messer R., Cieplak W. Jr., Peacocl
"Evidence for proteolytic cleavage of the 120-ki
membrane protein of rickettsiae: identification
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30-MAY-2000 (Rel. 39, Last annotation update)
OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCAS) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence of Rickettsia promitochondria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia prowazekii.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites
the S-layer protein antigens of Rickettsia typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92114896; PubMed=1370573;
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FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVEREI
                                                                                                                                                                                                                                                                                                                                                                      LAYER WITH HEXAGONAL SYMMETRY.
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                                              M37647; AAA26390.1; ALT_INIT AF161079; AAD42234.1; -. AJ235273; CAA15140.1; -.
  S-layer;
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, Podowski R.M., Naeslund and C.G.;
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Local Similarity 20.7%;
nes 182; Conservative 11
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                        GGYVIGGNLHTCSDKILSAA---FCQLFGRDRDYFVAKN-QGTVYGGTLYYQHNETYISL
                                                                                                                                                                                                                                                                                                                              NLIFANGT - -
KNFFAQGNAIFTLNKVKSKSQRYFFESNGKMSKQIAAGNYDNMTFGGNLIFGYD--YNAM
                                                                             IGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRGFRHLS
                                                                                                                                   ASGTVTSTAVTPDPIMGEKFHYGYQGTWGPIVWGTGAST----TATFNWTKTGYIPNPER
                                                                                                                                                              DPSDVATFVGAIATDTSAAVTTVNLNDTQKTQDLLSNRLGTL---RYLSNAETSDVAG-S
                                                                                                                                                                                                                    NDVLNVVTTAVGNSAIANAPGVS------QNISRCLESTNTAAYNNMLLAK
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                                                                                                          ATGAVSS-----
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257
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                                                                                                          -GDEAEVSY-GVWAKPFYNIAEQDKKGGIAGYKAKTTGVVVGLDT
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V -> A (IN STRAIN BRE
Y -> D (IN STRAIN BRE
A -> S (IN STRAIN BRE
A -> VC (IN REF. 1).
TTOEAPLICA -> INGRSS
T -> I (IN REF. 1).
Q -> L (IN REF. 2).
D -> S (IN REF. 2).
T -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 223; DB 1;
Pred. No. 9.6e-05
1; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AITKSCFNNTKGDLTFT--GN------
                                                                                                                                                                                                                                                                                                     -----YTGNIIFTGEKLSETEAAD-SKNLT
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                                                    INGLSFSLY
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                                                   GSQQLV
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RESULT 9
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01-FEB-1995 (Rel. 31, I
30-MAY-2000 (Rel. 39, I
HYPOTHETICAL 99.7 KDA F
YIL169C OR YI9402.07C.
                                                                                                                                                                                                                        STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitchead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1147
                                                               EMBL;
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                  Hypothetical protein; SIGNAL 1 2
                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fung1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P40442;
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                                                  S0001431; YIL169C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQGTVYGGTLYYQHNE--TYISLPCKLRPCSLSYVPTEIPVLFSGNLSYTHTDNDLKTKY 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGIFSNSTSMIVTTKANNGTVTYLGNAFV--GNIGDSDTPVASVR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-----STKTRRG-FRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAK 700
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                                                             Z46921; CAA87023.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Ascomycota; Saccharomycotina; Saccharomycetes;
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31, Last sequence update)
39, Last annotation update)
KDA PROTEIN IN SDL1 5'REGION
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 23
995
                                 Signal.
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POTENTIAL.
HYPOTHETICAL
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   PROTEIN
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                                                                                                            http://www.isb-sib.ch/announce/
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   YIL169C
                                                                                                                                                                         EMBL outstation
                                                                                                                                                                            a collaboration
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RESULT 10
OMPB\_RICPR
ID OMPB\_R
AC Q53020
DT 30-MAY

OMPB\_RICPR STANDAR Q53020; Q9ZCM0; 30-MAY-2000 (Rel. 39,

Created)

STANDARD;

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SEQUENCE
744
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hes 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSASFDGNKNGNFSVRESQEDAGTTYLFKGNVTLENIPGTGTAITKSCFNNTKGDLTFTG
 VTSECSKETSATTASPKSYTTVTVTHCDDNGCNTKTVT
                                                                                                                 VYTTTLDYVNATSTVVVS-----CS-----ETTDS----
                                                                                                                                                                                                                                DGTTGVLTATQGNRQFSFAIGTGFSS-----SDFSVSEGIFAGAYAYYLNYNGVVATSA
                                                                                                                                                                                                                                                                                                                                                                                                                         DLGTSAKMTALRSAAGRA-IYFYDPITTGSSTTVTDVL-----KVNETPADSALQYT-G 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSFPQSTSSASTASGSATSNSLSSITSSASSASATASNSLSSSDGTIYLPTTTI-SGDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STSVVSSSGSVSISSSIAE------TSSSATDILSSITQSA-SSTSGVSSSVG
                                                        TTVPCSSTTATITSCDETG----CHVSTSTGAVVTETVSSKSYTTATVTHCDDNGCNTKT
                                                                                                                                                                         ASSSTASGASASVTGSTSFGASVTGSTAST -- SFGASVTGSTASTS-FGASVTGS---TS
                                                                                                                                                                                       TFTGQTVVFKGEGVLAVD-----PTET---NATPIPVVGYTGKNQIAITADITA--LSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTGKVIATEGVVVAAGAKLTLLDGDKYSFSADLKVYGDL--LVKKSKETYPGTEFDISGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFSRNSVNGGTAPKGGA-IAIEDSGELSLSAD---SGDIVFLGNTVTSTTPGT--NRSSI 365
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                                                                                   ----CSDKILSAAFCQLFGRDRDYFVAKNQGTVYGGTLYYQHNETYISLPCKLRPCSLSY
                                                                                                                                             IDISSLHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRGFRHLSGGYVIGGNLHT--
                                                                                                                                                                                                                                                           SGTITLLDPT-----GTFYENHSLRNPQSYDILE-----LKASGTVTSTA 558
                                                                                                                                                                                                                                                                                                                     TLQTQAFTQQADSRLEMDVGTTLEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTL 518
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73; Conservative
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21.1%;
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Pred. No. 3.1e-05;
3; Mismatches 343;
 781
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30-MAY-2000

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01-OCT-2000
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SIGNAL
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                                                                                                                                                                 MGEKFHYGYQGTWGPIV 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVAGAAVNSSVVDKSTTFIGFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSK 161
Y-2000 (Rel. 39, Created)
Y-2000 (Rel. 39, Last sequence update)
T-2000 (Rel. 40, Last annotation update)
MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
                                                                                                                                        GGDNLHIGGDGKDGVYV 552
                                                                                                                                                                                          GDAADLTALQDDPQSTVLNGGVLDLSDFSTWQSGTSYNDGLEVSGSSGTVIGSQDVVDLA
                                                                                                                                                                                                                     NHSL-----RNPQSY------
                                                                                                                                                                                                                                             -----GNVTVNQGSFAGIIEGAGQLTIAQNGSYVLAGAQSMALTGDIVVDDGAVLSLE
                                                                                                                                                                                                                                                                       PADTSTINNLVINISS ----IDGAKKAKIETK ---- ATSKNLTLSGTITLLDPTGTFYE
                                                                                                                                                                                                                                                                                                  THCQDDPQDCYGLT---IGSIDQYQNQAELNVGSTQQTFVHALTGFQNGTLNIDAG----
                                                                                                                                                                                                                                                                                                                           KLSETEAADSKNLTSKLLQPVTLSGGTLSLKHGVTLQT--QAFTQQADSRLEMDVGTTLE
                                                                                                                                                                                                                                                                                                                                                     VD---SIAGTGLITKTGSG----DLVLNADNNDFTGEMQIEN--GEVTLGRSNSLMNVGD
                                                                                                                                                                                                                                                                                                                                                                                                          GGVLVDENNSAAGYGDGPSSAAGGFMYLGLSEVTFDIADGKTLVIGNT-----ENDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGLTLFSRNSVNG---GTAPKGGAIAIEDSGELSLSADSGDIVFLGNTVTSTTPGTNRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRVTNAMFRNNIANDGKGGAIY----TINNDVYLSDVIFDNNQAYTSTSYSDGD--GGA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTVTGEYNNGGAIFAKENSTLNLT----DVIFSGNVAGGYGGAIYSSG----TNDTGAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLSGITQDWSIADGQ--WLVFSDMTNNAS-GGAVFLQQGA---EFSLLPENETGMTLFAN 102
                                                                                                                                                                                                                                                                                                                                                                              IDLGTSAKMTALRSAAGRAIYFYDPITTGSSTTVTDVLKVNETPADSALQYTGNIIFTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDVTDNNSDSKHPSGYTIVNN--TAFTNNTAEGYGGAIYTNSVTAPYLIDISVDDSYSQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICAYKTSTDTK----VTLTGNQMLLFSNNTSTTAGGAIYVKKLEL-------AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 4.8%;
Similarity 24.1%;
34; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                      STANDARD;
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LV -> PG (IN REF. 3).

S -> Q (IN REF. 3).

AG -> SA (IN REF. 3).

A -> R (IN REF. 3).

E -> S (IN REF. 3).

V -> M (IN REF. 3).

V -> M (IN REF. 3).

PP -> AT (IN REF. 3).

PP -> AT (IN REF. 3).

PAYOPVLNAKVGGYLNNLRAANQAFMMERRDHAGGDGQTLN

LRVIGG -> LLTSEC (IN REF. 4).

152 MW; 17F98C05E299FC95 CRC64;
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Pred. No. 2.4e-05;
4; Mismatches 209
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POTENTIAL.
HYPOTHETICAL PROTEIN YFAL
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                                                                      PRT;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB003681; BAA20138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN MHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-YH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; S-layer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequencing of the gene encoding the protein japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uchiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B) (CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTI (120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
 338
                                                                                                                                                                      610
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                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                          386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY). FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: CELL WALLAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATETYLDSSASFDGNKNGNFSVRESQEDAGTTYLFKGNYTLE-NIPGTGTAITKSCFNNT 80
 SLSADSGDIV-FLGN-TVTSTTPGTNRSSIDLGTSAKMTALRSAAGRAIYFYDPITTGSS
                                  NVGEGVNLYATNITTTDAN----VGSFVFNAGGKNIVS-GTVGGQQGNKFNTVAL-----
                                                                LTGNOMLLFSNNTSTTAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAIAIEDSGEL
                                                                                                   TTNAAGQGKIIF----NPVVNNNTTLAAGTN--LGSAANPLAEINFGS-----KGARADTVL
                                                                                                                                    ---SSDSGAAIFTEASVTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVT
                                                                                                                                                                      TISG-TIGIIGANNTTLGQFNIGSSKTTLNGGNVAINE--LVIGNNGSVQFAHNTYLITR
                                                                                                                                                                                       SLTGTTMSALFSENT-----SSK---KGGAIQTSDALTITGNQGEVSFSDNT-----
                                                                                                                                                                                                                                     LG-GANIISANGGTINFQANGGTIKLTSTQNNIVVDCDLAIATDQTGVVDASSLTNAQTL
                                                                                                                                                                                                                                                               TGKGA--VSCSTGSLKFDKN---VSLLFSKN-----FSTDNGGAI-----TAKTL
                                                                                                                                                                                                                                                                                                       ADGTVINGKVNQTVLVGGVLAAGAITLDGSATITGDIGNGGGGAALQSITLANDATKTLT
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528
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1656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 229.5; DB 1;
Pred. No. 4.3e-05;
0; Mismatches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 KDA SURFACE-EXPOSED 32 KDA BETA PEPTIDE. POLY-GLY.
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Matches 127
  YFAL_ECOLI S'
P45508; P45507;
01-FEB-1995 (Rel
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.

DOMAIN 166 379
SEQUENCE 881 AA; 89152 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00837; V5TPXLIKE.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
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SGD; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z49353; CAA89370.1; -. EMBL; X85502; CAA58492.1; -. EMBL; X88551; CAA61314.1; -. HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001283; - Pfam; PF00188; SCP; 1.
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                                                                                                           -----GTTLEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSTSTTSDTVST--ISSSIMPAVAQGYTTTVSSAASSSSL--KSTTINPAKTATLTASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                SCENNTKGDLTFTGNGNSLLFQTVDAG---TVAGAAVNSSVVDKSTTFIGFSSLSFIASP
                                                                                              TNCSSIVKTTTLENSSTTTITAIT-----KSTTTLATTANNSTRAATAVTIDPT
                                                                                                                                             ITSETAQASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPA
                                                                                                                                                                 KLSETEAADS - - - KNLTSKLLQPVTLSGGTLSLK-HGVTLQTQ-AFTQQADSRLEMDV - -
                                                                                                                                                                                                                                                              LTLFSRNSVNGGTAPKGGAIAIED-SGELSLSADSGDIVFLGNTVTSTTPGTNRS--SID
                                                                                                                                                                                                                                                                                          PLSST
                                                                                                                                                                                                                                                                                                              ASSSTTGDMSGGAICAYKTSTDTKVTLTGNQM---LLFSNNTSTTAGGAIYVKKLELASGG
                                                                                                                                                                                                                                                                                                                                                            SSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTG
                                                                                                                                                                                                                                                                                                                                                                                                            GSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGAITAKTLSLTGTTMSALFSENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHFTQVVWKSTAEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNFS--VRESQEDAGTTYLFKGN-----VTLENIPG------TGTAITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S0003614; YJL078C.
                                                                                                                                                                                          LGSSSRSSGAVSSSAVSQSVLNSVIAVNTDVSVTSVSSTAHTTKDTA---TTSVTASES
                                                                                                                                                                                                                LGTSAKMT - - ALRSAAGRAIYFYDPITTGSSTTVTDVLKVNETPADSALQYTGNIIFTGE
                                                                                                                                                                                                                                         -TVFSAQTTSSVSASLSSSVAADDIQGSTSKEATSS----VSEHTSIVTSATNAAQYATR
                                                                                                                                                                                                                                                                                                                                        TS---
                                                                                                                                                                                                                                                                                                                                                                                     STVITSSTESVGSSTVSSASSSSV----TTSYATSSSTVVSSDATSSTTTTSSVATSSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
  (Rel.
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                                                                                                                                                                                                                                                                                         -----LTTSTASSRSVTSNSVNSVKFANT----
 STANDARD; PRT; 1250 AA.; P4556; P77487; P4556; P39441; P76468; P77487; P131, Created) P1. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.9%;
23.6%;
                                                                                                                                                                                                                                                                                                                                      -TSSTAAASSSDPASSSAAASSSASTENAASSSSAISSSSSMVSA
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Pred.
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; 37DBAC660CA9D12A CRC64;
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No. 9.
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                                                                                                                                                                                                                                                                                       361
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  STRAIN=K12 / EMG2;
Estep P., O'Keeffe T., Political Submitted (JUN-10)
EMBL;
EMBL;
EMBL;
EMBL;
                                                                     entities re
or send an
                                                                                                                                                                                                                                                  MEDLINE=96032851;
Borodovsky M., Mc
                                                                                                                                                                                                                                                                                                 Hussain K., Elliott E.J., Salmond "The parD-mutant of Escherichia cc "The complete sequence of gyrA.", Mol. Microbiol. 1:259-273(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gregor J., Davis N.W., Kirkpatrick Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (Rel. 4
HYPOTHETICAL 131.2
                                                                                                                                                                                                                                                                                                                                                             STRAIN-OV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-K12
                                                                                                                                                                                                                     "Detection of new genes
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88201664; PubMed=2834621;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1180-1250 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia
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                                                                                                                                                                                                                                                                            DENTIFICATION
                                                                                                                                                                    MANY FRAMESHIFTS
AE000313; AAC75293.1; -.
D90855; BAA16052.1; ALT_INIT
D90854; BAA16050.1; ALT_INIT
K02672; -; NOT_ANNOTATED_CDS
U30459; AAA74094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria;
                                                                                                                                                                                                                                                   McIninch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40, Last annotation update)
2 KDA PROTEIN IN UBIG-NRDA INTERGENIC REGION
                                                                                                                                                                                                                                                              PubMed=7567469;
                                                                                                                                                                                                                                                                                                                                                                                                            Robison K.,
                                                                                                                                                                                                                                                   J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   three gene classes.";
Nucleic Acids Res. 23:3554-3562(1995).
-!- SIMILARITY: TO E.COLI YDEK.
-!- CAUTION: REF.3: SEQUENCE DIFFERS EXTENSIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H. Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K. Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
STRAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-84272624; PubMed-6087316; Carlson J., Fuchs J.A., Messing J.; Carlson J. Fuchs J.A., Messing J.; "Primary structure of the Escherichia coll ribonucleoside reductase operon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY SEQUENCE OF 1-938 FROM N.A.
equires a license agreement (; email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koonin E.V., Rudd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hackstadt T., Messer R., Cieplak W., Peacock M.G.; "Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mapping of monoclonal antibody binding sites on the S-layer protein antigens of Rickettsia typhi prowazekir";
Mol. Immunol. 29:95-105(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-WILMINGTON; MEDLINE-94040787;
                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant deficient in processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92104668; PubMed=1729180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ching W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92114896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WILMINGTON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.; "Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi."; gene 133:129-133(1993).
                230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION OF CLEAVAGE SITE
                                                                   189
                                                                                                                            130
                                                                                                                                                      737
                                                                                                                                                                                  70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. The by non-profit institutions as long if if and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ect. Immun. 60:159-165(1992).

FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNOSEN DURING INFECTION.

FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR. SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                              MIATETVLDSSASFDGNKNG------NFSVRESQEDAGTTYLFKG-NYTLENIPGTG
                                       --TLNKQGAYFGVLKQVMVSG-PGNIAFNEIGNGVAHAIAVDSISFENASLGASLFLLSG
                                                                   ENTSSKKGGAIQTSDALTITGNQGEVSFS--
                                                                                                                         SPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDN-GGAITAKTLSLTGTTMSALFS
                                                                                                                                                                                 TAITKSCFUNTKGDLTFTGUGUSLLFQTVDAGTVAGAAVUSSVVDKSTTFIGFSSLSFIA
                                                                                                                                                                                                              IVAADPINTDTALADGTNLGSAESPLSNIHFATKAANGDS-ILHIGKGVNLYANNITTTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L04661; AAB48987.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                    Conservative
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              TEASVTISN-NAK---VSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTK
                                                                                                                                                      GSLHFRSGGTSIVSGTV--GGQQGLKLNNLILDNGTTVKFLGDITF--
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                                                                                               -NGGTKIEGKSILQISSNYITDHIESADNTGTLEFVNTDPITV--
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                                                                                                                                                                                                                                                                                                                      32 KDA BETA PEPTIDE.

MEMBRANE ANCHOR (POTENTIAL):

H -> N (IN REF. 2).

V -> I (IN REF. 2).

G -> A (IN REF. 2).

G -> S (IN REF. 2).

G -> S (IN REF. 2).

MW; OCB5641C7EB185EE CRC64;
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Pred. No. 1.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell wall.
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Rickettsia
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RESULT 6
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P47033;
O1-FEB-1996 (Rel. 33
O1-FEB-1998 (Rel. 33
15-JUL-1998 (Rel. 36
                             with
                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                    1476
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             and
                                                                                                                                         STRAIN-S288C
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                                            Saccharomyces cerevisiae
                                                                          Zimmermann F.K.;
                                                                                         Miosga T., Schaaff-Gerstenschlaeger I., Chalwatzis N.,
Boles E., Fournier C., Schmitt S., Velten C., Wilhelm |
                                                                                                                       MEDLINE-96093911;
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                    YJL078C OR J1027
                                                         "Sequence analysis of a 33.1 kb fragment from the left arm
                                                                                                                                                                                                                                                                                                                                                 YJH8_YEAST
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             leucine zippers, a fungal Z
a putative alpha 2-SCB-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                  KQIAAGNYDN----ITFGGNLMFGYDYNALQGVLVTPMAGLSYLKSSNENYKETGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQHNETYISLPCKLRPCSLS-YVPTEIPVLFSGNLSYTHTDNDLKTKYTTY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLGNRL------GALRYLSNSETADVGGSETGAVSSGDEAIDQVSYGVWAKPFYNIAEQ 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKGDKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKKGGLAGYKAKTAGVVVG--LDTLANDNLMIGAAIGITKTD-----IKHQD------Y 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSTKTRRGFRHLSGGYVIGGNLHT-CSDKILSAAFCQLFGRDRDYFVAKNQGTVYGGTLY 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVPNSLWNAFIDISSLHYL--METANEG------LQGDRAF------WCAGLSNFFHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTLGAPNFDVTGNNIFVKYELIRDANQDYVLTRTNDVLNV-VTTAVGNSAIANAPGVHQN 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLSTTLNVSNGNVGQIVIAEGAQVNATTTGTTTIKIQDNANANFSGTQTYTLIQGGARFN 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSTKANQ-----GTVTYLGNALVGNIGSSDIPVASVRFTGNDSGVGLQGNI-----H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIIATNVTINDDVTLTTGGIAGTDFDGKITLGSINGNANVKFVDRTFSHPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAICLESTDTAAYNNMLLAKDSSDVATFIGAIATDTGAA-VATVNLNDT------QKTQD 1322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PTVKGSWGNDSFALEFGGRAPICLDESALFEQYM-PFMKLQFVYAHQEGFKEQGT
putative alpha 2
11:681-689(1995)
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                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DIKGLSFSLYGAQQLVKNFFAQGSAIFTLNKVKSKSQRYFFDANGKMN
                                                                                                                        PubMed=7483841;
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36,
8DA
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                                                                                                                                                                                                                      Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
PROTEIN IN SCP160-SMC
                                                                                                                                                                                                                                                                                                                   Created)
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             e chromosome X, including putative proteins
fungal Zn(II)2-Cys6 binuclear cluster doma
SCB-alpha 2 binding site.";
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Query Match Best Local Similarity

5.0%; 24.8%;

Score 240.5; Pred. No. 5.4

.5; DB 1; 5.4e-06;

Length

35;

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SLAP_CAUCR
P35828; Q46015;
01-JUN-1994 (Rel. 2
01-OCT-1994 (Rel. 3
30-MAY-2000 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FINAL CB15;
STRAIN-ATCC 19089 / CB15;
MEDLINE-93007489; PubMed=1393820;
MEDLINE-93007489; PubMed=1393820;
Glichrist A., Fisher J.A., Smit J.K.;
Glichrist A., Fisher J.A., Smit J.K.;
Glichrist A., Fisher J.A., Smit J.K.;
Crescentus paracrystalline surface layer protein.";
crescentus paracrystalline surface layer protein.";
microbiol. 38:193-202(1992).
                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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               Cell wall; INIT_MET
                                      Pfam; PF00353; hemolysinCabind; PRINTS; PR00313; CABNDNGRPT.
                                                                            EMBL; AF062345; AAC38665.1; HSSP; P01549; 2MCM.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CB
                                                                                                                                                                                                                                                                                                                                                                                                                                        Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fisher J.A., Smit J.K., Agabian N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE STRAIN-ATCC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
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                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98292737; PubMed=9620954;
                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Transcriptional analysis of the major Caulobacter crescentus.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89008089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=76;
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                                                                                                                                                                                                                           SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                IPR001343;
                                                                                                                                                                                                                                                                                                                                                          Smit J.K.;
               s-layer;
 1025 AA;
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1. 30, Last sequence update)
1. 39, Last annotation update)
1. 39, Last annotation update)
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                          Calcium-binding
98209 MW;
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AFC8B519820B1A5F CRC64;
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                                         P96589;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0UTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGE)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGE)
            Rickettsia typhi.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
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   CHAIN
                              Antigen; Repeat; Signal; SIGNAL 1 28
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                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeated, near-identical sequences.";
Infect. Immun. 58:2760-2769(1990).
-i- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
190 KDA ANTIGEN PRECURSOR (CELL SURFACE ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
"A protective protein antigen of Rickettsia rickettsii has tandemly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90354033; PubMed=2117568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: GLYCOSYLATED (POSSIBLE).
DISEASE: PROBABLY PLAYS AN IMPORTANT ROLE IN THE PATHOGENESIS AND IMMUNITY TO ROCKY MOUNTAIN SPOTTED FEVER.
                                                                                                 ; M31227; AAA26380.1; A41477; A41477.
                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Furobean Bioinformatics Institute There are no restrictions on its
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S-layer; Glycoprotein POTENTIAL.
190 KDA ANTIGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 VTFTN-PVVVTGAIDNTGNANNGIVTFTGNSTVTGDIGNTNALATVNVG--AGTATLGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VTLENIPGTGTAITKSCFNNTKGDLTFTGN-----GNSLLFQTVDAGTVAGAAVNSSV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                TNSLATISYGA-GTATLGGAVIKATTTKLTDAASAVKF-----TNPVV-VTGAIDNTG
                                                                                                                                             PQSYDILELKASGTVT-----STAVTPDPIMGEKFHYGYQGTWGPIVWGTGA-----
                                                                                                                                                                         GGAVIKATTTKLTNAASVLT-LTNANAVLTGAIDNTTGGDNVGVLNLNGALSQVTGDIGN
                                                                                                                                                                                                                                                             EAADSKNLTSKLLQPVTLSGGTLSLKHGVTLQTQAFTQQADSRLEMDVGTTLEPADTSTI
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                                                       NANNGIVTFTGNSTVTGNVGNTNALATVNVGAGLLQVQGGVVKANTINLTDNASAVTFTN
                                                                                                                                                                                                    NNLVINISSIDGAKKAKIETKATSKNLTLSGTI---TLLDPTGTFYENHSLR-----N
                                                                                                                                                                                                                                  TGGDNV------GVLNL-NGALSQVTGDIGNTNSLATISVG-----AGTATL
                                                                                                                                                                                                                                                                                          NSLATISVGAGTA-----TLGGAVIKATTTKL--TNAASVLTLTNANAVLTG-AVDNT
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A (TYPE I).

B (TYPE II).

C (TYPE II).

C (TYPE II).

C (TYPE I).

E (TYPE I).

E (TYPE I).

F (TYPE I).

G (TYPE I).

I (TYPE I).

J (TYPE I).

I (TYPE I).
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Pred. No. 1.2e-06;
O; Mismatches 325;
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M (TYPE II).
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                                                                                    ----GSLVPNSLWNAFIDISSLHYLM
   -GNV - -GNTNALATVNVGA
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CHILTR STANDARD; PRT; 1034 An.
0MOE CHITR STANDARD; PRT; 1034 An.
03008; 084878;
01-CCT-1994 (Rel. 30, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 Rel. 39, Last annotation update
                        Stephens R.S., Kalman S., Lammel C.J., For Mitchell W.P., Olinger L., Tatusov R.L.,
                                                SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
PubMed=9784136;
                                                                                                      Chlamydia trachomatis.
Bacteria; Chlamydiales;
NCBI_TaxID=813;
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obligate
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pathogen
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SEQUENCE
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Outer membrane; Signal.
25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-L2/434/BU;
Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.
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Science 282:754-759(1998).
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                                                                                                                                      TLEPADTSTIN----NLVINISSIDGAKKAKIE-----TKATSKNLTLSGTITLLDPTG
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Pred. No. 4.3e-19;
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Result
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Maximum Match 100%
Listing first 45 summaries
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FIG2_YEAST
YDBA_ECOLI
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120K_RICRI
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OMPB_RICRI

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OMPF_CHLTR
190K_RICRI
SLAP_CAUCR
OMPB_RICTY
YJH8_YEAST
YFAL_ECOLI
  APMU_PIG
SLAP_CAMFE
TROP_HUMAN
YS8A_CAEEL
N100_YEAST
YQU3_CAEEL
ICEA_PANAN
MUC4_HUMAN
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p15921 rickettsia
p35828 caulobacter
p96989 r outer mem
p47033 saccharomyc
p4508 escherichia
006653 r outer mem
p40442 saccharomyc
p35653 saccharomyc
p35656 escherichia
p42835 saccharomyc
p3020 r outer mem
p3293 saccharomyc
p3658 clostridium
p32323 saccharomyc
p14914 rickettsia
p42916 escherichia
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P33924 escherichia			P47179 saccharomyc	P08640 sacc	P28968 equi	P32051 esch		P12255 bord	Q10168 schizosacch		P03764 bacteriopha

## ALIGNMENTS

Db Qy	Db 09	Db Qy	W W S	SOFT	88888888	CCCRRRRRRRRRR CCCCRTT	RESUI OMPE AC DT DT DT DT OS OS
169 GAI-TAKTLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNOGEVSFSDNTSS 222	118 TFIGFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNG 168	62 LENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDKST 117  :	Query Match 11.3%; Score 540.5; DB 1; Length 964; Best Local Similarity 25.4%; Pred. No. 1.4e-22; Matches 244; Conservative 138; Mismatches 402; Indels 175; Gaps 46;	1360; AAC68467.1; rane; Signal.	his SWISS-PROT entry is copyright. It is produced throuetween the Swiss Institute of Bioinformatics and the he European Bioinformatics Institute. There are no rese by non-profit institutions as long as its contendified and this statement is not removed. Usage by notities requires a license agreement (See http://www.isr.send.an email to license@isb-sib.ch).	STRAINED/JUW-3/CX; STRAINED/JUW-3/CX; STRAINED/JUW-3/CX; Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.; "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."; Science 282:754-759(1998)1- SUBCELJULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).	CHLTR CHLTR OMPE_CHLT 084877; 30-MAY-20 30-MAY-20 30-MAY-20 PUTATIVE PMPE OR C Chlamydia Bacteria; NCBL Taxxi

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EMBL; AJ133035; CAB37083.1;
EMBL; AE002235; AAF38561.1;
TIGR; CP0761;
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.,
McClarty G., Salzberg S.L., Elsen J., Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99206606; PubMed-10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
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01-MAY-1999 (TremBLrel. 10, Last sequence update)
01-MAR-2001 (TremBLrel. 16, Last annotation update)
0UTER MEMBRANE PROTEIN 7 (POLYMORPHIC MEMBRANE PROTEIN G FAMILY).
0MP7 OR PMP_2 OR CP0761.
                     12 TFAIFPLSMIATETVLDSSASFDG-NKNGNESVRESQEDAGTTYLFKGNVTLENIPGTGT 70
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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TLSMSNILGAATTEELSASNSFDGTTSTSFSSKTSSATDGTNYVFKDSVVIENVPKTGE 74
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	ILARQA 886        LARQA 799		
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                                                MEDLINE=96406378; Pubmed=8810511;
                                                                                            Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlam
                                                                                                              POMP91B PRECURSOR.
              Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring "Identification of a multigene family coding for the 90 kDa p of the ovine abortion subtype of Chlamydia psittaci."; FEMS Microbiol. Lett. 142:277-281(1996).
                                                                    SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=83554;
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MEDLINE=98187897; PubMed=9529048;
Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
Molecular cloning and characterization of the genes coding for the
"Molecular cloning and characterization envelope proteins from t
highly immunogenic cluster of 90-kilodalton envelope proteins from t
chlamydia psittaci subtype that causes abortion in sheep.";
Infect. Immun. 66:1317-1324(1998).
EMBL; U65943; AAC1593.1; -.
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                                                                                                                                            ---TATTSSSTVTPPETNLKNYTPPTHYGYQGAW-TVTWKQGSSAQEKTATLTWEQTGYS
                LPCKLRPCSLSYVPT-----
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846
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--ISYMNTWNTLLQNTLGAEAPLVLNAQLTYCHASNNMKTNMTNTYTPKNVTP
                                                                                                                                                                                                                                                                                             16 P
846 P
90834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. POMP91B.
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                   -EIPVLFSGNLSYTHTDNDLKTKYT-----
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Query Match 34.5%; Sometimes 34.2%; Property Matches 380; Conservative 132;
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Submitted (CCT-1996) to the
EMBL; U65943; AAC15924.1; -.
EMBL; U65942; AAC15922.1; -.
Interpro; IPR003357; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003368; - Pfam; PF02385; OMP; 1. Pfam; PF02415; DUF145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-OVINE ENZOOTIC ABORTION ISOLATE S26/3;
Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
[2]
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                                                         STKTRRGERHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGTVYGGTLYYQ
                                                                                                                                       WTKTGYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRAFWCAGLSNFFHKD
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|KLSDEEKARAENLASTFNQPITLSAGSLVLKDGVSVTAKQVTQEAGSTVVMDLGTTLQTP
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HNETYISLPCKLRPCSLSYVPTEIPVLFSGNLSYTHTDNDLKT--
                                  GSDTKRKFRHNSAGYALGVYAKTPSDDIFSAAFCQLFGKDKDYLVSKNNANIYAGSLYYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                    IDLGT-GKFTKLRAKDGFGIFFYDPITGGGS----DELNINK---KETVDYTGKIVFSGE
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839 F
89824 MW;
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POMP90B.
4581C7CBAF7FF4C4
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Matches 376
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P71132;
01-FEB-1997 (TrEMBLrel. 02, 0
01-FEB-1997 (TrEMBLrel. 02, 1
01-MAR-2001 (TrEMBLrel. 16, 1
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Pfam; PF02415; DUF1
SEQUENCE 847 AA;
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"Identification of a multigene family coding for the 9
of the owine abortion subtype of Chlamydia psittaci.";
FEMS Microbiol. Lett. 142:277-281(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-OVINE ENZOOTIC ABORTION ISOLATE MEDLINE=96406378; PubMed=8810511;
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                                                                                                                                                              LDISGFSLFSCAYCPPGA--TGYGAIK-AVGNTTIKDNSSLVFHKNCSTGEGGAIQCKAS
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SNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVTLTGNOMLLFSNNTSTTAGG
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DUF145; 1.
AA; 90694
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Pred. No. 6.76
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90 kDa protei
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                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Read T.D., Brunham R.C., Shen C., Gill.S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.", Nucleic Acids Res. 28:1397-1406(2000).
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Q9K299;
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Pfam; PF02415; DUF145; 1.
SEQUENCE 949 AA; 101357 MW;
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           GNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDKST 117
                                                               MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTS----ATTYSLT
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Pred. No. 3.6e-98;
71; Mismatches 332
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Chlamydia psittaci (Chlamydophila psittaci)
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SEQUENCE FROM NCBI\_TaxID=83554;

Chlamydiaceae; Chlamydophila

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01-MAR-2001 (TrEMBLrel. 16, Last an
OUTER MEMBRANE PROTEIN 4 PRECURSOR.
                                                                STRAIN-CDC/CWL-029/VR-1310;
Knudsen K., Madsen A.S., Mygind P.,
"Identification of two novel genes (
associated surface layer proteins in
 STRAIN-VR1310;
Hjerno K., Boe
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Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi Shiba T., IShii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
EMBL; AJ001311; CAA04672.1; -.
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Kalman S., Mitchell W., Marathe R., Lammel C., Fan o
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C.
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InterPro; IPR003368; -.
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Pfam; PF02415; DUF145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hjerno K., Boesen T., Daugaard L., Knudsen K., Christiansen G., Birkelund S.;
"Chlamydia proteins containing the GGAI-repeat of autotransporting pathogenicity factors."; submitted (JAN-1999) to the EMBL/GenBank/DDBJ dEMBL; AE001627; AD118590.1; -
EMBL; AE001627; AD11850.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; "Ast. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae (Cl
Bacteria; Chlamydiales;
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OUTER MEMBRANE PROTEIN
OMP11 OR PMP_8.
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                                                                                                                                                                                                                   GSTLLMQPGTKLK-ADTEAISLTKLVVDLSALEGNKSVSIETAGANKTITLTSPLVFQDS
                     DSRLEMDVGTTLEPADTSTIN--NLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDP
                                                                DSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPYTLSGGTLSLKHGYTLQTQAFTQQA
                                                                                                  TSTT-PGTNRSSIDLGTSAKMTALRSAAGRAIYFYDPI---TTGSSTTVTDVLKVNETPA
                                                                                                                                                       QGGAICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIAIADSGSLSLSANQGDITFLGNTL
                                                                                                                                                                    AGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAIAIEDSGELSLSADSGDIVFLGNTV
                                                                                                                                                                                                        SITQNSSLFFSGNTATDAAG-----KGGAIYCEKTGETPTLTISGNKSLTFAENSSVT
                                                 NSPLDYSGTIVFSGEKLSADEAKAADNFTSILKQPLALASGTLALKGNVELDVNGFTQTE
                                                                                                                                                                                                                                                         KTLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFTEAS
                                                                                                                                                                                                                                                                                                               LTFTGFSNLSFIAAPGTTVASGKSTLS-SAGALNLTDNGTILFSQNVSNEANNNGGAITT
                                                                                                                                                                                                                                                                                                                           TTFIGESSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTD---NGGAITA 173
                                                                                                                                                                                                                                                                                                                                                                                KGNYTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDKS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                            MKSSFPKFVFSTFAIFPLSM-IAT---ETVLDSSASFDGNKNGNFSVRESQEDAGTTYLF
                                                                                                                                                                                                                                                                                                                                                                 SGNVYI-NDAGKGTALTGCCFTETTGDLTFTGKGYSFSFNTVDAGSNAGAAA-STTADKA
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930
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DUF145; 1.
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es; Chlamydiaceae; Chlamydophila
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Pred. No. 2
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OUTER MEMBRANE PROTEIN 11
, 46A9B5E3BB913C4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Best Local Similarity
Matches 409; Conserv
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PRELIMINARY;
P71135;
P71135;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence upda:
01-MAR-2001 (TrEMBLrel. 16, Last annotation upo
PUTATIVE 98 KDA OUTER MEMBRANE PROTEIN.
Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamyd.
NCBI_TaxID-83554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-OVINE ABORTION $26/3;
Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U7249; AABIB188:1; -.
InterPro; IPR003357; -.
InterPro; IPR00336; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
SEQUENCE 926 AA; 98439 MW; 3E755E52F594750F CRC64;
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170
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ISCKAFSLTGSSKEISFTTNSTAKKGGAIAATGIAHLSDNQGTIRFSGNTAVNSGGAVYS
                             NTADKILTLTDFSKLSFKECPSSLVNTGKGAMK-SGGALNLANNASILFDQNYSAENGGA
                                                                                                                                        SVVDKSTTFIGFSSLSFIASPGSSITTGKGAVSCSTGSLKFDKNVSLLFSKNFSTDNGGA
                                                                                                                                                                                                                       GTIYNVESDISIVDV-GQTAALASSAFVQTADNLTFKGNNHSLSITNANAG-ANPAGINV
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2.4e-101;
hes 335;
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O9RB66;
O1-MAY-2000 (TrEMBLrel. 13, C
O1-MAY-2000 (TrEMBLrel. 13, L
O1-MAR-2001 (TrEMBLrel. 16, L
POLYMORPHIC OUTER MEMBRANE PR
                                                                                                                                                                                                                                                                                                             MEDLINE-20150255; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
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                                                                                                         Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
SEQUENCE 930 AA; 97639
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Bacteria: Chlamydiales; Chlamydiaceae; Chlamydop
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POLYMORPHIC OUTER MEMBRANE PROPOTEIN G FAMILY).

PMP_7 OR CP0308.

Chlamydia pneumoniae (Chlamydia Bacteria; Chlamydiales; Chlamydiales)
SEQUENCE FROM N.A
                         NCBI_TaxID=83558;
[1]
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                                                                     (Chlamydophila pneumoniae)
es; Chlamydiaceae; Chlamydo
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, Last annotation update)
PROTEIN G FAMILY (POLYMORPHIC MEMBRANE
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.,
McClarty G., Salzberg S.L., Elsen J., Fraser C.M.,
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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MEDLINE-20330349; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F.,
Shirai M., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumo
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
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Nucleic Acids Res. 28:1397-1406(2000).
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Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
ProDom; PD004952; -; 1.
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                                      GGAIYVKKLELASGGLTLFSRNSVNGGTAPK--GGAIAIEDSGELSLSADSGDIVFLGNT
                                                     LEMDVGTTLEPADTS-TINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTF
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Pred. No. 9.7e-104;
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EMBL; AJ133034; CAB37069.1;
EMBL; AP002546; BAA98655.1;
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Nucleic Acids Res. 28:1397-1406(2000).
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                      TAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAIAIEDSGELSLSADSGDIVELGNT
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SFISSNKAISFINNSVTATSA-----TGGAIYCSSTSAPKPVLTLSDNGELNFIGNTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                  SSISLS-LNPNLTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAANNGGAIYTEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNLTGDVSITN-AGSPTALTASCFKETTGNLSFQGHGYQFLLQNIDAG--ANCTETNTAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLFKGNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKSSLHWFLISSSLALPLSLNFSAFAAVVEINLGPTNSFSG--PGTYTPPAQTTNADGTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE002192; AAF38163.1; CP0306; -.
                                                                                                                                                                                                                  {\tt TSGGAIYTDNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLSALGGDITFEGNT}
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928 AA;
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928 O
98332 MW;
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45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %; Score 1977; DB 2;
%; Pred. No. 2.7e-105;
149; Mismatches 329;
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; 58910A8F04F12219 CRC64;
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                                                                                                                                                                                                                Matches
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EMBL; AE001627; AAD18589.1; -.
InterPro; IPR003357; -.
InterPro; IPR003358; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
SEQUENCE 936 AA; 100079 MW; 8
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Q9Z898;
Q12898;
Q12898;
Q13898;
Q14899;
Q15899;
Q1589
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Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalman S., Mitchell W., Marathe R., Lammel C., Folinger L., Grimwood J., Davis R.W., Stephens R. Comparative genomes of Chlamydia pneumoniae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-CWL029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=83558;
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EGISNFFHKDSTKINKGFRHISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKNRA
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                                                                                                                                    MKSSFPKFVFSTFAIF-PLSMIATETVLDSS-ASFDGNKNGNFSVRESQE-DAGTTYLFK
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SDYSFQNAGALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSSAGTVASTSAADKNL 120
                                                  GNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDKST 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTNLARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF 928
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                                                                                                           MKSSVSWLFFSSIPLFSSLSIVAAEVTLDSSNNSYDGSNGTTFTVFSTTDAAAGTTYSLL
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                                                                                                                                                                                                          h 40.8%; Score 1951; DB 2; Similarity 43.1%; Pred. No. 8.5e-104; 08; Conservative 179; Mismatches 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Chlamydophila pn
es; Chlamydiaceae;
                                                                                                                                                                                                                                                                                                                                                    8881D78A53D194EC CRC64;
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me; Chlamydophila
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Best Local (
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O86163;
O1-NOV-1998
O1-NOV-1998
O1-MAR-2001
                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
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01-NOV-1998 (TrEMBLrel. 08, Last sequence upda:
01-MAR-2001 (TrEMBLrel. 16, Last annotation upo
OUTER MEMBRANE PROTEIN 5 PRECURSOR (FRAGMENT).
OMP5.
                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            STRAIN-CDC/CWL-029/VR-1310;
Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelu "Identification of two novel genes encoding outer membrane coassociated surface layer proteins in Chlamydia pneumoniae.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001311; CAA04671.1; -.
InterPro; IPR003357; -.
InterPro; IPR003368; -.
                                                                                                                                                                                                                                                                                                                            Pfam; PF02385; Pfam; PF02415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydop
                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                              Local Similarity
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                                                                                   MKSSFPKFVF-STFAIF---PLSMIATETVLDSSASFDGNKN-GNFSVRESQEDAGTTYL
TGNCTITGNTSLVFSENSVT----ATAG--NGGAL----SGDADVTISGNQSVTFSGNQ
                    EASYTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLFSNNT
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Q9Z398;
                                                            MEDLINE-99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., I Olinger L., Grimwood J., Davis R.W., "Comparative genomes of Chlamydia pna Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN PRECURSOR (POLYMORPHIC MEMBRANE
                                         SEQUENCE FROM N.A.
                                                                                                                    STRAIN=CWL029;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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                                                                                                                                                                                    Q9RB65 PRELIMINARY; PRT; 928 AA.
Q9RB65; Q9RB64; Q9S6P2;
01-MAY-2000 (TrembLrel. 13, Created)
01-OCT-2000 (TrembLrel. 15, Last sequence update)
01-MAR-2001 (TrembLrel. 16, Last annotation update)
POLYMORPHIC OUTER MEMBRANE PROTEIN G FAMILY (OUTER MEMBRANE PROTEIN G FAMILY).
PRECURSOR) (POLYMORPHIC MEMBRANE PROTEIN G FAMILY).
PMP_10 OR OMP5 OR CP0303.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
Hjerno K., Boesen T., Daugaard L.,
Christiansen G., Birkelund S.;
"Chlamydia proteins containing the
of autotransporting pathogenicity f
                                               STRAIN-VR1310;
                                                        SEQUENCE FROM N.A.
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Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AP002546; BAA98657.1; -.
EMBL; AJ133034; CAB37071.1; -.
EMBL; AE002192; AAF38160.1; -.
TIGR; CP0303; -.
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.
Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.
McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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                                                                                         PTGTTYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEKFHYGYQGTWGPIVW----
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                                                                                                                                                                                 PADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGGTLSLKHGVTLQTQAFTQ
                                                                                                                                                                                                                                                              AVANGGAIYAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITF
                                                                                                                                                                                                                                                                             STTAGGAIYVKKLELAS--GGLTLFSRNSVNGGTAPKGGAIAIEDSGELSLSADSGDIVF
                                                                                                                                                                                                                                                                                                                        KNLSLKNSTGSISFEGNKSSATGKKGGAICATGTYDITNNTAPTLFSNNIAEAAGGAINS
                                                                                                                                                                                                                                                                                                                                                                     KTLSLTGTTMSALFSENTSS---KKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNT--TTGIDYT
                                            -GTGASTTATENWTKTGYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRAF
                                                                              NQGNAYENHDLGKTQDFSFVQLSALGTATTTDVPAVPTVATPTHYGYQGTWG
                                                                                                                           {\tt TAGSSVIMDAGTTLKASTEEVTLTGLSIPVDSLGEGKKVVIAASAASKNVALSGPILLLD}
                                                                                                                                                                                                                                                                                                             TGNCTITGNTSLVFSENSVT----ATAG--NGGAL----SGDADVTISGNQSVTFSGNQ
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Pred. No. 1.5e-110;
1; Mismatches 319;
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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O9rb71 chlamydia
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O9z398 chlamydia
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O9z542 chlamydia
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O9rb69 chlamydia
P71135 chlamydia
O9k299 chlamydia
P71132 chlamydia
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01-MAR-2001
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PMP_3.

Chlamydia pneumoniae (Chlamydophila pneumoniae).

Bacteria; Chlamydiales; Chlamydiaceae; Chlamydop

NCBI_TaxID=83558;
                                                                                                                                                                                                InterPro; IPR003368; -. Pfam; PF02385; OMP; 1. Pfam; PF02415; DUF145; SEQUENCE 772 AA; 829
                                                                                                                                                                                                                                                                          Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                   EMBL; AP002545; BAA98226.1; -. InterPro; IPR003357; -.
                                                                                                                                                                                                                                                                                                                                             STRAIN=J138; MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
 277 TLTGNQMLLFSNNTSTTAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAIAIEDSGE 336
                                                                                           61
                                         SDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKV 276
                            SDNTSSDSGAAIFTEASYTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKV
                                                                              MLFSKNFSTDNGGAITAKTLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSF
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2 AA; 82931 MW;
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99.9%;
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Last sequence update)
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Pred. No. 9.5e-221;
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                                                                                                                                                                                                                                                      AAATAGCTTCTTCGAAAGCTCTAGTGATGGCCGTGGTTTTAGTATTGGAAGGCTGCTTAA 2684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTATAGAAAAATTCCCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAG 2444
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                                                                                                                                           CCTCTCGATTCCTGTGGGTGCGAAATTCGTGCAGGGGGATATCGGAGATTCCTACACCTA 2744
                                                                                                                                                                                                                                                                                                                            TOGGTCTTGGGTGGATACCCACACGCCATTTCTAAACCTAGAGATGATCTATGCACATCA 26483
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TGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTAATGATCCAGGCTGCACGACAAC 26657
                                                                                                           TCTAGCGGTTCCTGTAGGGATAAAATT----TGAGAAATTCTCCGATAAGTCTACGTA
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Search completed: October 2, 2001, 00:28:56 Job time: 42409 sec

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Query Match 14.8
Best Local Similarity 51.3
Matches 1388; Conservative
                                                                                                                                 24447 TICTGGGATTACGAAATTCTCAGGATTTTCAACTCTTCGGATGCTTGCAGCTCCTAG--- 24503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24207
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AACGGTTACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATAT
                                                                                                                                                                                                                                                                                                                                                                          AACGTTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCTG---CATCTACAACAGC 533
                                                                                                                                                                                                                           AAATAAGAATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCTCCTAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGACAGTTGTTTTAAGCAAACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACATATTCTCTAACAGGAGATGTCTTCTTTTACGAGCCTGGAAAAGGCACTCCCTTATC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTGATACAAGCACCACAGAATTTACTCCTAAAGCGGCAACTTCTGATGCTAGTGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATGATAGCTTTAATGGAAATATCGATTCAGGAACGTTTACTCCAAAAACTTCAGCCAC 356
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ARDRLTDQSSKENQKELEKAEQEYISSWERVKKFEIERVQERIQAIQKLYPNILEREE
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DPRFQDSDTQLRALTIRLQEAKASLEEEIKRFSNLENDIAEERRLLKESKQTFERAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIEMTLRMVELPLLFMKNTFEKASLQYNSCKEMLAKVEPQCKESPTYRSSQERLERLN
QDLQTAYTNCQERLQGFSDLESKVRTCRDHLREQMKHFEVQGLNFINEELLMVGAELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFYECEKAKIQRDGRFKWL<sup>®</sup>
11485. ,12792
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LKRSVKEVMDRFMRVTWKSWEASVMLDHSYGVARELFKKAVGVLEESVYKILFKSYRD
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13104 15428
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Pred. No. 1e-89;
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B 8	654 24558	TGTAAACTTGTAGTTGCTGGGAATTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGC 713	17
ΔÃ	71	CTTTCCTTTTAACTGCACTTCTGGAGATGCTCTTTTTAGTAACACTCTTCATCAAC 77	
DЪ	24618		77
Qy	774	AAAGGGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACACAGGTTATGT 833	
DЬ	24678	ACAAGGGGGAGCGATCTATGCTTCTGGTGACTCTGTGATTTCTGAGAATGCAGGAATCTT 247	37
Q <sub>Y</sub>	8.	AGATTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTC 893	
DЬ	24738	AACAGTGCGACAACATCAGGAGGCGCGATCTCTGCTGAAGGGAACCT 247	9/
, 04	. 89	ATACTATCGAACAACTATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGG 95	,
₽	24798	ATCTCCAATAACCAAAATATCTTTTTCGATGGCTGCAAAGCAACTACAAATGGCGG 2	7
Qy	95	10	_
B	24858	AGCTATTGATTGTAACAAAGCAGGGGCGAACCCCAGACCCTATCTTGACTCTTCAGGAAA 249	17
Qy	1008	TAAGACTCTGATCTTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	7
망	24918	GAGAGCCTGCATTTTCTGAATAACACAGCAGGAAATAGTGGAGGTGCGATTTATACCAA 249	77
Qy	1068	AAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATC 1124	
ઠ	24978	AAAATTGGTGTTATCCTCAGGACGAGGAGGAGGGTGTTATTTTCTAACAACAAGCTGCGAA 2503	7
Qy	1125	AGCAACTCCTAAGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGC 1184	
В	25038	TGCTACTCCTAAAGGAGGGGCAATTGCGATTCTAGATTCTGGAGAGATTAGCATTTCTGC 2509	7
Qy	1185	AGACAGGAAACATT	-
Db	25098	TCGAGGGCAATACTACGAGCACTACAGGAA	7
Qy	1245	GGCTGC 130	
Ę	0CTC2	MIGCININGNICIIGCNICGNNIGCNNNNIIIIINNNICICCGNGCGNC 232	-
Qy	13	AAAAATCATACAATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCAGACGT 13	
Db	25218		14
Qy	1365	ATTGAAGATAAATAACGGCTCTGCGGGGAGCTCTCAATCCATATCAAGGAACGATTCTATT 1424	
Ъ	25275	GCTCTCTTTGAATAAAGCTGACGCAGGATCTGGAAATACCTATGAAGGCTACATCGTTTT 253	34
Qy	1425	TTCTGGAGAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATT 1484	
DЪ	25335	CTCTGGAGAGAACTCTCAGAAGTAAGAAACCTGACAATCTGAAGTCTACATT 2538	7
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Qy	1545	TCAAGAGGCCGGTTCTCTCTCCTCGGCATGGATTCAGGAAC	
В	25448	T 255	07
Qy	1605	CTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGA	
В	25508	TGAGGCAAGCGCTGAGGGGGTCACTCTCAATGGCCTAGCCATTAATATAGATTCCTTAGA 2556	7
Qγ	1665	TCAGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATCTG	
В	25568	GGGACAAATAAAGCTATCATTAAGGCGACGGCAGCAAGTAAGGATGTTGCCTT	7

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JOURNAL
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Direct Submission

Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.

Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.

Mutsunori Shirai, Yamaguchi University School of Medicine,

Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
755-8805, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,

Tel:81-836-22-2227, Fax:81-836-22-2415)

On Aug 31, 2000 this sequence version replaced gi:6172286
gi:6172388 gi:6172310 gi:6172312 gi:6172314 gi:6177316 gi:6172318
gi:6172320 gi:6172312 gi:6172314 gi:6635160 gi:6635162
gi:6635164 gi:6635166 gi:6635168 gi:6635170 gi:6635172 gi:8547422
gi:8547426 gi:8547430 gi:8978373
AB033780-AB033781, AB033792-AB033799: Submitted (14-Feb-2000)

AB03671-AB03678: Submitted (18-Dec-2000).
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NUCLEIC Acids Res. 28 (12), 2311-2314 (2000)
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Chlamydophila pneumoniae J138
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene=
                                                                                                                                                             /product="Glu tRNA Gln amidotransferae (A subunit)"
/protein_id="BAA98213.1"
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KHQIRVVRSSLKAMVPEFLDIRRIFEEEEEFFFLSARKRLIDLATTLVERKILTEQLER NNLRKAFSYLYQDSIFKKIIDNFEKLAWKFMILSKSICRFTIIFENHEHGVAKSLLHK

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2144	2085 TATIGGAACACAAACAAGGTTTCCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGG	Qy
4204	2023 ATGGGGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGG	B 5
2024 4264	965 GACCAAAACAGGATTTGTTCCCAGCCCCGAAAGAAAATCTGCGTTAGTATGCAATACCC	Db Qy
1964 4324	1905 ATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTG	DЪ
1904 4384	1845 CAGCAGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACA	DP QV
1844 4433	CAGCTCTTC	Db Qy
1784 4493	1725 GAAGCTCAACCTGATTGATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGA	Db Qy
1724 4553	1665 TCTTAAGCAGCCCGTCAGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATCTGG	р V
1664 4613	1605 ATCAACTACAGCTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGG	Дb
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1424 4846	1365 ATTGAAGATAAATAACGGCTCTGCGGAGCTCTCAATCCATATCAAGGAACGATTCTATT	рь
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1184 5083	1125 AGCAACTCCTAAGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGC	Db Oy
1124 5143	1068 AAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCCATC	Qy db
5203		Db

VERSION

ACCESSION

AP002545 299650 bp DNA BCT 08-DEC-2000 (Chlamydophila pneumoniae J138 genomic DNA, complete sequence, section 1/4. AB033781 AB033792 AB033793 AB033794 AB033795 AB033796 AB033797 AB033798 AB033799 AB036071 AB036072 AB036073 AB036075 AB036076 AB036076 AB036076 AB036078 AB038345 AB038346 AB038347 BA000008

e,	AP002545 299650 bp DNA BCT 08-DEC-200 Chlamydophila pneumoniae J138 genomic DNA, complete sequence section 1/4.	SULT 15 002545 . CUS FINITION	RESULT AP0025, LOCUS DEFINIT
	ATTITA 3337	3342	Db
	ATTCTA 2990	2985	Qy
3343		3402	뫄
2984	CGCTATGGAACTCCGTGGATCTTCAAGGAACTACAATGTAGATGTTGGTACCAAACTCCG	2925	Qy
3403	TCTTGTACGTGCTGGAAATCATGCCTTTGCTTCAAACTTTGAAGTTTTCAGTCAG	3462	Db
2924	ATTA	2865	Qy
3463		3522	Ър
2864	- 13	2805	Qy
3523		3582	DЬ
2804	TGATCTCTCAGGATTCTTTGTTTCCGATGTCTATCGTAACAATCCCCAATCTACAGCGAC	2745	Qy
3583	CCTAGCGGTTCCTGTAGGGATAAAATTTGAGAAATTCTCCGATAAGTCTACGTA	3636	Db
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3637	GAATGACTTTAAGGAAAACGGCACAGAAGGCCGTTCTTTCCAAAGTGAAGACCTCTTCAA	3696	ДЪ
2684		2625	Qy
3697	TCGGTCTTGGGTGGATACCCCACACGCCATTTCTAAACCTAGAGATGATCTATGCACATCA	3756	В
2624	- >	2565	Qy
3757	GGACG	3816	рь
2564		2505	Qy
3817	CCATACCGACAATAACATGACCACAAAGTACACTGGCTATTCTCCTGTTAAGGGAAGCTG	3876	дь
2504		2445	γQ
3877	GATTTTGTCAGGAAATTCTGACTCCCTACCTTTTGTCTTCAATGCTCGGTTTGCTTATGG	3936	ф
2444	TCAG	2385	Qy
3937	CCTCGGAGAGTCTAAGACCCTCGCTAA	3963	Db
2384	CTCTCATACCCTACAACCCCAAAACTATTTGAGATTAGGAAGAGCAAAGTTTTCTGAATC	2325	Qy
3964	GACCATCTTGTGGCTAAGAACCATACCCATGTATATGCAGGGGCAATGAGTTACCGACA	4023	Db
2324	- >	2265	Qy
4024	CTTCACGGCTTCTGAAAATTTCTTTAATTTTGCTTTTTGTCAGCTTTTTTGGCTACGACAA	4083	Db
2264		2205	Qy
4084	GAAAGGAAACCAACGTAGTTATCGTCATTCTAGCGCGGGTTATGCATTAGGAGGAGGAGTT	4143	Db
2204	TGC	2145	Qу
4144	GTTATCTTCGTCAACAAATTTGTGGGTATCAGGAATCGCGGACTTTTTGCATGAAGATCA	4203	Db

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PUBMED
REFERENCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-MAR-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA On Jun 1, 2000 this sequence version replaced gi:7189672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
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Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 28 (6), 1397-1406 (2000) 20150255
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                                                                                                                                                                                                                                                                                                                /note-"This region contains a gene with one or more premature stops or frameshifts, and is not the result of a sequencing artifact; similar to GP:4455886; identified by sequence similarity; putative; polymorphic membrane protein G family, degenerate" complement(6325. .9110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  causing a premature stop, and is not the result of a sequencing artifact; similar to GP:4455886; identified by sequence similarity; putative;polymorphic membrane protein G family authentic point mutation"
                                                                                                                                                                                                     putative;polymorphic membrane
frameshift"
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/gene="CP0758"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="synonym: Chlamydia pneumoniae AR39"
complement(150. .2987)
/gene="CP0757"
                                                                                                                                                                                                                                         is not the result of a sequencing artifact; similar GP:4455886; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SISTKGVSCLELHREIAR" complement(3336. .6086)
  /product="polymorphic
/protein_id="AAF38561.
                                                                               /note="similar to GP:4376270;
similarity; putative"
                                                                                                                                          complement(9393. .11918)
                                                                                                                                                             /gene="CP0761"
                                                                                                                                                                              complement(9393. .11918)
                                                                                                                                                                                                                                                                                                   /gene="CP0760"
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/protein_id="AAF38560.1"
/db_xref="GI:7189673"
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/strain="AR39"
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                                          transl_table=11/
                                                        codon_start=1
                                                                                                                                                                                                                                                                                 note="This region contains an authentic frame shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MRLLLSCPMLFIAACASFFGFQEEMQGRNIQSLDANASSLGELF"
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VSILLGEGGLREILLPYVSKTLPCSFYGOLSYGHTDHRMKTESLPPPPPTLSTDHTSW
GGYVMAAGELGTRVAVENTSGRGFFQEYTPFVKYQAVYARQDSFYELGALSRDFSDSHL
YNLAIPLGIKLEKRFAAEQYYHVVAMYSPDVCRSNPKCTTTLLSNOGSWKTKGSNLARQ
AGIYQASGFRSLGAAAELFGNRGFEWRGSSRSYRVDAGSKIKF"
A 2722 c 2431 g 3441 t 1 others
                                                                                                                                                                                                                                            ITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKEYTGTIVPSGEKLTEAE
AKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDLGTSLVANTESI
ELTINLEINIDSLRNGKIKLSAATAGKDIRITNFVVLAISDESFYQNGFLNEDHSYD
ILEIDAGKDIV ISADSKKIKLSAATAGVGFYGYGGKWIDRVVLATSGATVSWAKOSFNFTAEQ
EAPLVPNLLWGSFIDVRSFQNFIELGTEGAPYEKRFWVAGISNVLHRSGRENQRKFRH
VSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNTNFAKTYAGSLRLQHDASLYSV
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FQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATGTVSHSAIDLGTSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKIPLRFLLISLYPTLSMSNLLGAATTEELSASNSFDGTTSTTS FSSKTSSATDGTNYVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFS NIDATTASGAAIGSEAANKTVTLSGFSALSFLKSPASTVTNGLGAINVKGNLSLLDND
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Query Match
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TGTGATCTCCAATAACCAAAATATCTTTTTCGATGGCTGCAAAGCAACTACAAATGGCGG
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                                                  AGCTATTGATTGTAACAAAGCAGGGGGGGAACCCCAGACCCTATCTTGACTCTTTCAGGAAA
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1; Mismatches 1234;
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2093 3988	CTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGGTATGGAACA	2034 3929
2033 3928	AGGATITGITCCCAGCCCCGAAAGAAANTCIGCGITAGTAIGCAATACCCTAIGGGGAGI	1974 3869
1973 3868	GACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTGGACCAAAAC	1920 3809
1919 3808	TGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACAATGGAATGTTAATTG	1860 37 <b>4</b> 9
1859 3748	ATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACATCAGCAGCCGTTATCCC	1800 3701
1799 3700	TGATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGACCAGCTCTTCTCTCT	1740 3641
1739 3640	CAGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATCTGGGAAGCTCAACCTGAT	1680 3581
1679 3580	GAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAGCAGCCCGT	1620 3521
1619 3520	TCAAGAGGCCGGTTCTCCTCCTCGGCATGGATTCAGGAACGACATTATCAACTACAGCTGG	1560 3461
1559 3460	CCTATCCGGAGGAAGTTATTGCTACAAAAGGGAGTCACTTTAGAGAGCACGAGCTTCTC	1500 3401
1499 3400	AACAGCAGATGAACTTAAAGTTGGTGACAATTTAAAATCTTCATTCA	1440 3341
1439 3340	CGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGAFTCTATTTTCTGGAGAAACCCT	1380 3287
1379 3286	TTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCAGACGTATTGAAGATAAATAA	1320 3227
1319 3226	GATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATACAAT	1260 3167
1259 3166	TACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGGATACTCCTAAACGTAATGC	1200 3110
1199 3109	GGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAACAT	1140 3050
1139 3049	TTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATGATCTCCTACAGCAACTCCTAAGGG	1080 2990
1079 2989	CTTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	1020 2930

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ACCESSION VERSION KEYWORDS SOURCE

genome. AE002235 AE002161 AE002235.2 GI:8163495 AE002235 12127 bp | Chlamydophila pneumoniae

AR39, section

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Chlamydophila pneumoniae AR39

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                                                                                                                                                   GGAACTCCGTGGATCTTCAAGGAACTACAATGTAGATGTTGGTACCAAACTCCGATTCTA 2990
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NDVSLEAGTLYLSSGAGLLVDSFTOKEGSLIVENGGTSIITNVTPASEGLOSRSTPPS
PKNALPVIRAVSKYLASSLINLEREADSGAGAVPTIEESPDOSITTINLAVAULDEL
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VSTOPISNKVMDLAFCOMLGKSKDYRLADARSHVYAASIHTKCEKLVNHYTFSKRKGA
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/db_xref="taxon:83555"
/clone="$112"
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RSVDSILETRRGLWVSGIGNFFHKDRNAENRKFRHISSGYVLGATTNTSREDSLSVAF
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HPAIEELFPFVKLHIVFVQQEDFKETQGGTENRNFQSAHFVNVSLPLGVRFEKTNKLN
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/db_xref-m[01:1657777"
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/transl_table=11
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/note="submitted as Chlamydia
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                                                                   CCACGTTGCTTTTAGCAACAATGCTGTTTCCGGTTCATCTGATGGTTGCGGTGGAGCTAT
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1964	1905 ATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTG
1904 1709	1845 CAGCAGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACA
1844 1661	1785 CCAGCTCTTCTCTCTATTAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACAT
1784 1601	25 GAAGCTCAACCTGATTGATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGA
1724 1541	1665 TCTTAAGCAGCCCGTCAGCCTAACAGCAAAAAGGTGCTTCAAATAAAGTGATCGTATCTGG
1664 1481	1605 ATCAACTACAGCTGGGAGTATTACAATCAGGAACCTAGGAATCAATGTTGACTCCTTAGG
1604 1421	1545 GAGCACGAGCTTCTCTCAAGAGGCCGGTTCTCTCCTCGGCATGGATTCAGGAACGACATT
1544 1361	1485 CACGCAGCCAGTCTCCCTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTTAGA 
1484 1301	1425 TTCTGGAGAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATT
1424 1241	1365 ATTGAAGATAAATAACGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATT
1364 1181	1305 TAAAAATCATACAATTTTCTATGATCCCATCACTTCAGAAGGAAG
130 <b>4</b> 1124	1245 TCCTAAACGTAATGCGATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGC
1244 1064	1185 AGAGACAGGAAACATTACCTTTGTAAGAAATACCCTTACAACAACCAGGAAGTACCGATAC
118 <b>4</b> 1004	1125 AGCAACTCCTAAGGGGGGTGCTATCAGCATGGATGCCTCAGGAGAGCTCAGTCTTTCTGC
1124 944	1068 AAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATC
1067 884	1008 TAAGACTCTGATCTTTGCTTCAAACGTAGCAGAAACAAGCGGTGGGGGCGATCCATGCTAA
1007 824	954 TGCGATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAA
953 764	894 GATACTATCGAACAACATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGG
893 704	834 TAGATTCCTATCTAACATAGCGTCTACGTCAGGAGGGGCGCTATCGATGATGAAGGCACGTC

Db Qy

Qy Qy Db

Db Db

	985 ATTCTA 2990 	Qу 298	_
SAACTACAATGTAGATGTTGGTACCAAACTCCG 2984 	925 CGCTATGGAACTCCGTGGATCTTCAAGGAACTACAATGTAGATGTTGGTACCAAACTCCG 	Qy 2925 Db 2691	_ ~
TTACAACTCCAATTGTGAGCTCTTCGGACATTA 2924	865 TTTACTGAGGGGTAGCAACAACTACGTCTACAACTCCAATTGTGAGCTCTTCGGACATTA	Oy 286 Db 263	
AATTCGCGGTGGCAATCTTTCAAGACAGGCATT 2864                                   ACATGTGGTACAAGCTTGTCTAGACAAGCTCT 2630	305 TCTTGTGATGAGCCCAGACTCTTGGAAAATTCGCGGTGGCAATCTTTCAAGACAGGCATT 	Qy 2805 Db 2571	
IGTCTATCGTAACAATCCCCAATCTACAGCGAC 2804	745 TGATCTCTCAGGATTCTTTGTTTCCGATGTCTATCGTAACAATCCCCAATCTACAGCGAC 	Qy 2745 Db 2511	
CGTGCAGGGGATATCGGAGATTCCTACACCTA 2744	CCTCTCGATTCCTGTGGGTGCGAAATTCGTGCA 	Qy 2685 Db 2457	
TGGCCGTGGTTTTAGTATTGGAAGGCTGCTTAA 2684	AAATAGCTTCTTCGAAAGCTCTAGTGATGGCC 	Qy 2625 Db 2397	
ACAGATGAAAGTCGAAATGGTITATGTATCACA 2624 	2565 ACATCCTCTTTCAAGACCTTCATTCCACAGATGAAAGTCGAAATGGTTTATGTATCACA	Qy 256 Db 233	
CGGCCTAGACCTTCCTTTGTTCCTTTCCAACCC 2564	2505 GAGCAACGAGTGTATAGCTGGTGGTATCGGCCTAGACCTTCCTT	Qy 250 Db 227	
CTATACCTCATTGCCAGAATCCGAAGGTTCTTG 2504	2445 CCATTCAGACAACCGTATGGAAACGCACTATACCTCATTGCCAGAATCCGAAGGTTCTTG	Oy 24, Db 221	
TCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAG 2444	2385 AGCTATAGAAAATTCCCTAGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAG	Oy 238 Db 21!	
TTTGAGATTAGGAAGAGCAAAGTTTTCTGAATC 2384	GAG	Oy 231 Db 211	
TAGAACCTACGGTGGAACTTTATTCTTCAAGCA 2324	2265 AGATTGTTTATCGCTCACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCA	Oy 220 Db 201	
CTTTGCGTTCTGCCATCTCTTTGCTAGAGACAA 2264 	2205 TCACACTCCTAAAGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGACAA	Qy 220 Db 201	
TACCTCTGGAGGCTACGTCATCGGTGGAAGTGC 2204	2145 AGATGAAAATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGC	Qy 21, Db 199	
TTCCTCCATGACGAACTTCCTGCATAAGACTGG 2144 	2085 TATGGAACACAAACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGG	Qy 208 Db 189	
TCTGCAACAGCTTGTAGAGATCGGCGCAACTGG 2084	2025 ATGGGGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCGAACTGG	Qy 201 Db 181	
CGAAAGAAATCTGCGTTAGTATGCAATACCCT 2024 	1965 GACCAAAACAGGATTTGTTCCCAGCCCCGAAAGAAATCTGCGCTTAGTATGCAATACCCT 	Qy 190 Db 177	
		Db 17:	

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AGATGAAAATCGCAAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGC
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                     TTTACTGAGGGGTAGCAACAACTACGTCTACAACTCCAATTGTGAGCTCTTCGGACATTA
                                                                                                        TCTTGTGATGAGCCCAGACTCTTGGAAAATTCGCGGTGGCAATCTTTCAAGACAGGCATT
                                                                                                                                                                                                                                                                      CCTCTCGATTCCTGTGGGTGCGAAATTCGTGCAGGGGGATATCGGAGATTCCTACACCTA 2744
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TCTTATGGTTTCTGGGGGATTCTTGGTCGACATGTGGTACAAGCTTGTCTAGACAAGCTCT
                                                                                                                                                              TGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTAATGATCCAGGCTGCACGACAAC
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                                                                                                                                                                                   AGGGAATCTTGACCAAAATGAAAATGCCTCTAGTGAAAATGGGGGGAGCCATCAATACGAA
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                     ACAAGGGGGAGCGATCTATGCTTCTGGTGACTCTGTGATTTCTGAGAATGCAGGAATCTT
                                                                                                    GACTTTGTCTTTGACTGGGAGTACGCGGTTTGTAGCGTTCCTTGGCAATAGCTCGTCGCA
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Pred. No. 1.1e-94;
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Length 2757; Indels

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Madsen,A. and Birkelund,S.
NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
PATENT: WO 9858953-A 11 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
LOCATION/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
564 c 642 g 78
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  GTCTTTCCTTTTAACTGGCACTTCTGGAGATGCTCTTTTTTAGTAACAACTCTTCATCAAC
                                                                                                                                                                                                                                                                                       AAATAAGAATCTTACCTTCTCAGGGTTTTTCCTTACTGAGTTTTGATTCCTCCTAGCAC
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                                                     AGGGAATCTTGATCTTAATGAAAATGCCTCTAGTGAAAATGGGGGAGCCATCAATACGAA
                                                                                                  TCGTAAACTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGC
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CGAIVLSGVISGLSALIVCGLGISTISLGVVLFVLGLILLLRKRELTLEQIEAKQIAE
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RQLFDEEKIELLSGERLLEFIAANLFKQGRDVYLNLGNLADIRAYMGPNNYKVAMVIE
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RLRELTQNFEIQGFNFMKEDFKAAAKDLYIRSTAEQKMNFDVPCMELFRRYHEEVNKP
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QDVKDLARTQELEEQDIEAKREEAAEDLRSLNERLKKSKTMLDRAKWHIENAEDSITW
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DSERWNHKVLIQKLEDNYEKLLEESSKESTEANKKLLSDLVDRLEDAKTKFFLKKQEE
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/db_xref="GI:4455897"
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                                                 GCCTATCATGCTTGTAGATGCTCAGGGGAACTATTATGAGCATCATAATCTCAGTCAACA
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Submitted (21-JAN-1999) Boesen T., Department of Medical
Microbiology and Immunology, University of Aarhus, The Bartholin
Building, DK-8000 Aarhus, DENMARK
Location/Qualifiers
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ERVQERIRAIQKLYNILERBEETTGQETVPFTVQGTTASSDLTDILGRIEVSSREDN
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           /gene="hb2"
7150. .8058
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SISAERGTITFOGNRTSLFTLWGIHLLQARKELKLQARNGCSLEFYDFITSEADGSTQ
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AYQODFKETTADGRRFSNGSITSISVPLGIRFEKLALSQDVLYDFSFSYIFDIFRKDP
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QSKTKGGAISGANVTIVGNYDSVSFYQNAATFGGAIHSSGPLQIAVNQAEIRFAQNTA
KNGSGGALYSDGDIDIDQNAYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFS
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KHLSYFKKVNNKKEVQYAKFRLKVLESDLEGILAQTESAESLLTQEELPILATRGALE
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/db_xref="GI:4455892"
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/strain="VR1310"
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1184 4199	AGCAACTCCTAAGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGC	1125 4140

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ACCESSION VERSION KEYWORDS RESULT 11 CPN133035 LOCUS DEFINITION

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CPN133035 26920 bp DNA 27-FEB-2001 Chlamydia pneumoniae GGAI-protein family cluster B, genes omp6, hb1, hb2, hb3, hb4, hb5, hb6, hb7, omp7, pseudogenes omp8, omp91 omp15, strain VR1310.

SOURCE ORGANISM

REFERENCE AUTHORS omp15, strain vR1310.

AJ133035

Gene; hb3 gene; hb4 gene; hb5 gene; hb6 gene; hb7 gene; omp8 gene; omp9 gene; omp9 gene; omp9 gene; omp9 gene; ompmembrane protein 6; outer membrane protein 7; pseudogene.

Chlamydophila pneumoniae.

Chlamydophila pneumoniae

Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.

1 (bases 1 to 26920)

Daugaard, L., Hjerno, K., Knudsen, K., Madsen, A.S., Christiansen, G.

gene; outer

Birkelund, S.

gene

Sg

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 ANAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATC - - -
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SGLRISEIVAVNKQDFDLSTHLIRIRGKGKKERIIPVTSNAIQWIQIYLNHPDRKRLE
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                                                                                                                                               TTCCGATGTCTATCGTAACAATCCCCAATCTACAGCGACTCTTGTGATGAGCCCCAGACTC
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                                        TTGGACTTCGCTATGTAAAAACCTCGCACGACAAGCCTTCTTAGCAAGTGCTGGAAGCCA
                                                                              TTGGAAAATTCGCGGTGGCAATCTTTCAAGACAGGCATTTTTACTGAGGGGTAGCAACAA
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Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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Kalman,S., Mitchell,W., Mara
Grimwood,J., Davis,R.W. and
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                                                AGGAGCCTTAAATCTTACCGATAATGGAACGATTCTCTTTAGCCAAAACGTCTCCAATGA
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Madsen, A. and Birkelund, S.
NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
PATENT: WO 9858953-A 15 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
LOCATION/Qualifiers
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                                                                                                                                         TACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAGCAGCCCGTCAGCCT
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TAGCGGCAATTTTTATGAAAGCCATACGATAAACCAAGCCTTCACGCAGCCTTTGGTGGT
                                                           TGAAACAGCAGGAGCCAACAAAACTATAACTCTAACCTCTCCTCTTGTTTTCCAAGATAG
                                                                              CAGTCTTACCAAACTTGTCGTTGATCTTTCTGCCTTAGAGGGAAATAAGAGTGTGTCCAT-1517
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1745	6 AACAGCAAAAAGGTGCTTCAAATAAAGTGATCGTATCTGGGAAGCTCAACCTGATTGAT	168	.₽
13688	b TACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAGCAGCCCGTCAGCCT 	1362	B &
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1328	9 AGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATACAATTTTCTTCTA	126	g Q
13328		1326	
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1208	9 CAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAACATTACCTTTGT	114	β
13211		1315	δ
1148	2 CTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAGGGGGGTGCTAT	109	유
13151		1309	양
1091	2 CGTAGCAGAAACAAGCGGTGGCGCCATCCATGCTAAAAAGCTAGCCCTTTCCTCTGGAGG	103	β
13091		1303	δ
1031	2 GGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTGATCTTTGCTTCAAA	97	g
13031		1297	2
971	1 TTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCGATCTGCAACACCAA	92	д
12971		1291	Q
920	GTCGATACTATCGAACAACAATTTCTATA	86	요 성
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860	AGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGATTCCTATCTAACATAGCGTCTAC	801	ρ
12851		12792	γ
800	AGATGCTCTTTTAGTAACAACTCTTCATCAACAAAGGGAGGAGCAATTGCTACTACAGC	741	g
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740	0 AGATGGTGGAGCTATCAAAGGAGCGTCTTTCCTTTTAACTGGCACTTCTGG	69	д
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689	AGGAGGCGTAAATTTAGAAAATATTCGTAAACTTGTAGTTGCTGGGAATTTTTCTACTGC	630	P
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TTCCGATGTCTATCGTAACAATCCCCAATCTACAGCGACTCTTGTGATGAGCCCAGACTC 2	TCGGTTAGAAAAATCTCCGAAGATGAAAAAAAATAATTTCGAGATTTCTCTAGCCTACAT	GAAATTCGTGCAGGGGGATATCGGAGATTCCTACACCTATGATCTCTCAGGATTCTTTGT	TAGTGATGGCCGTGGTTTTAGTATTGGAAGGCTGCTTAACCTCTCGATTCCTGTGGGTGC 2	CATTCCACAGATGAAAGTCGAAATGGTTTATGTATCACAAAATAGCTTCTTCGAAAGCTC 2	TGGTATCGGCCTAGACCTTCCTTTTGTTCTTTCCAACCCACATCCTCTTTTCAAGACCTT 2	AACGCACTATACCTCATTGCCAGAATCCGAAGGTTCTTGGAGCAACGAGTGTATAGCTGG 2	GGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAGCCATTCAGACAACCGTATGGA:	AAACTATTTGAGATTAGGAAGAGCAAAGTTTTCTGAATCAGCTATAGAAAAATTCCCTAG	CAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCACTCTCATACCCTACAACCCCA	ATTTACCTTTGCGTTCTGCCAICTCTTTGCTAGAGACAAAGATTGTTTTATCGCTCACAA	CCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGCTCACACTCCTAAAGACGACCT	CTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGGAGATGAAAATCGCAAAGGCTT	TCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGGTATGGAACACAAACAA	CAGCCCGAAAGAAAATCTGCGTTAGTATGCAATACCCTATGGGGAGTCTTTACTGACAT	GGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTGGACCAAAACAGGATTTGTTCC:	TGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACAATGGAATGTTAATTGGACTAC 1	AATCACGGTTGATGCTGATGTTGATACGTTGACATCAGCAGCCTTATCCCTGTTCC	TGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGACCAGCTCTCTCT	
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VSTKKCLMIEDNENVSLSGNTATVSGGAIYAFKCALHGNTTLIFDGNTAGTAGTTTTQ
ETEDFTLIGSTGTVTFSTNTAKTAGALHTKGNTSFTKNKALVFSGNSATATATTTTDQ
EGCGGAILCNISESDLATKSLIFLTENESLSFINNTAKRSGGGIYAPAKCVISGSESINF
DGNTAATTSGGAIYSKNLSITALFENESLSFINNTAKRSGGGIYAPAKCVISGSESINF
UGNTAATTSGGAIYSKNLSITANGPVSFTNNSGGKGGAIYIADSGELSLEALDGDITFS
GNRATEGTSTPNSIHLGAGAKITKLAAAPGHTIFFYDDTTMEAPASGGTIEELVINPX
VKAIVPPOPKNGFIASVPVVPVAPANPNTGTVFSSGKLPSDDASIPANTTTILNOK
INLAGGNVVLKEGATLQVYSFTQQPDSTVFMDAGTTLETTTNNUTDGSIDLKNLSVNL
VKLDSKYNLTIAVNSTSGGLKISGDLKFHNNESSFYDNFGLKANLNLPFLDLSSTSGT
VNLDDFNPIBSSMAAPDYGYGGSWTLVFKVOAGGKVTLVAERQALGYTPKFELRATLV
VLDDFNPIBSSMAAPDYGYGGSWTLVFKVOAGGKVTLVAERQALGYTPKFELRATLV
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IVGGSMTTPQEYTFAVAFSQLFGKSKDYVVSDIKSQVYAGSLCAQSSYVIPLHSSLRR
HVLSKVLPELPGETPLVLHGQVSYGRNHHNWTTKLANNTQGKSDWDSHSFAVEVGGSL
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                                                                                                                                                                                                                                                                                           AKPPSALLLTLGYAVDAYRDHPHCLTSLTNGTSWSTFATNLSRQAFFAEASGHLKLLH
GLDCFASGSCELRSSSRSYNANCGTRYSF"
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GNSSLTGNTNLLFSGNKATGPSNSSANQEGCGGAILAFIDSGSVSDKTGLSIANNQEV
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3275. .4528
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/codon_start=1
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note="CPn0444"
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CPn0445"
      Outer Membrane Protein G Family"
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Best Local :
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TGNKNLSFTNNTALTYGGAISGLKVSLSAGGFTLFQSNISGSSAGGGGGGAINIASAG
ELALSATSGDITFNNNQVTNGSTSTRNAINIIDTAKVTSI IRAATGQSIYFVDPITNPG
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QLTFAFCQLFARDRNHITGKNHGDTYGASLYFHHTEGLFDIANFLWGKATRAPWVLSE
                                  GSAHIYNVDCGLRYSF"
                                                                                                                        IFSVAFCQLFGKDKDLFIVENTSHNYLASLYLQHRAFLGGLPMPSFGSITDMLKDIPL
ILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNNSGALELGGSLALYLPKEAPFFQGYFP
FLKFQAVYSRQQNFKESGAEARAFDDGDLVNCSIPVGIRLEKISEDEKNNFEISLAYI
                                                                                                                                                                                                                                        LSLSANGGDITFLGNTLTSTSAPTSTRNAIYLGSSAKITNLRAAQGQSIYFYDDIASN
LSLSANGGDITFLGNTLTSTSAPTSTRNAIYLGSSAKITNLRAAQGQSIYFYDDIASN
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TLQQIMTSQANSIYQQRGLWASGTANFFHKDKSGTNQAFRHKSYGYIVGGSAEDFSEN
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12172. .14964
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LKEVEPFVKVQYIYAHQQDFYERHAEGRAFNKSELINVEIPIGVTFERDSKSEKGTYD
                                                                             GDVYRKNPRSRTSLMVSGASWTSLCKNLARQAFLASAGSHLTLSPHVELSGEAAYELR
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AGSSAGTVASTSAADKNLLFNDFSRLSIISCPSLLLSETGQCALKSVGNLSLTGNSQI
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Matches 1430;
12552 TTCCTTCATTGCAGCTCCTGGAACTACAGTTGCTTCAGGAAAAAGTACTTTAAGTTCTGC 12611
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                                                         570 GAGTTTTGATTCCTCCTAGCACAACGGTTACTACAGGTCAGGGAACGCTTTCCTCAGC 629
                                                                                                                                                                                                                                                                                                                                                                                                                          390 CGAGCCTGGAAAAGGCACTCCCTTATCTGACAGTTGTTTTAAGCAAACCACGGACAATCT 449
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                                                                                                                                                                                AGGTGCTGCTGCATCTACAACAGCAAATAAGAATCTTACCTTCTCAGGGTTTTCCTTACT 569
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52.6%;
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Pred. No. 1.4e-106;
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                                         CTAGTTCTTCTAGGGAG
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AE001627 AE001363
AE001627.1 GI:4376721
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Kalman,S., Mitchell,W.,
Grimwood,J., Davis,R.W.
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651. .1289
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Matches 1432; Conserv
GGCTGCAAGTATTTCAGGAAACACCGGCCAGTTAGTCTTTATGAATAATAAAGGAGAAAC
                                                      AGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGATTCCTATCTAACATAGCGTCTAC
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TSGGLKISGDLKFHNNEGSFYDNPGLKANLNLPFLDSJSSTSGTVNLDDENPIPSSMAA
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SLSGNTATVSGGAIYATKCALHGNTTLTFDGNTAETAGGAIYTETEDFTLTGSTGTVT
FSTNTAKTAGALHTKGNTSFTKNKALVFSGNSATATATTTDQEGCGGAILCNISESD
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NLSITANGPVSFTNNSGGKGGAIYIADSGELSLEAIDGDITFSGNRATEGTSTPNSIH
LGAGAKITKLAAAPGHTIYFYDPITMEAPASGGTIEELVINPVVKAIVPPPQPKNGPI
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SSNTATDKGGIYSKEKDSTLDANTGVYEKSNTAKTGGAWSSDDLALTGNTQVLFQ
ENKTTGSAAQANNPECGGAICCYLATATDKTGLAISQNEMSETSNTTTANGGAIYSK
TKCTLDGNTTLTFDQNTATAGCGGAIYTETEDFSLKGSTGTVTFSTNTAKTGGALYSK
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/protein_id="AAF38166.1"
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Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae aR39
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Chlamydophila pneumoniae AR39
Bacteria; Chlamydiales; Chlamydophila.
                Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T. Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B
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Submitted (01-MAR-2000) The Institute for Genomic Research,
Medical Center Dr, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTPKSTADANGTNYVLSGNVYINDAGKGTALTGCCFTETTGDLTFTGKGYSFSENTVD
AGSNAGAASSTADANGTNYULSGNVYINDAGKGTALTGCCFTETTGDLTFTGKGYSFSENTVD
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similarity; putative"
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                                                             complement(6013. .9843)
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                                                                                                                                  FAFEVRSSSRNYNTNLGSKFCF"
                                                                                                                                                       LTLMYILDAYRRNPKCQTSLIASDANWMAYGTNLARQGFSVRAANHFQVNPHMEIFGC
                                                                                                                                                                             LKEVEPFVKVQYIYAHQQDFYERYAEGRAFNKSELINVEIPIGVTFERDSKSEKGTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="polymorphic membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDVYRKNPRSRTSLMVSGASWTSLCKNLARQAFLASAGSHLTLSPHVELSGEAAYELR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MKSSVSWLFFSSIPLFSSLSIVAAEVTLDSSNNSYDGSNGTTFT"
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strain="AR39"
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                  GP:4376727; identified by sequence
                                                                                                          .9843)
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81	321 TTCTTCTATGATCCCATCACTTCAGAAGGAACCTCCATCAGACTGCTATTGAAGATAAATAA	261 ATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATACAATT 132	01 ACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGATACTCCTAAAACGTAATGCG 1 	141 GGTGCTATCAGCATGCATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAACATT 120 	081 TCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAGGGG 114 	1021 TTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	TGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTGATC 102 	TCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCGATC	841 CTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATACTA 900 	781 GGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGATTC 840 		661 CTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCTTTC	601 ACTACAGGTCAGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGTAAA	541 AATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCTCCTAGCACAAGGGTT 	TTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCTGCATCTACAACAGCAAATAAG	421 AGTTGTTTTAAGCAAACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCCTTAACG 480	361 TATTCTCTAACAGGAGATGTCTTCTTTTACGAGCCTGGAAAAAGGCACTCCCTTATCTGAC 420 	301 GATAGCTTTAATGGAAATATCGATTCAGGAACGTTTACTCCAAAAAACTTCAGCCACAACA 360 
Qy 2461 ATGGAA	Qy 2401 CCTAGGC	Qy 2341 CCCCAA         Db 9949 CCCCAA	Qy 2281 CACAAC.         Db 9889 CACAAC	Qy 2221 GACCTAT	Qy 2161 GGCTTCC          Db 9769 GGCTTCC	Oy 2101 GGTTTC:           Db 9709 GGTTTC:	Qy 2041 GACATTO	Qy 1981 GTTCCC/         Db 9589 GTTCCC/	Qy 1921 ACTAC         Db 9529 ACTAC	1861 9469	1801 9409	Qy 1741 GATATTY        Db 9349 GATATTY	Qy 1681 AGCCTAJ        Db 9289 AGCCTAJ	9	Qy 1561 CAAGAG          Db 9169 CAAGAG	Qy 1501 CTATCO         Db 9109 CTATCO	9049	8989
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SOURCE
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AUTHORS
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Ralman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
Direct Submission
Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
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99206606
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Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.

Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
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Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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AE001628.1 GI:4376730
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                                                                                                                                                                                                                                               AQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                           241
                                                                                                                                                             181
                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                            61
                                GTGTTAGCTTTCTCATGTCACCTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGAT
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Local Similarity
                                                                                                                                                                                                                                                                                     1 CAATGTCGAAGAGAAGACCAACCAAGGAAAATTGCGATTTCATAAACCCACTTTATTATTA 60
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                                                                                                                                                                                                               AATTCTTACTTGCGTCATATAAAATAGAAAACTCAGAGAGTCAAGATAAAAATTCTTGAC 120
                                                                                                                                                                                                                                                               CAATGTCGAAGAGAGAGCACTAACCAGGAAAATTGCGATTTCATAAACCCACTTTATTATTA 7668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3228
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRNTLITTGSTDTPKRNAINIGSNGKETELRAAKNHTIFFYDPITSEGTSDVLKINN
GSAGALMPYQGTLESGETLTADELKYADNLKSSETQDVSLSGEKLLLQKGVTLESTS
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FARDKDCFIAHNNSRTYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVEMYYVSQNSFFESSSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSD
VYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
SRNYNVDVGTKLRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAASTTANKNLTESGESLLSFDSSPSTTVTTGOGTLSSAGGVNLENIRKLVVAGNFS
TADGGALKGASFLLTGTSGDALFSNNSSSTKGGALATTAGAFLANNTGVFELSNIA
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VAETSGGAIDHETKKLALSSGGFTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6715.
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/note="CPn0450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Translation="MEMMSPFQQPEQCHEDVVGSFLRPESLTRARSDFEEGRIVYEQM

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EQFLWIHNLVMKDRPEDLFVSLHVCRGDYQAEFFSRRAYDSIEEPLFAKTDVDSYHYY

WALDDKYSGGAEPLAYVSGEKHVCLGLISSNHSCIEDRDAVVSRIYEAASYIPLERLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVQVSFSHSDNRMETHYTSLPESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (4865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="pmp_11"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7813. .10599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contains frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="CPn0449"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4865. .6769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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/note="CPn0451"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSPQCGFASCEGDHRMTEEEQWKKIAFVKEIAKEIWG"
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                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                   98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .10599
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                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2065 g
                                                                                                                                                                                                                                                                                                                                                                                        Score 3149;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phic Outer Membrane Protein shift"
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .7650)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10757;
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                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                     7788
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  240
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7908

209708 OY 1980 Db 209768 QY 2040 Db	О Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф Ф	209528	209408 Qy 1680 Db 209468 Qy 1740 Db			1380 Oy 209168 Db 2 1440 Oy	N N	28 QY Db 2	1020 Oy 208808 Oy 1080 Db 2 208868 Oy 208868 Op 2
3001 ACTCCCTAGTTCTTCTAGGAGTTTTCTCATACTTTTAGGAI			2701 GGTGCGAAATTCGTGCAGGGGGATATCGGAGATTCCTACACC	9 1 9	210249 ATGGAAACGCACTATACCTCATTGCCAGAATCCGAAGGTTCT 2521 GCTGGTGGTATCGGCCTAGACCTTCCTTTTGTTCTTTCCAAC	2401 CCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTCCTTC.	9 1 9	09949 GCCTTCCGTCATACCTCTGAGGCTACCGTCATCGGTGGAAGT 2221 GACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGAC	2041 GACATTCGCTCTTGCAACAGTTGTAGAAGTCGGCGCAACT 2041 GACATTCGCTCTTGCAACAGTTGTAGAAGTCGGCGCAACT 1111111111111111111111111111111111

3120 210908	TGCTTTCCTTGCAAACTGTAAAAAATAACATTTGTCCCTCTTCAAAAAAAA	y 3061 b 210849	Qу
3060	ACTCCCTAGTTCTTCTAGGGAGTTTTCTCATACTTTTAGGGAAATATTTGCTATAGGGAA	y 3001	4d
210848		5 210789	40
3000	GGATCTTCAAGGAACTACAATGTAGATGTTGGTACCAAACTCCGATTCTAGATTGCTAAA	y 2941	Db
21 <b>0788</b>		b 210729	Qy
2940	AACAACTACGTCTACAACTCCAATTGTGAGCTCTTCGGACATTACGCTATGGAACTCCGT	y 2881	Qy
210728		b 210669	dd
2880	GACTCTTGGAAAATTCGCGGTGGCAATCTTTCAAGACAGGCATTTTTACTGAGGGGTAGC	y 2821	Db
210668		b 210609	Db
2820	TTTGTTTCCGATGTCTATCGTAACAATCCCCAATCTACAGCGACTCTTGTGATGAGCCCA	y 2761 b 210549	Qy db
2760 210548	GGTGCGAAATTCGTGCAGGGGGATATCGGAGATTCCTACACCTATGATCTCTCAGGATTC	y 2701 b 210489	pb 49
2700	AGCTCTAGTGATGGCCGTGGTTTTAGTATTGGAAGGCTGCTTAACCTCTCGATTCCTGTG	y 2641	40
210488		b 210429	VQ
2640	ACCTTCATTCCACAGATGAAAGTCGAAATGGTTTATGTATCACAAAATAGCTTCTTCGAA	y 2581	da
210428		b 210369	VQ
2580	GCTGGTGGTATCGGCCTAGACCTTCCTTTGTTCTŤTCCAACCCACATCCTCTTTTCAAG	y 2521	da
210368		b 210309	Vo
2520	ATGGAAACGCACTATACCTCATTGCCAGAATCCGAAGGTTCTTGGAGCAACGAGTGTATA	y 2461	Qy
210308		b 210249	Db
2460	CCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAGCCATTCAGACAACCGT	y 2401	dg
210248		b 210189	VQ
2400 210188	CCCCAAAACTATTTGAGATTAGGAAGAGCAAAGTTTTCTGAATCAGCTATAGAAAAATTC	y 2341 b 210129	pb dy
2340	CACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCACTCTCATACCCTACAA	y 2281 b 210069	Db Qy
2280	GACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGACAAAGATTGTTTTATCGCT	y 2221	dd
210068		b 210009	Qy
2220 210008	GGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGCTCACACTCCTAAAGAC	y 2161 b 209949	Ωy
2160	GGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGGAGATGAAAATCGCAAA	y 2101	Qy
		b 209889	Db
2100	GACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGGTATGGAACACAAACAA	y 2041	Qy
209888		b 209829	Db
209828	GTTCCCAGCCCCGAAAGAAATCTGCGTTAGTATGCAATACCCTATGGGGAGTCTTTACT	ъ 209769	۵

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LTVLHAGGKFDKDSYKVSGGLHGVGVSCVNALSEKLVATVFKDKKCYQMEFSRGIPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIGQGNEGSIDSDP AAANKYTEARLTHSAMYLMEDLDKDIVDIVPNYDETKHEPVVFP
SKEPNLLCNGSSGIAVGMATNIEPHNIGELIEATLLLANPQASVDEILQVNGSDEP
TGGIICGSEGIAVGMATNIEPHNIGELIEATLLLANPQASVDEILQVNGSDEP
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LALDKNIAPTMSIHRM.SAMIRHRKEVIRRETTRYELKAFTRAVLEGYLKALSSCLDA
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KKVSLDAFSNERKKGIRALEIDEGDELIAACHIVSDEKVMLFTHLGMAVRFPHEKVR
                                                                                                                         complement(10812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8391. .10808)
/gene="gyrB_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMGRTARGVRGVSLKNEEDKVVSCQIVTENQSVLIVCDQGFGKRSLVEDFRETNRGGV
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complement(5871.
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GIAEGLGADFVADLCSKVVGFTPFLPNFVLLLDIPADIGLQRKHRQKVFDKFEKKPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="WHLEEENQGWEALLRKYYHQEVPPAILLHGFTLPYLQDKAEQLA
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ILCSKETFSYLFRYAQCEIPVTEVSQIIKESSETDKQVLRDKYORFMEVLLELYRDRY
                                                                                                                                                                                                           LGEMNADQLWDTTMNPEQRTLIHVSLKDAVEADHIFTMLMGEEVPPRREFIESHALSI
                                                                                                                                                                                                                                                      LKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCYTLEEVINYLKNLGRKGIEIQRYKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="gyrB_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEGDALVSMEKLSSNENDDEVLSGSEEECSDTVSLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YHNRIREGFLSLASADPSRYLVLDARESLASLIDKVMLHTQLGLCT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVSLQYKEKELVSVSPGQDLSN"

complement(5246. .5866)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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gene CDS

gene CDS

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901

TCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCGATC

960

gene CDS

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                                                         В
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CTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATACTA
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                                                                                                                                                           AL Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.

Mutsunori Shirai, Yamaguchi University School of Medicine,
Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
75-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-227, Fax:81-836-22-2415)
On Sep 15, 2000 this sequence version replaced gi:6172290
gi:6172292 gi:6172294 gi:6172296 gi:6172326 gi:6172382 gi:6172382
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gi:8547438 gi:8978640.
AB033782-AB0338349: Submitted (14-Feb-2000)
AB036079-AB036082: Submitted (18-Dec-2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGPCSHGLESTVVASDPLYIYREGLISRSVIENIAGTEAKIFHRTSHAFSKHIKIYTV
KNQEQLVSFLSGSLDFKGVVCEHPKPKNFYTRLREALKKKTPSIVFIYDINTSDYPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEAHPVLNQLIHRIFSKGKAESILSSRAEKFLKQVIVEQVNPKITDVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGVIGLNLVRSYVGDSLGDLEKHVLHAENLGILSSIVLGSDFFYANEDENFFFNECSS
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tau"
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TGGG 1295 TGGG 1295 CGTC 1680             CGTC 1301		168	Ş
 TGGG 1295	AGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAGCAGCC	1621 12951	g Qy
TGG	CAAGAGGCCGGTTCTCCTCCGCATGGATTCAGGAACGACATTATCAACTACAGC 	1561 12891	д У
CTCT 1560	CTATCCGGAGGAAGTTATTGCTACAAAAGGGAGTCACTTTAGAGAGCACGAGCTTC 	1501 12831	₽ 2
CTCC 1500        CTCC 12830	ACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATTCA	1441 12771	gy Qy
CCTA 1440	1 GGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATTTTCTGGAGAAAA 	1381 12711	g Qy
ATAAC 1380       ATAAC 12710	TTCTTCTATGATCCCATCACTTCAGAAGGAACCTCAT	1321 12651	g Qy
PAATT 1320       PAATT 12650	1 ATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATAC 	1261 12591	ду 29
NATGCG 1260        ATGCG 12590	ACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGGATACTCCTAAACGTI	1201 12531	Dy Qy
ACATT 1200 	1 GGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTCTGCAGAGACAGGAAA 	1141 12471	Qу
16666 1140        16666 12470	1 TCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAA 	1081 12411	dg VQ
CCTT 1080	TTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	1021 12351	g 9
PGATC 1020        GATC 12350	1 TGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCT 	961 12291	ОУ
GATC 960        GATC 12290	1 TCGAACAACTATCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGC 	901 12231	요 왕
ГАСТА 900        AСТА 12230	1 CTATCTAACATAGCGTCTACGTCAGGAGGGCGCTATCGATGATGAAGGCACGTCGAT	841 12171	유 성
HTTC 840	1 GGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACACAGGTTATGTTAG 	781 12111	B 6
AGGGA 780        AGGGA 12110	1 CTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTCTTCATCAACAAA 	721 12051	Qу

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Qy 2821 GACTCTTG	Qy 2761 TTTGTTTC	Qy 2701 GGTGCGAP	Qy 2641 AGCTCTAC          Db 13971 AGCTCTAC	Qy 2581 ACCTTCAT         Db 13911 ACCTTCAT	Qy 2521 GCTGGTGG           Db 13851 GCTGGTGG	Qy 2461 ATGGAAAC          Db 13791 ATGGAAAC	Qy 2401 CCTAGGG         Db: 13731 CCTAGGGG	Qy 2341 CCCCAAAA         Db 13671 CCCCAAAA	Qy 2281 CACAACAA         Db 13611 CACAACAA	ОУ 2221 GACCTATT         Db 13551 GACCTATT	Qy 2161 GGCTTCCC         Db 13491 GGCTTCCC	Qy 2101 GGTTTCTC          Db 13431 GGTTTCTC	Qy 2041 GACATTCC	Oy 1981 GTTCCCAC Db 13311 GTTCCCAC	Qy 1921 ACTACGGATACAGG	QY 1861 GTTCCTGCTGAGGA 	Qy 1801 TTAAAAAT         Db 13131 TTAAAAAT
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2880 14210	2820 14150	2760 14090	2700 14030	2640 13970	2580 13910	2520 13850	2460 13790	2400 13730	2340 13670	2280 13610	2220 13550	2160 13490	2100 13430	2040 13370	1980 13310	1920 13250	1860 13190

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Chlamydophila pneumoniae.
Chlamydophila pneumoniae
Chlamydophila pneumoniae
Bacteria; Chlamydiales; Chl
1 (bases 1 to 17280)
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                                                                                               Boesen, T.

Boesen, T.

Boesen, T.

Direct Submission

Submitted (21-JAN-1999) Boesen T., Department of Medical Submitted (21-JAN-1999) Boesen T., Department of Medical Microbiology and Immunology, University of Aarhus, The Building, DK-8000 Aarhus, DENMARK

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPN133034 17280 bp DNA
Chlamydia pneumoniae GGAI-protein
(partial), ompl1, ompl0, omp5, omp
ORF1, strain VR1310.
                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                           Daugaard, L., Hjerno, K., and Birkelund, S.
                                                                                                                                                                                                                                                                                                                                                                   AJ133034
AJ133034.1 GI:4455881
AJ133034.1 GI:4455881
Aypothetical protein; omp10 gene; gene; omp14 gene; omp4 gene; omp5
protein; outer membrane protein 11
outer membrane protein 14; outer m
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omp4, omp13 and omp14 (partial) and
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11; outer membrane
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GSAHIYNVDCGLRYSF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=2
/transl_table=11
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="omp10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="omp10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="omp11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="omp11"
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}85. .3677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein 12"
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cps

sig\_peptide

oy oy	Оу	Qу	Qу	Оу	Qy Db	Оу	Qу	Оy	Оу	Qу	ОУ	Qy	Оy	Оу	ОУ	Дb	DЬ
1501 CTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTTAGAGAGCACGAGCTTCTCT 1560	1441 ACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATTCA	1381 GGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATTTTCTGGAGAAACCCTA 1440	TTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCAGACGTATTGAAGATAAATAA	1261 ATCAACATAGGAAGTAACGGGAAATTCACGGGAATTACGGGCTGCTAAAAATCATACAATT 1320	1201 ACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGGATACTCCTAAACGTAATGCG 1260	1141 GGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAACATT 1200 	1081 TCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAGGGG 1140	1021 TTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	961 TGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTGATC 1020 	901 TCGAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCGATC 960 	841 CTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATACTA 900	781 GGAGCAATTGCTACAGCAGGCGCCTCGCATAGCAAATAACACAGGTTATGTTAGATTC 840	721 CTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTCTTCATCAACAAAGGGA 780	661 CTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCTTTC 720	601 ACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGTAAA 660 	541 AATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCCTAGCACAACGGTT 600	
מ עס פע עס אם	S	Qy Qy	др	Qy Db	Qy Db	Qy Db	Db Qy	Ду Дъ	Qy Db	Qy Db	dd Yy	ob Qy	o da	) B &	2 B .	מם <sub>מ</sub> ם	Qy Db
2361 ACCITCATICCACAGAIGAAAGICGAAATIGGITTATGIAICACAAAATIAGCITCTICGAA 2040 [		ATGGAAACGCACTATACCTCATTGCCAGAATCCGAAGGTTCTTGGAGCAACGAGTGTATACATAC	CCTAGGGAAATTCCCCTAGCCTTGGATGTCCAACTTTCGTTCAGCCATTCAGACAACCGT	2341 CCCCAAAACTATTTGAGATTAGGAAGAGCAAAGTTTTCTGAATCAGCTATTAGAAAAATTC 2400 	CACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCACTCTCATACCCTACAA	2221 GACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTACAGACAAAGATTGTTTATCGCT 2280	2161 GGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGCTCACACTCCTAAAGAC 2220	GGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGCAGATGAAAATCGCAAA	GACATTCGCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGGTATGGAACACAAACAA	1981 GTTCCCAGCCCCGAAAGAAATCTGCGTTAGTATGCAATACCCTATGGGGAGTCTTTACT 2040	ACTACGGATACAGCTACAAATACAAAAAGAGGCCACGGCAACTTGGACCAAAACAGGATTT ACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTGGACCAAAACAGGATTT	GTTCCTGCTGAGGATCCTAATTCAGAATAGGGATCCAAGGACAATGGAATGTTAATTGG	TRABABATICACGGTTGATGCTGATGTTGATACGTTGACATCACCAGCCTTATCCCT	GATATIGANGGGANCALITATIGANAGICATATGTICAGCCATGACCAGCICITCTCTCTCTA 		ACCOMMAN ACCOMMAN ACCOMMAN A ACCOMMAN A ACCOMMAN ACCOMMAN ACCOMMAN ACCOMMAN ACCOMMAN ACCOMMAN ACCOMMAN A ACCOMMAN A ACCOMMAN ACCOMMAN A ACCOMMAN A ACCOMMAN A ACCOMMAN A ACCOMMAN A ACCOMMAN ACCOMMAN A ACCOMMAN	3507 CAAGAGGCCGGTTCTCCTCGGCATGGATTCAGGAACGACATTATCAACTACAGCTGGG 3448 1621 AGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAGCAGCCCGTC 1680

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/note="conserved hypothetical protein; identified
Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CP0305"
8329. 9444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTFSGNOAVANGGAIYAKKITLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECŠL
SAEAGDITFNCHÄIVATTPQTTKNSIDIGSTAKITHKRAISGISIFFYDPITANTAA
DSTDTINLINAKALDAGNISTDYSGSIVFSGEKLSBEDEAKVADNITSTLKQPYTLTAGNLVL
KRGVTLDTKGFTQTAGSSVIMDAGTTLKASTEEVTLTGLSIPVDSLGEEKKVVIAASA
ASKNVALSGPILLLDNQGNAVENHDLGKTQDDFSFVQLSALGTRTTDVPAVTPTATPT
HYGYQGTWGMTWVDDTASTPKTKTATLAWTUNGGYLPNPERQGPLYPNSLUGSFSDIQA
1QGVIERSALTLCSDRGFWAAGVANFLDKDKKGEKRKYRKKSGGYAIGGAAQTCSENL
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LKDKISVSKHPFIEHFEFVKTFEKGNAKAKQTIPSPSQFFHEMIFAPNLKNTRKFYPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8170.
/gene="CP0304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPEKNTTTGIDYTLTGDITLONLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKS
SAEGAALSVTTDKNLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTDNNGTILF
KODVCEENGGAISTKNLSLKNSTGSISFEGNKSSATGKKGGALCATGTVDITNNTAPT
LFSNNIAEAAGGAINSTGNCTITGNTSLVFSENSVTATAGNGGALSGDADVTISGNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNNSRTYGGTLFFKHSHTLQPQNYLRL
GRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLPESEGSWSNECIAGGIG
LDLFFYLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGFSIGRLLNLSIPVGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVSLSGGKLLLQKGVTLESTSFSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLG
LKQPVSLTAKGASNKVIVSGKLNLIDLEGNIVSHMFSHDQLFSLLKITVDADVOTNV
DISSLLIPVPAEDPNESTGFQGQMVNUNTTDTPAINTKBATATWTKTGFPVSPERKSALV
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/protein_id="AAF38161.1"
/db_xref="GI:7189231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRIYNVDLGGKFQF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CP0303"
5026. .7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KASGSPELIISNNKTLIFASNVAETSGGAIHAKKLALSSGGFTEFLRNNVSSATPKGG
AISIDASGELSLSAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGKFTELRAAKNHT
IFFYDPITSEGTSSDYLKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSAGGVNLENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIAT
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                                                                                                           /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="CP0304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(8170. .8292)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIRNDPKCTTALVISGASWETYANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLNLTYIRQDSFSEKGTEGRSFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="polymorphic membrane protein G family"
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/db_xref="G1:7189230"
/translation="MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANEELLSPDDSFNGNIDSGTFTPKTSATTYSLTGDVFFYEPGKGTPLSDSCFKQTTDN
LTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAF38159.1"
/db_xref="GI:7189229"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEGQLAYSHVSNDLKTKYTAYPEVKGSWGNNAFNMMLGASSHSYPEYLHCFDTYAPYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GP:4376729; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CP0303"
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                                                                                                                                                                                                                                                                                                                                                                                   'gene="CP0305"
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ORIGIN
                                  BASE COUNT
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                                  3580
                                                                                                                             DAGANCTETNITAANKLLSESGESYLSLLQTINATTGGALXSTGACSIQSKYSCYFOQ
NESNDNGGALQGSSISLSLNENLTEAKNKATOKGGALYSTGGIT NUTLASASESENT
AANNGGALYTEASSETSSNKAISEINSTATGAGITSAKREPUTLASASESENT
AANNGGALYTEASSETSSNKAISEINSTATGAGITCSSTSARRPUTLTLSDNGE
LNETGUTATTSGGALYTDINLYLSSGEPTLEKNISAIDTAAPLGGALIAIADSGSLSLSISA
LGGDITFEGNTYVKGASSSQTTTRNSINIGNTNAKIVQLRASQGNTIYFYDPITTSIT
AALSDALNILMGEDLAGNEAYOGTIVESGEKLSEAEAAEADLKSTIOOPLITLAGGGLS
LKSGYTLVAKSESQSPGSTLLMDAGTTLETAGDITINILVLNVDSLKETKKATLKATQ
ASOTYTLSGSLSLVUDESGNVEDVSMNNEQVESGLTLTAADDEANHITDLAADPLEKN
PIHWGYQGNWALSWQEDTATKSKAATLTWTKTGYNPNERRGTLVANTLWGSFVDVRS
IQOLVATKVRQSQETRGIWCEGISNFEHKDSTKINKGFRHISAGYVVGATTTLASDNL
ITAAFCQLEGKDRADHFINKNRASAYAASLHLOHLATLSSPSLRYLPGSESEOPVLFD
AQISYIYSKNYMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLEHAYFPFIK
VERSYIHODSFKERNTTLVRSFDSGDLINVSVPJGITFERFSRNERASYEATVIYVAD
VERSYIHOSFKERNTTLVRSFDSGDLINVSVPJGITFERFSRNERASYEATVIYVAD
                                  a
                                                            SRSYNADLGGKFQF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQELIDDIVFYYRQVIQDLYAAGCRNLQLDDCAWCRLLDIRAPSWYGVDSHDRLQEIL
EQFLWIHNLVMKDRPEDLFVSLHVCRGDYQAEFFSRRAYDSIEEPLFAKTDVDSYHYY
WALDDKYSGGAEPLAYVSGEKHVCLGLISSNHSCIEDRDAVVSRIYEAASYIPLERLS
                                                                                                          VYRKNPDCTTALLINNTSWKTTGTNLSRQAG I GRAG I FYAFSPNLEVTSNLSME I RGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="polymorphic membrane protein G family"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(9785. .12571)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTPPAQTTNADGTIYNLTGDVSITNAGSPTALTASCFKETTGNLSFQGHGYQFLLQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSPQCGFASCEGDHRMTEEEQWKKIAFVKEIAKEIWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CP0306"
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                                  2890
                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane protein
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gene CDS

Qy 밁 δÃ Ş 밁 Qγ 밁 ₽ Qy 밁 Ş B δÃ 밁 8 В δÃ Query Match Best Local Similarity Matches 3200; 4647 4767 4827 4887 4947 5007 481 301 181 361 241 121 61 AATTCTTACTTGCGTCATATAAAATAGAAAACTCAGAGAGTCAAGATAAAAATTCTTGAC AGCTGTTTTGTCATCTTTAACTTGATTTACTTATTTTGTTTCTATATTGATGCGAATAGT 180 TATTCTCTAACAGGAGATGTCTTCTTTTACGAGCCTGGAAAAGGCACTCCCTTATCTGAC 420 TTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCTGCATCTACAACAGCAAATAAG 540 AGTTGTTTTAAGCAAACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG AGTTGTTTTAAGCAAACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG TATTCTCTAACAGGAGATGTCTTCTTTACGAGCCTGGAAAAGGCACTCCCTTATCTGAC GATAGCTTTAATGGAAATATCGATTCAGGAACGTTTACTCCAAAAACTTCAGCCACAACA GATAGCTTTAATGGAAATATCGATTCAGGAACGTTTACTCCAAAAACTTCAGCCACAACA 360 GTGTTAGCTTTCTCATGTCACCTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGAT GTGTTAGCTTTCTCATGTCACCTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGAT 300 Conservative 100.0%; Score 3200; 100.0%; Pred. No. 0; 0; Mismatches DB 0 Ļ. Length 12676; .. Gaps 480 4648 4708 4768 4888 4948 4588 4828 120 240 0;

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to		CAGTTA         CAGTTA	TTGTCC               TGTCC	ACTTTT       ACTTTT	GTACCA        GTACCA	TCTTCC 	CAAGAC               CAAGAC	AATCTA        AATCTA	ATTCCT ATTCCT	GAAGGO         GAAGGO	TTTATO	TTCTTI	CCGAAG CCGAAG	AAGTTI       AAGTTI	AGTTTT       AGTTTT	TATTCI             TATTCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae Infect. Immun. 67 (1), 375-383 (1999)
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Chlamydia pneumoniae omp5
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Chlamydophila pneumoniae.
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LFSNNIA AEAAGGA INSTGNCTITGNTSLVFSENSVTATAGNGGALSGDADVTISGNQS
VTFSCNGA VANGA ITAKKLTLASGGGGI ISENNIVOGTTAGNGGALSGDADVTISGNQS
VTFSCNGA VANGA ITAKKLTLASGGGGGI ISENNIVOGTTAGNGGA ISILAAGECSL
SAEAGDITFNGNA ITAKKTTAGATTAKTIDIGSTRAKITNIKA ISGHSIFFEDDITANTAA
DSTDTLNLNKADAGNSTDYSGSIVFSGEKLSEDEAKVADNLTSTLKQPVTLTAGNLVL
KRGVTLDTKGETQTAGSSVLMDAGTTLKASTEEVTLTGLSIFVDSLGECKKVVIJAASA
ASKNVALSGPILLLDDAGNAYENHDLGKTQDFSFVQLSALGTATTDVPAVPTVATPT
HYGYQGTWGWWYDDTASTPKTKTATLAWTNTGYLPNERGOFLVPNSLWGSFSDIQA
IQGVIERSALTLCSDRGFWAAGVANFLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENL
                                                                                                                                                                            TYTPKNTTTGIDYTLTGDITLQNLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKS
SAEGAALSVTTDKNLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILF
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/db_xref="GI:3255935"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(<1. .2742)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1. .2804)
/gene="omp5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="elementary body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Chlamydophila pneumoniae"
/isolate="CDC/CWL-029/VR-1310"
/db_xref="taxon:83558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .6030
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/clone_lib="pEX2"
                                                                                                                                                                                                                                                                                                                                                                                                           'note="putative lipoprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="omp5"
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CAATGTCGAAGAGCACTAACCAGGAAAATTGCGATTTCATAAACCCACTTTATTATTA 2760
                    CAATGTCGAAGAGAGCACTAACCAGGAAAATTGCGATTTCATAAACCCCACTTTATTATTA 60
                                                                                        3200;
                                                                                                                                                                                                                        1760
                                                                                        Conservative
                                                                                                                                                                                                                                                                                     /product="outer membrane protein
5698. .5726
                                                                                                                                                                                                                                                                                                                                                                                SRNYNVDVGTKLRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGMEHKQGFWVSSMTNFLHKTGDENRKGFRHTSGGYVIGGSAHTPKDDLFTFAFCHL
FARDKDCFIAHNNSRTYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSAGALNPYQGTILFSGETLTADELKYADNLKSSFTQPVSLSGKLLLQKGVTLESTS
FSQEAGSLLGKDSGTTLSTTAGSITITNLGINVDSLGSSLLFVPSGKASNKVIVSGK
FSQEAGSLLGKDSGTSLDGLFSLLKTIVDADVDTNVDLSSSLLFVPABDPNSSVGFQG
QMNVNWTTDTATNTKEATATWTKTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIAS
TSGGAIDDEGTSILSNNKFLYFEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASN
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GAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQGTLSSAGGVNLENIRKLYVAGNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative"
complement(2799.
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LEGQLAYSHVSNDLKTKYTAYPEVKGSWGNNAFNMMLGASSHSY PEYLHGFDTYAPYI
KLNLTYIRODSFSEKGTEGRSFDDSNLFNLSLPIGVKEKEFSDCNDFSYDLTLSYYPD
LIRNDPKCTTALVISGASWETYANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGS
                                                                                                                                                                                                                      /note="putative"
1341 c 1195
                                                                                                                                                                                                                                                                                                                                                                                                   VYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVQVSFSHSDNRMETHYTSLPESEGSWSNECTAGGIGLDLPFVLSNPHPLFKTFIPQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRNTLTTTGSTDTPKRNAINIGSNGKFTELRAAKNHTIFFYDPITSEGTSSDVLKINN
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complement(2698. .2742)
                                                                                                                                                                                                                                                                /gene="omp4"
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1860	1801 TTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACATCAGCAGCCTTATCCCT 1 	Qy Db
1800	1741 GATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGACCAGCTCTTCTCTCTA 1	Оу
L740 L740	1681 AGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATCTGGGAAGCTCAACCTGATT 1	pb Qy
1680	1621 AGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAGCAGCCGGTC 1	Qy Db
L620 L620	1561 CAAGAGGCCGGTTCTCCTCGGCATGGATTCAGGAACGACATTATCAACTACAGCTGGG 1	ОУ
L560 L560	1501 CTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTTAGAGAGCACGAGCTTCTCT 1	Qy Db
1500	1441 ACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATTCA	Оy
1440 1440	1381 GGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATTTTCTGGAGAAACCCTA 1	Qу Db
1380 1380	1321 TTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCAGACGTATTGAAGATAAATAA	Qу Дъ
L320 L320	1261 ATCAACATAGGAAGTAACGGGAAATTCACGGGATTACGGGCTGCTAAAAATCATACAATT 1	Qу Db
L260	1201 ACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGATACTCCTAAACGTAATGCG 1	Qу
1200	1141 GGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAACATT 1	Оу
L140 L140	1081 TCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAGGGG 1	Оу
080	1021 TTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	Oy Db
1020	961 TGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTGATC 1 	Qу
960	901 TCGAACAACAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCGATC 9 	Db Qy
006	841 CTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATACTA 9 	Db Qy

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NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
Patent: WO 9858953-A 1 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
Location/Qualifiers
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AE001586 Chlamydia
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FSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQPYSLTAKGASNKVIVSGK
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SRNYNVDVGTKLR\*
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GGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGATTC CTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCTTTC GATAGCTTTAATGGAAATATCGATTCAGGAACGTTTACTCCAAAAACTTCAGCCACAACA GTGTTAGCTTTCTCATGTCACCTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGAT AATTCTTACTTGCGTCATATAAAATAGAAAACTCAGAGAGTCAAGATAAAAATTCTTGAC ACTACAGGTCAGGGAACGCTTTCCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGTAAA TTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCTGCATCTACAACAGCAAATAAG TCTCTAAAAAACAAAAGCATTACCATGAAGACTTCGATTCCTTGGGTTTTAGTTTTCCTCC AGCTGTTTTGTCATCTTTAACTTGATTTACTTATTTTGTTTCTATATTGATGCGAATAGT CTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCTTTC AATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCTCCCTAGCACAACGGTT ACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGTAAA AATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCTCCTAGCACAACGGTT AGTTGTTTTAAGCAAACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG GATAGCTTTAATGGAAATATCGATTCAGGAACGTTTACTCCAAAAACTTCAGCCACAACA TCTCTAAAAAACAAAAGCATTACCATGAAGACTTCGATTCCTTGGGTTTTAGTTTCCTCC Similarity Conservative 100.0%; 0; Score 3200; Pred. No. 0; Mismatches DB 9; 0; Length Indels 0, Gaps 360 60 840 840 660 600 480 480 420 300 60 660 600 540 420 240 780 240 180 0;

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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AE001627 Chlamydia	AE001628 Chlamydia AE002193 Chlamydon	AP002546 Chlamydop	AJ133034 Chlamydia	AE002192 Chlamydop	AJ001311 Chlamydia	A81827 Sequence 1	Description

2691 2587	2632 TTCTTCGAAAGCTCTAGTGATGGCCGTGGTTTTAGTATTGGAAGGCTGCTTAACCTCTCG 2	
2631 2527	2572 CTTTTCAAGACCTTCATTCCACAGATGAAAGTCGAAATGGTTTATGTATCACAAAATAGC 2	
2571 2470	2512 GAGTGTATAGCTGGTGGTATCGGCCTAGACCTTCCTTTTGTTCTTTCCAACCCACATCCT :	
2511 2410	2452 GACAACCGTATGGAAACGCACTATACCTCATTGCCAGAATCCGAAGGTTCTTGGAGCAAC :	
2451 2350	2392 GAAAAATTCCCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAGCCATTCA :	
2391 2305	2332 ACCCTACAACCCCAAAACTATTTGAGATTAGGAAGAGCAAAGTTTTCTGAATCAGCTATA :	
2331 2245	2272 TTTATCGCTCACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCACTCTCAT :	
2271 2191	2212 CCTAAAGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGACAAAGATTGT 2	
2211 2131	2152 AATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGCTCACACT :	
2151 2071	ATAAGACTGGAGATGAA        ataaagataagaaaggg	
2091 2011	AGCTTGTAGAGATCGGCGCAACTGGTATGGAA                gtgtcatagagagaagtgctttgactctttgt	
2031 1951	CCCCGAAAGAAATCTGCGTTAGTATGCAATACCCTATGGGGA 	
1971 1891	1918 TGGACTACGGATACAGCTACAAATACAAAAGAGGGCCACGGCAACTTGGACCAAA :	
1917 1831	CCCTAATTCAGAATACGGATTCCAAGGACAATGGAATGTTAAT	
1857 1771	1798 CTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACATCAGCAGCCTTATC :	
1797 1723	1738 ATTGATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGACCAGCTCTTCTCT :	
1737 1663	1678 GTCAGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATCTGGGAAGCTCAACCTG :	
1677 1603	1618 GGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAGCAGCCC :	

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01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to drown regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies of the according to preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of the protein of the component of the component of the protein of the component of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a Chlamydia antigen of the invention, designated CPN10635. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptide antigens from Chlamydia useful preventing, diagnosing and treating diseases such as community accommunity bronchitis, sinusitis and asthmatic bronchitis, adult-c
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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This DNA sequence codes for the novel 97.2 kDa surface exposed protein Omp5 (see AAW88418) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The cantibody was used to identify the genes (see AAX06816-27) encoding Omp4-Omp15 proteins (see AAW88417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2-gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89.6-100,3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by pCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA
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916 98929	57 CTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATACTATCGAACAACAATTTC 9	у 8 b 988	B 5
856 98869	97 CAGCAGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGATTCCTATCTAACATAGCGT 8	y 7 b 988	gg VQ
796 98809	46 CTCTTTTTAGTAACAACTCTTCATCAACAAAGGGAGGAGCAATTGCTACTA 7	у 7 b 987	₽ &
745 98749	86 CTGCAGATGGTGGAGCTATCAAAGGAGCGTCTTTCCTTTTAACTGGCACTTCTGGAGATG 7	у 6	B 6

2876	CCCAGACTCTTGGAAAATTCGCGGTGGCAATCTTTCAAGACAGGCATTTTTACTGAGGGG	2817	οv
100804	gatcccaaatgcactacagc	100745	Db
2816	TECTTTGTTTCCGATGTCTATCGTAACAATCCCCAATCTACAGCGACTCTTGTG	2757	Qy
2756	TGTGGGTGCGAAATTCGTGCAGGGGGATATCGGAGATTCCTACACCTATGATCTCTCAGG	2697	dd
100744		100685	VQ
2696		2637	Qy
100684		100625	Db
2636		2577	Qy
100624		100565	Db
2576	TATAGCTGGTGGTATCGGCCTAGACCTTCCTTTTGTTCCAACCCACATCCTCTTTT	2517	Qy
100564		100508	Db
2516 100507	CCGTATGGAAACGCACTATACCTCATTGGCAGAATCCGAAGGTTCTTGGAGCAACGAGTG	2457 100448	Оу
2456	ATTCCCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAGCCATTCAGACAA	2397	Qy
100447		100403	Db
2396	ACAACCCCAAAACTATTTGAGATTAGGAAGAGACAAAGTTTTTCTGAATCAGCTATAGAAAA	2337	Qy
100402		1003 <b>43</b>	Db
2336 100342	CGCTCACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCACTCTCATACCCT	2277 100289	Ф
2276	AGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGACAAAGATTGTTTTAT	2217	Qy
100288		100229	Db
2216	CAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGCTCACACTCCTAA	2157	Qy
100228		100169	Db
2156 100168	ACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGGAGATGAAAATCG	2097 100109	Qу
2096	TACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGGTATGGAACACAA	2037	Qy
100108		100049	Db
2036 100048		1977 99989	Qу
1976	TACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTGGACCAAAACAGG	1923	Qy
99988		99929	Db
1922	TCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACAATGGAATGTTAATTGGAC	1863	Qy
99928		99869	Db
1862	AAAAATCACGGTTGATGCTGATGTTGATACGTTGACATCAGCAGCCTTATCCCTGT	1803	Qy
99868		99821	Db
1802	TATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGACCAGCTCTTCTCTCTATT	1743	Qy
99820		99761	Db

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Isolated nucleic acid for use in diagnostic and analytical encodes genomic sequence of Chlamydia pneumoniae -
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08-APR-1999;
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Claim 2: Page 128-320; 320pp; English.

proteins; (6) a
weight % of P1;
peptide of (6). pneumoniae protein (P1), given in the specification. The isolated nucleic acid is useful for diagnostic and analytical methods, such as, hybridization-based assays or amplification-based assays. The protein may be used for diagnostic purposes, for their enzymatic or structural activity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizing fragment of N1; (2) an isolated nucleic acid (N2) that hybridizes under stringent conditions to N1; (3) an expression cassette comprising N1 under the transcriptional regulation of a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional in an expression host, and cassette into the host cell, and the cellular progeny of the host cell; (5) a method for producing a Pl comprising growing a cell of (4) where the protein is expressed and isolating the protein free of other proteins; (6) a purified polypeptide composition comprising at least 50 weight % of Pl; and (7) a monoclonal antibody binding specifically to the second control of the protein second contr transcriptional termination region; (4) a cell comprising an expression cassette of (3) as part of an extrachromosomal element or integrated into the genome of a host cell as a result of induction of the expression This invention describes a novel nucleic acid (N1) encoding a Chlamydia

Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other

Query Match

14.3%;

Score 458.6; DB 21 Pred. No. 9.2e-105;

DB 21;

Length 273254;

В Ş 밁 Ωy 밁 δÃ 밁 δÃ 밁 Qy 밁 QΥ B Q 밁 Ъ Qy DЪ δÃ γ 밁 ρ Best Local Similarity Matches 1534; Conserv 98035 98273 98155 tatatgacgcaagtaagaatttaataataaagtgggtt--tatgaaatcgcaattttcct 224 44 AACCCACTTTATTATAAATTCTTACTTGCGTCATATAAAATAGAAAACTCAGAGAGTCA 103 CAGCAGGAGGCGTAAATTTAGAAAATATTCGTAAACTTGTAGTTGCTGGGAATTTTTCTA ctttcttagcggccccatcatcggtaatcacaaccccctcaggaaaaggtgcagttaaat GTTT---gcgcagcactttctgttacaactgataaaaatctgtcgctaacaggattttcgagtctta GTGCTGCTGCATCTACAACAGCAAATAAGAATCTTACCTTCTCAGGGTTTTTCCTTACTGA gctttgccggtaaggggtactcactttcttttttaaatattaagtct---agtgctgaag CCTTCTTGGGGAACGGTCATAGCTTAACGTTTGGCTTTATAGATGCTGGCACTCATGCAG accttggggattcggcagctttaacgaagggttgtttttctgacactacggaatctttaa AGCCTGGAAAAGGCACTCCCTTATCTGACAGTTGTTTTAAGCAAACCACGGACAATCTTA ctcctaaaaatacgactactggaatagactatactctgacaggagatataactctgcaaa CTCCAAAAACTTCAGCCACAACA-----TATTCTCTAACAGGAGATGTCTTCTTTACG ctgctgaaaatataggcccctctgatagctttgacggaagtactaacacaggcacctata ACGAGGAACTTTTATCACCTGATGATAGCTTTAATGGAAATATCGATTCAGGAACGTTTA 337 ggttagtgctctcttcgacattggcatgttttactagttgttccactgtttttgctgcaa GGGTTTTAGTTTCCTCCGTGTTAGCTTTCT-----CATGTCACCTACAGTCACCTAGCTA ATATTGATGCGAATAGTTCTCTAAAAAAACAAAAGCATTACCATTACCATGAAGACTTCGATTCCTT gttaaagatgacaaaacagctgtcaagaatttttatcttgactctctgagttttctattt 98154 AGATAAAAATTCTTGACAGCTGTTTTGTCATCTTTAACTTGATTTACTTATTTTTGTTTCT 163 aatgcttttgtttttagagaactattcgcatcaatatagaaacaaaataagtaaatcaa 98094 Conservative -TGATTCCTCTCCTAGCACAACGGTTACTACAGGTCAGGGAACGCTTTCCT 0; Mismatches 1364; Indels 97; Gaps 685 277 98689 571 391 98629 98509 98392 98452 98272 98569 98212 16;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 other;
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                                                                                                                                                                                                      TCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAG---CAACTCCTAAG 1137
                                                                                                                                                                                                                                                                       GCAGGAGGCGTAAATTTAGAAAATATTCGTAAACTTGTTAGTTGCTGGGAATTTTTTCTACT 687
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                                                  attgtctttttagggaatacagtcacttctac----tactcctgggacgaatagaagt 1189
                                                                     ATTACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGGATACTCCTAAACGTAAT 1257
                                                                                                                  ggtggagccatagctatcgaagatagtggggaattgagtttatccgccgatagtggtgac 1135
                                                                                                                                                    GGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAAC 1197
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			2272 TTTATCGCTCACAACAACTCTAGAACCTACGGTGGAACTTTATTCTT	212 CTANAGKUNGKUTATTIACCTTICCTTICCTTICCTAGNAKANANITGI 	ט ני	2152 AATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGCTCACACT	2009 ggagaccgtgcttttggtgtgctggattatctaacttcttccataaggatagtacaaaa	2092 CACAAACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGGAGATGAA	1949 gcatttatagatattagctctctccattatcttatggagactgcaaacgaagggttgcag	2032 GTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCG	1889 actggctatattcctaatcccgagcgtatcggctctttagtccctaatagcttatggaat	1972 ACAGGATTTGTTCCCAGCCCCGAAAGAAATCTGCGTTAGTATGCA	1835 ccaattgtttgggggacaggggcttctacgactgcaaccti	AAAG	1776 -tgactccagatcctataatgggtgagaaattccattacggctatcagggaacttggggc	1852 CTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACAATGGAAT		1792 TTCTCTCTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACATCAGCAGC	1667 actttattggacccgacgggcacgttttatgaaaatcatagtttaagaaatcctcagtcc	1732 AACCTGATTGATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGACCAGCTC		1672 CAGCCCGTCAGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCG	150gctgatactagcaccataaacaatttggtcattaacatcagttctatagacggtgca	1612 ACAGCTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAG		1552 AGCTTCTCTCAAGAGGCCGGTTCTCTCCTCGGCATGGATTCAGGAA	1430	1492 CCAGTCTCCCTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCA		1432 GAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATTCA		1372 ATAAATAACGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATTTTCTGGA		1318 ATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCAT	1190 agtatcgacttaggaacgagtgcaaagatgacagctttgcgttctgctgctggtagagcc
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The present sequence is the 98kDa putative outer membrane protein gene cc from Chlamydia pneumoniae. The genomic sequence was amplified using two CC PCR primers. The 5' primer contains a Noti restriction site, a ribosome binding site, an initiation codon and a sequence close to the 5' end of CC the 98kDa putative outer membrane protein coding sequence. The 5' primer CC contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a serging sequence. The 3' primer CC contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BsrG1 restriction site. The stop codon was cc excluded and an additional nucleotide was inserted to obtain an in-frame CC terminal fusion with the Histidine tag. The PCR product was cloned to not a eukaryotic expression vector (pCA-Myc-His) by restricting both CC the vector and the PCR product with NotI and BamH1 and performing a Cliqation reaction. This expression vector was injected intramuscularly cand intramasally into mice, which were subsequently inoculated with CC chlamydia pneumoniae. The chlamydial lung titers of the immunised mice were lower than those of the controls. Thus the 98kDa putative outer membrane protein can be used as a vaccine to provide protection against Chlamydia infections, especially Chlamydia pneumoniae infections.

The polypeptide may also be administered orally to treat Chlamydia
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01-MAR-1999;
27-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Chlamydia 98 kDa putative outer membrane protein antigen, for vaccination and protection against Chlamydia infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY94327
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99US-0122066.
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                                                                                                                                                                                                                                                                                                                                                                                                      was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAW06816-27) encoding C dmp4-Omp15 proteins (see AAW088417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89,6-100.3 kba and C about 56.1 kba. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines may also prevent atherosclerosis and bronchial asthma,
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1372; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This DNA sequence codes for the novel 90.0 kDa surface exposed protein Omp8 (see AAW88421) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
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Mygind P;
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Pred. No. 2.1e-107;
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Omp8; outer membrane protein 8; surface exposed infection; diagnosis; vaccine; atherosclerosis;

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Mygind P;
This DNA sequence codes for the novel 96.7 kDa surface exposed protein Omp9 (see AAW88422) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
                                                                                                                                                                                                                                                                                                                                 Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encoded to the content of the conte
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P-PSDB; AAW06822.
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Pred. No. 1.3e-115;
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tgagagcctgcattttctgaataacacagcaggaaatagtggaggtgcgatttataccaa

1604	545 GAGCACGAGCTTCTCTCAAGAGGCCGGTTCTCTCCTCGGCATGGATTCAGGAACGACATT	
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1544		Qy
1401		ф
1484	NGAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATT	Qy
1341		Db
1424	AACGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATT	Qy
1281	 tgataa	
1364	AATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCAGACGT	Qy
1224	1165 tytgaccagaaatyctatagatcttycatcgaatycaaaatttttaaatctccgaycgac	Db
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1184	1125 AGCAACTCTAAAGGGGGTGCTATCAGCATCGCTCAGGAAGCCTCAGTCTTCTGC	} Q
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1124	1068 AAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATC	Qy
984	925 tgagagoctgcattttctgaataacacagcaggaaatagtggaggtgcgatttataccaa	Db
1067	AGACTCTGATCTTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	Qy
924	attga	Дb
1007	954 TGCGATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAA	Qy
864	805 tgtgatctccaataaccaaaatatctttttcgatggctgcaaagcaactacaaatggcgg	Db
953	894 GATACTATCGAACAACTTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGG	Qy
804	745 gagcttcggaaacaatgtggacaacatcaggaggcgcgatctctgctgaagggaacct	뮹
893	834 TAGATTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTC	Qy
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773	714 GTCTTTCCTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTCTTCATCAAC	P 04
624	65 aggg	DЪ
713	54 T	Qy
564	511gaccacaggtaaaggagccattaaaattaccgatggtctggtgtttgagagtat	Db
653	594 AACGGTTACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTTAGAAAATAT	Qy
510	34 AAATAAAATETTACCTTCAGGTTTTCCTTACTGAGTTCTGATTCCTCCTGCTGGAGCAC	₽ 5
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2684	AAATAGCTTCTTCGAAAGCTCTAGTGATGGCCGTGGTTTTAGTATTGGAAGGCTGCTTAA	2625	Qy
2624 2496	ACATCCTCTTTTCAAGACCTTCATTCCACAGATGAAAGTCGAAATGGTTTATGTATCACA	2565 2437	Оу
2436	GAGCAACGAGTGTATAGCTGGTGGTATCGGCCTAGACCTTCCTT	2505	Дb
7 7	CATICAGACAACCGTAT	- ω -	Db 49
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2444	AGCTATAGAAAAATTCCCTAGGGAAATTCCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAG	2385	Qy
2384 2256	CTCTCATACCCCTACAACCCCAAAACTATTTGAGATTAGGAAGAGACAAAGTTTTCTGAATC	2325 2230	Qy Db
2229	ggaccatcttgtggctaagaaccatacccatgtatatgcaggggcaatgagttaccgaca	2170	DB V
16	cttcacggcttctgaaaatttctttaattttgctttttgtcagctttttgcacgacaa	2110	g d
2264	GTTC	2205	Qy
2109	gaaaggaaaccaacgtagttatcgtcattctagcgcgggttatgcattaggaggaggatt	2050	Db
2204	GATGAAAATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGT	2145	Qy
2049	TATGGAACAACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGG	1990	Db Qy
1989	gtgggttcttttgtcgatgtccgctccattcagagcctcatggaccggagcacaagttc	1930	ДЬ
2084	ATGGGGAGTCTTTACTGACATTCGCCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGG	2025	Qy
1929	gactaaaacaggatacaagccgaatccagaacgtcagggacctttggttcctaatagcct	1870	ДD
2024	ACCAAAACAGGATTTGTTCCCAGCCCCGAAAGAAATCTGCGTTAGTATGCAATACC	1965	Qy
1869	Algebra of the light theoret and the lill	1810	dd Ay
` 0	cgataccccaattctaaatactacgaatcactatgggtatcaagggaa	1762	) Db
1904	CAGCAGCCTTATCCCTGTTCCTGCTGAGGATTCCAGAATTCAGAATTACGGATTCCAAGGACA	1845	Qy
1761		1702	Дb
1844	CCAGCTCTTCTCTCTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACAT	1785	Qy
1784 1701	GANGCTCAACCTGATTGATGTAAAGGGAACATTTATGAAAGTCATGATCAGCCATGA	1725 1642	dg Vy
1641	tgggacaaataaagctatcattaaggcgacggcagcaagtaaggatgttgccttatcagg	1582	Db
1724	TCTTAAGCAGCCCGTCAGCCTAACAGCAAAAAGGTGCTTCAAATAAAGTGATCGGTATCTGG	1665	Qy
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on .	ATCAACTACAGCTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGG	60	Q
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                TCTTCAAGGAACTACAATGTAGATGTTGGTACCAAACTCCGATTC
                                                                                     AACTACGTCTACAACTCCAATTGTGAGCTCTTCGGACATTACGCTATGGAACTCCGTGGA 2943
                                                                                                                                                          TCTTGGAAAATTCGCGGTGGCAATCTTTCAAGACAGCATTTTTACTGAGGGGTAGCAAC
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tcagcacacatctacaatgtagattgtgggctaagatactcattc
                                                                 ca-tctgactctcccctcatgtagaactctctggggaagctgcttatgagcttcgtggc
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20-AUG-1998;
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20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
27-AUG-1998;
17-AUG-1999;
                                                                                                                                                                                                                                                     AAZ61502-09 encode Chlamydia pneumoniae polypeptides. The polypeptides are present in the bacterial membrane structure, in the external vicinity of the membrane structure, in the inclusion membrane structure, in the external vicinity of the inclusion membrane structure, and in the cytoplasm of the infected cell. The polypeptides may be used to prevent, treat and detect the presence of Chlamydia infection and/or the presence of Chlamydia in a sample. The polypeptides may also be used to induce an immune response in a mammal. The vaccine vector comprising the polynucleotides is used to induce an immune response in a mammal. Antibodies directed against the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antigens and corresponding DNA molecules that can be used to prevent, treat and diagnose disease caused by Chlamydia infection in mammals, especially humans \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                             Sequence 2957
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 15-E; 201pp; English.
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                                                                                                                                  297 TGATGATAGCTTTAATGGAAATATCGATTCAGGAACGTTTACTCCAAAAACTTCAGCCAC 356
cacaagttgtttttctaacactgcaggaaatcttaccttcttagggaacggattttctct
              TGACAGTTGTTTTAAGCAAACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTT
                                                             AACATATTCTCTAACAGGAGATGTCTTCTTTTACGAGCCTGGAAAAGGCACTCCCCTTATC 416
                                                   tggtgatacaagcaccacagaatttactcctaaagcggcaacttctgatgctagtggcac
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                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding preventing, diagnosing pneumonia, bronchitis,
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                                                                                                                                                                                                                                                                                                                                  AGATGCTCTTTTTAGTAACAACTCTTCATCAACAAAGGGAGGAGCAATTGCTACTACAGC
TTTTGAAGGGAATGCAGCGAAAACTACT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggagccttaaatcttaccgataatggaacgattctcttttagccaaaacgtctccaatga
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                                                       tgggggtggggctctgggctttgaagccagctcctcgattactcaaaatagctccctttt
                                                                                                               GTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATACTATCGAACAACAAATTTCTATA
                                                                                                                                                                             ggctgcaagtatttcaggaaacaccggccagttagtctttatgaataataaaggagaaac
                                                                                                                                                                                                                                        AGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGATTCCTATCTAACATAGCGTCTAC
                                                                                                                                                                                                                                                                                                   ttctataaccttcactagtaatagcgcaaaaaaattaggtggagcgatctatagctctgc
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52.6%;
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and treating diseases such as community acquired
sinusitis and asthmatic bronchitis, adult-onset
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tttccccttcttaaagttccaggcagtctacagccgccaacaaaactttaaagagagtgg
                                                         CATTCCACAGATGAAAGTCGAAATGGTTTATGTATCACAAAATAGCTTCTTCGAAAGCTC
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                                                                                                                                                                                                                                                                                                               agatattcctctcattttgaatgcccagctaagctacagctacactaaaaatgatatgga
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Best Local Similarity Matches 1416; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein Ompli (see AAW88424) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding Omp4-Ompl5 proteins (see AAW88417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae. The test comprises detecting antibodies specific for omp4-omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the other, and encode polypeptides of about 89.6-100.3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia
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infection; diagnosis;
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                                                 cgatgctgggaaaggcacagcattaacaggctgctgctttacagaaactacgggtgatct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A sequence codes for the novel 97.6 kDa surface exposed Ompl1 (see AAW88424) of the human respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                2793 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                               possibly associated with C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae surface exposed protein Omp11
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Nucleic acids encoding preventing, diagnosing
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pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
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                                                                 Fig 7;
                                                                174pp;
                                                                 English.
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This sequence encodes a Chlamydia antigen of the invention, designated CC CPNI06639. The nucleic acids (and their complementary sequences) may be cu used as diagnostic agents for detecting the presence of nucleic acids cand their complementary sequences) may be complementary sequences of nucleic acids conding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate cards may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The confictions. Chlamydia is a pathogen implicated in the development of infections. Chlamydia is a pathogen implicated in the development of confections. Chlamydia is a pathogen implicated in the development of confections community acquired pneumonia, upper respiratory tract disease (especially borochitis and sinusitis, asthmatic bronchitis, confections of asthma and acute exacerbations of asthma in adults. be may

Sequence 3000 BP; 858 A; 726 C; 592 G; 824 T; 0 other;

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Pred. No. 7.6e-130;
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1285 TTCACGGAATTACGGCTGCTAAAAATCATACAATTTTCTTATGATCCCATCACTTCA 1344	1105 CTACGAAATAATGTCTCATCAGCAACTCCTTAAGGGGGGGTGCTATCAGCATCGATGCCTCA 1164	925 GAAGGGAATGCAGCGAAAACTACTGGCGGTGCATCTCGAACACCAAGGCGAGTGGATCT 984 [	GCTCTTTTTAGTAACAACTCTTCATCAACAAAGGGAGGAGCAATTGCTACTACAGCAGGC	565 TTACTGAGTTTTGATTCCTCCTAGCACAACGGTTACTACAGGTCAGGGAACGCTTTCC 624 [	
	2185 TACGT 1	1799 gcgti 2065 GTAGZ [      1859 gtagZ 2125 AACTT       1919 aactt		1439 atcaa 1705 AATAA 1705 AATAA 1705 AGTCA 1765 AGTCA 1559 agtca	Db 1259 gacaatttaaaatcttcattcacgcagccagtctccctatccggaggaaagttattgcta  Qy 1525 CAAAAGGGAGTCACTTTAGAAGAGACACGAGCTTCTCTCAAGAGGCCGGTTCTCTCCTCCGGC  Qy 15319 caaaagggagtcacttttagagagcacgagcttctctcctaagaggccggttctctcctcggc  Qy 1585 ATGGATTCAGGAACGACATTATCAACTACAGCTGGGAGTATTACAATCACGAACCTAGGA  Qy 1585 ATGGATTCAGGAACGACATTATCAACTACAGCTGGGAGTATTACAATCACGAACCTAGGA  Qy 1585 ATGAATCTTGACTCCTTAGGTCTTAAGCAGCCCGTCAGCACAAAGGTGCTTCA  Qy 1645 ATCAATCTTGACTCCTTAGGTCTTAAGCAGCCCGGTCAGCCAAAAGGTGCTTCA
	CCTTTGCCGTTCTCC 2244	ctctgcaacagctt 1858 ctctgcaacagctt 1858 ctrTCCTCCATGACG 2124 [	16 19 17 17 20	caaaagttgcttca 1498 GGAACATTTATGAA 1764 [	ggaaagttattgcta 1318 GGTTCTCCTCGGC 1584                             ATCACGAACCTAGGA 1644                 atcacgaacctagga 1438 GCAAAAGGTGCTTCA 1704

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c bronchitis; adult-onset asthma;
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                                                                        bronchitis;
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                                                           nitis; sinusitis; exacerbations of
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Location/Qualifiers

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                                                                                                                                                                                                                                                    This sequence encodes a Chlamydia antigen of the invention, designated CPN100634. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays, Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
                                                                                                                                                                          Query Match
Best Local S
Matches 2782
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01-DEC-1998;
01-DEC-1998;
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01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding preventing, diagnosing pneumonia, bronchitis,
                                                                                                                                                                                                                                                  Sequence
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mes 2782; Conserv
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                                                                                                                 ATGAAGACTTCGATTCCTTGGGTTTTAGTTTTCCTCCGTGTTAGCTTTCTCATGTCACCTA
 tcaggaacgtttactccaaaaacttcagccacaacatattctctaacaggagatgtcttc
               TCAGGAACGTTTACTCCAAAAACTTCAGCCACAACATATTCTCTAACAGGAGATGTCTTC
                                                          cagtcactagctaacgaggaacttttatcacctgatgatagctttaatggaaatatcgat
                                                                        CAGTCACTAGCTAACGAGGAACTTTTATCACCTGATGATAGCTTTAATGGAAATATCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide antigens from Chlamydia useful for
and treating diseases such as community acquired
sinusitis and asthmatic bronchitis, adult-onset
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1021 agcaactcctaaggggggtgctatcagcatcgatgcctcaggagagctcagtctttctgc 1080 1185 AGAGACAGGAAACATTACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGATAC 1244	901 LAAAAAGCLAGCCCLLCCCLCCGGAGGCCLLCCACGAGGCLLCCACCGACACCCCACCCA	TAAAAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATC 1	CAATAAGACTCTGATCTTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	45 TACTGGCGGTGCGATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTTAA  [	85 AGGCACGTCGATACTATCGAACAACAAATTCTATATTTTGAAGGGAATGCAGCGACAACAC 1	AGGTTATGTTAGATTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGA 8	TTCATCAAAGGGAGGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACAC	CAAAGGAGCGTCTTTCCTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTC	645 AGAAAATATTCGTAAACTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTAT 704	585 TCCTAGCACAAGGTTACTACAGGTCAGGGAAGGCTTTTCCTCAGCAGGAGGCGTAAATTT 644	5 TACAACAGCAAATAAGAATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTC	CGGTCATAGCTTAACGTTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCTGCATC 5	CACTCCCTTATCTGACAGTTGTTTTAAGCAAACCACGGACAATCTTACCTTCTTGGGAA	AACTTCAGCCACAACATATTCTCTAACAGGAGTGTCTTCTTTTTACGAGCCTGGAAAAGG	ACTITIATCACCTGATGATAGCTITAATGGAAATATCGATTCAGGAACGTITACTCCAAA 3	GGTTTTAGTTTCCTCCGTGTTAGCTTTCTCATGTCACCTACAGTCACTAGCTAACGAGGA 2 	165 TATTGATGCGAATAGTTCTCTAAAAAACAAAAGCATTACCATGAAGACTTCGATTCCTTG 224 	105 GATAAAAATTCTTGACAGCTGTTTTGTCATCTTAACTTGATTTACTTATTTTGTTCTA 164
Qy 2265 AGATTGTTTTATCGCTCAÇAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCA 2324 	QY 2205 TCACACTCCTAAAGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGACAA 2264	Qy 2145 AGATGAAAATCGCAAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGC 2204	Qy 2085 TATGGAACAAACAAAGATTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGG 2144	Qy 2025 ATGGGGAGTCTTTACTGACATTCGCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGG 2084	Qy 1965 GACCAAAACAGGATTTGTTCCCAGCCCCGAAAGAAAATCTGCGTTAGTATGCAATACCCT 2024	Qy 1905 ATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTG 1964	Qy 1845 CAGCAGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACA 1904	Qy 1785 CCAGCTCTTCTCTCTATTAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACAT 1844	\ACCTGATTGARATTGAAGGGAACATTTATGAAGGTCATATGTTCAGGCATGA 	1665 TCTTAAGCAGCCCGTCAGCCTAACAGCAAAAAGGTGCTTCAAATAAAGTGATGGTATCTGG	1605 ATCAACTACAACTGGAATTACAATCACGAACCAGGAATCAATGTTGACTCCTTAGG	45 GAGCACGAGCTTCTCTAAGAGGCCGGTTCTCTCCTCGGCATGGATTCAGGAACGACATT	Qy 1485 CACGCAGCCAGTCTCCCTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTTAGA 1544	Qy 1425 TTCTGGAGAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATT 1484 	Oy 1365 ATTGAAGATAAATAACGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATCTATT 1424		Qy 1245 TCCTAAACCTAATGCGATCAACATRGGAAGTAACGGGAATTCACGGGATTAGGGGCTGC 1304 	

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                                               This sequence encodes a Chlamydia antigen of the invention, designated CC CPN100534. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (FCR) assays. Antisense sequences may be used to down regulate nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of closes (especially bronchitts and sinusitis, asthmatic bronchitts, cadult-onset asthma and acute exacerbations of asthma in adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding preventing, diagnosing pneumonia, bronchitis,
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and treating diseases such as community acquir
sinusitis and asthmatic bronchitis, adult-onse
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1080 519238	Qy 1021 TTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT
1020 519178	Qy 961 TGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTCTAACAATAAGACTCTGATC
960 519118	Qy 901 TCGAACAACAACTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCGATC
900 519058	GCTATCGATGATGAAGGCACGTCGATACTA 
840 518998	Qy 781 GGAGCAATTGCTACTACAGCAGGCGCCTCGCATAGCAAATAACACAGGTTATGTTAGATTC
780 518938	Qy 721 CTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTCTTCATCAACAAAGGGA
720 518878	Qy 661 CTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCTTTC
660 518818	Qy 601 ACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGTAAA
600 518758	Qy 541 AATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCCTAGCACAACGGTT
540 518698	Qy 481 TTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCTGCATCTACAACAGCAAATAAG 
480 518638	Qy 421 AGTTGTTTTAAGCAAACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG
420 518578	Qy 361 TATTCTCTAACAGGAGATGTCTTCTTTTACGAGCCTGGAAAAGGCACTCCCTTATCTGAC
360 518518	Qy 301 GATAGCTTTAATGGAAATATCGATTCAGGAACGTTTACTCCAAAAACTTCAGCCACAACA
300 518458	Qy 241 GTGTTAGCTTTCTCATGTCACCTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGAT
240 518398	Qy 181 TCTCTAAAAAACAAAAGCATTACCATGAAGACTTCGATTCCTTGGGTTTTAGTTTCCTCCC
180 518338	Qy 121 AGCTGTTTTGTCATCTTTAACTTGATTTAGTTTTGTTTCTATATTTGATGCGAATAGT
120 518278	Qy 61 AATTCTTACTTGCGTCATATAAAATAGAAAACTCAGAGAGTCAAGATAAAAATTCTTGAC
60 518218	Qy 1 CAATGTCGAAGAGAGCACTAACCAGGAAAATTGCGATTTCATAAACCCACTTTATTATA
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Query Match Best Local Similarity

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                     The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY34584735879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
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21-NOV-1997;
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CC hybridization-based assays or amplification-based assays. The protein may CC be used for diagnostic purposes, for their enzymatic or structural CC activity, or as a vaccine. The invention also describes (1) a probe CC comprising a hybridizing fragment of N1; (2) an isolated nucleic acid CC (N2) that hybridizes under stringent conditions to N1; (3) an expression CC cassette comprising N1 under the transcriptional regulation of a CC transcriptional initation region functional in an expression host, and a CC transcriptional itermination region; (4) a cell comprising an expression CC cassette of (3) as part of an extrachromosomal element or integrated into CC cassette into the host cell as a result of induction of the expression CC cassette into the host cell, and the cellular progeny of the host cell; (5) a method for producing a P1 comprising growing a cell of (4) where CC the protein; (6) a purified polypeptide composition comprising at least 50 weight % of P1; and (7) a monoclonal antibody binding specifically to the CC peptide of (6).
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Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other;

1860	TTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACATCAGCAGCCTTATCCCT	1801	Qy
1800 96436	GATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGACCAGCTCTCTCT	1741 96495	Db Oy
1740 96496	AGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATCTGGGAAGCTCAACCTGATT 	1681 96555	рь <i>Q</i> у
1680 96556	AGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAGCAGCCCGTC	1621 96615	Qу
1620 96616	CAAGAGGCCGGTTCTCCTCGGCATGGATTCAGGAACGACATTATCAACTACAGCTGGG 	1561 96675	ру
1560 96676	CTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTTAGAGAGCACCAGGCTTCTCTT	1501 96735	Db Qy
1500 96736	ACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATTCA	1441 96795	Db Qy
1440 96796	GGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATTTTCTGGAGAAACCCTA	1381 96855	pb dg
1380 96856	TTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCAGACGTATTGAAGATAAATAA	1321 96915	Db Qy
1320 96916	ATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATACAATT	1261 96975	Db Qy
1260 96976	ACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGATACTCCTAAACGTAATGCG	1201 97035	Db Qy
1200 97036	GGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAACATT 	1141 97095	Db Qy
1140 97096	TCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAGGGG	1081 97155	Qy Db
1080 97156	TITGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	1021 97215	Qy Db
1020 97216	TGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTGATC	.961 97275	Db Qy
960 97276	TCGAACAACTATTTTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCGATC	901 97335	Db Qy
900 97336	CTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATACTA	841 97395	Qy Db
840 97396	GGAGCAATTGCTACTACAGCAGGCGCTCGCATAGGAAATAACACAGGTTATGTTAGATTC	781 97455	Qy Db
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This invention describes a novel nucleic acid (N1) encoding a Chl. pneumoniae protein (P1), given in the specification. The isolated acid is useful for diagnostic and analytical methods, such as,

Chlamydia nucleic

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Best Local Similarity
Matches 3200; Conserva
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1620	PAGAGGCCGGTTCTCTCCTCGGCATGGATTCAGGAACGACATTATCAACTACAGCTGG	5	Οy
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1560	TATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTTAGAGAGCACGAGCTTCTC!		Qy
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1500	CAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATTCA	1441	Qy
1440	gctctgcgggagctctcaatccatatcaaggaacgattctattttctggagaaacccta	1381	DЪ
	GCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATTTTCTGGAGAAACCCT	1381	Qy
1380	cttctatgatcccatcacttcagaaggaacctcatcagacgtattgaagataaataa	w	DЬ
1380	TCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCAGACGTATT	1321	Qy
1320	atcaacataggaagtaacgggaaattcacggaattacgggctgctaaaaatcatacaatt		Db
1320	TCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATACAAT	26	Qy
1260	acctttgtaagaaatacccttacaaccagcagtaccgatactcctaaacgtaatgcg	1201	Db
1260	CCTTTGTAAGAAATACCCTTACAACAACGGAAGTACCGGATACTCCTAAACGTAATGC	20	Qy
	gtgctatcagcatcgatgcctcaggagagctcagtctttctgcagagacaggaaacatt	1141	Db
1200	GTGCTATCAGCATCGATGCCTCAGGAGAGAGCTCAGTCTTTCTGCAGAGACAGGAAAAC	14	Qy
1140		1081	В
1140	CCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAG	1081	Qy
1080	agcagaaacaagcgg	1021	Db
1080	TTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCAT	1021	Qy
1020	tgcaacaccaaggcgagtggatctcctgaactgataatctctaacaataagactctgatc	961	ф
1020	GCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTGAT		Оу
960			В
960	CGAACAACAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCGAT	õ	Ωу
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900	TATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGAAGGCACGTCGATACT		Qy
840	ggagcaattgctactacagcaggcgctcgcatagcaaataacacaggttatgttagattc		Db
840	GAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGATT	80	Qy
780	cttttaactggcacttctggagatgctctttttagtaacaactcttcatcaacaaaggga	721	Дb
780	TTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTCTTCATCAACAAAGG	N)	Qy
720	cttgtagttgctgggaatttttctactgcagatggtggagctatcaaaggagcgtctttc		뫄
720	TTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCTTT		Qy
660	actacaggtcagggaacgctttcctcagcaggaggcgtaaatttagaaaatattcgtaaa		Db
660	CTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGT	0	Qy
600	aatcttaccttctcagggttttccttactgagttttgattcctctcctagcacaacggtt	541	DЬ
600	TCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCTCCTAGCACAACGG	541	Qy

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                               SUMMARIES
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2510.320 Million cell updates/sec
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                                Chlamydia pneumoni
Nucleotide sequenc
Chlamydia antigen
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Chlamydia the C
                                                                                                                                                                                                                      Description
Chlamydia pneumoni
Chlamydia pneumoni
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Chlamydia pneumoni
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ALIGNMENTS

Oligonucleotide D2	AAF58262	22	936		112	45	
	AAF58259	22	936	3.5	112	44	
Oligonucleotide D1	AAF58257	22	936		112	43	
	AAF58254	22	936		112	42	
	AAF58252	22	936		112	41	
	AAF58255	22	938		113.2	40	o
Oligonucleotide D2	AAF58262	22	936	٠	113.2	39	o
	AAF58259	22	936		113.2	38	a
	AAF58257	22	936		113.2	37	ဂ
Oligonucleotide D1	AAF58254	22	936		113.2	36	C
	AAF58252	22	936	٠	113.2	35	C
Chlamydia antigen	AAA30849	21	2950		142	34	C
	AAA27342	21	3150	•	143.8	<u>ω</u>	
	AAX06830	20	1830	•	184.6	32	
	AAX06824	20	840	•	191.8	31	
Chlamydia pneumoni	AAX06818	20	3052		252.6	30	
-	AAA50035	21	2950	•	255.8	29	
	AAX06828	20	3000	•	300	28	a
g	AAX06827	20	2838	9.6	307.6	27	
DNA encoding the C	AAZ61508	21	3050	•	323.2	26	
C. pneumoniae CPN1	AAA28690	21	2750	10.7	341	25	
niae	AAA28691	21	2526	10.7	341	24	
Chlamydia pneumoni	AAX06819	20	2526	•	341	23	
Chlamydia antigen	AAA30850	21	2784	11.9	382	22	
	AAA48839	21	2808	•	405.2	21	
Chlamydia antigen	AAA30852	21	2784	•	422.8	20	
	AAX06822	20	2787	•	423.2	19	
Chlamydia antigen	AAA30851	21	2950	13.3	425.2	18	
Chlamydia pneumoni	AAX06828	20	3000	. 13.5	432.4	17	
-	AAA48838	21	3050	13.6	433.6	16	
Chlamydia antigen	AAA30849	21	2950	13.8	441.6	15	
-	AAX06817	20	2815	14.2	456	14	
	AAC81914	21	273254	14.3	8	13	
	AAA27021	21	3000	14.6		12	

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AAX06816
                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                    Key
CDS
WPI; 1999-105610/09
                Birkelund S,
Mygind P;
                                         (BIRK/) BIRKELUND S. (CHRI/) CHRISTIANSEN G.
                                                                     23-JUN-1997;
                                                                                     19-JUN-1998;
                                                                                                        30-DEC-1998
                                                                                                                         W09858953-A2
                                                                                                                                                                             Chlamydia pneumoniae.
                                                                                                                                                                                             Omp4; outer membrane protein 4; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
                                                                                                                                                                                                                       Chlamydia pneumoniae surface exposed protein Omp4 DNA
                                                                                                                                                                                                                                        26-APR-1999 (first entry)
                                                                                                                                                                                                                                                          AAX06816;
                                                                                                                                                                                                                                                                           AAX06816 standard; DNA; 3200
                         Christiansen
                                                                    97DK-0000744
                                                                                      98WO-DK00266
                                                                                                                                                   Location/Qualifiers 205..2991
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                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 1.2%; Score 39.2; DB 3; Length 2960; Best Local Similarity 50.0%; Pred. No. 0.73; Matches 98; Conservative 0; Mismatches 98; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 07-073043
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00777
FILING DATE: 26-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: OHBA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 777-4528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6028250
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GENERAL INFORMATION:
APPLICANT: OHBA, Toshiharu
APPLICANT: TAKAHASHI, Shuichi
APPLICANT: ANMA, YOShiko
APPLICANT: ANMA, YOShiko
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: PLANT PROMOTER AND METHOD FOR GENE
TITLE OF INVENTION: EXPRESSION USING SAID PROMOTER
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,842
2118 TTTAGTCCCTCATTTT 2103
                                                                                               2178 TCTGGAATTTATATTATAAAATATGTATTTTTTTGGGTCCATATTATTTTATGTAGTT 2119
                                                                                                                                                                                                    2238 AAAATATTTGATAAATAATTTATTATCTTATCTTTAATATCTTTTTTTACTTAATTGTAAT 2179
                                                                                                                                                                                                                                                                                                      2298 AGTTTTTTTTTAAATTTTAGAAAAATAAAATTTAAATAACAAATTTTATAAATTAAATTA 2239
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LENGTH: 2960 base pairs
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ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 7th Street N.W., Ste. 300
CITY: washington
STATE: D.C.
                                                                                                                                                                                                                               109 AAAATTCTTGACAGCTGTTTTGTCATCTTTAACTTGATTTACTTTATTTTGTTTCTATATT 168
                       229 TTAGTTTCCTCCGTGT 244
                                                                                                                                                  169 GATGCGAATAGTTCTCTAAAAAAACAAAAGCATTACCATGAAGACTTCGATTCCTTGGGTT 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Search completed: October 2, 2001, 03:25:12 Job time: 50105 sec

ORIGINAL SOURCE:

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RESULT 14
US-08-544-332-1
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; LOCATION:
US-07-991-867B-1
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Best Local Similarity
Matches 99; Conser
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                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3171 CAATAATCTATTCTTATT 3188
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                                                                                                                                                                                                                                                                                                        APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7318 TATTAATCTTCTCATAGT 7335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7198 AGAGAAATTAATATTTTTTGTAAACTCGGAAAATTCAGCAAGTTTTCTTTTAATCATATC 7257
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                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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NAME/KEY:
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LOCATION:
                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                    STREET: 2421 N.W. CITY: Gainesville
APPLICATION NUMBER: US 07/991,867 FILING DATE: 07-DEC-1992
                                                                            APPLICATION NUMBER:
                                                                                                                                                                                             ZIP: 32606
                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                            ΞĽ
                                                                                                                                                                                                                                                        E: Gerard H. Bencen
2421 N.W. 41st Street,
                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                         Hall, Richard L.
                                                                                                                                                                                                                                                                                                                                                                      Moyer, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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3080..6091
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1474.
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2502..2987
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                                                                             US/08/544,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.6; DB 1; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                          Suite A-1
                                                                                                            Version
                                                                                                               #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8457;
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RESULT 15
US-08-913-842-3/c
· Sequence 3, Application US/08913842
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                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: US-08-544-332-1
                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                       7198
                                                                                                   7318
                                                                                                                                                                                         3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 8457 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                     3051 CTATAGGGAATGCTTTCCTTGCAAACTGTAAAAAATAACATTTGTCCCTCTTCAAAAAAA 3110
                                                                                                                                                                                                                                                                                                            2991 GATTGCTAAAACTCCCTAGTTCTTCTAGGGAGTTTTCTCATACTTTTAGGGAAATATTTG 3050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US OFFITTING DATE: 19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO 93 FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                   TATTAATCTTCTCATAGT 7335
                                                                                                                             CAATAATCTATTCTTATT 3188
                                                                                                                                                           ATTATATTCTATATTATCTAAATCTCCTTTTATTTTAAGATCATAAAAAGCAAATGAAGA 7317
                                                                                                                                                                                                                       AGAGAAATTAATATTTTTTGTAAACTCGGAAAATTCAGCAAGTTTTCTTTTAATCATATC 7257
                                                                                                                                                                                                                                                                                 GATTGGTAAATTAGTTTTTATTTTATATTATCATTTTAAAAACTTTCAATAAAAGATTC 7197
                                                                                                                                                                                        l Similarity 50.(
99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bencen, Gerard
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3080..6091
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1474..2151
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2502..2987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2239..2475)
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                                                                                                                                                                                                                                                                                                                                        Score 39.6; DB 2;
Pred. No. 0.89;
0; Mismatches 99
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                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/827,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3051 CTATAGGGAATGCTTTCCTTGCAAACTGTAAAAAATAACATTTGTCCCTCTTCAAAAAAG 3110
                                                                                                                                                                                                                                                          FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
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CTTY: Gainesville
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0' FILING DATE: 30-JAN-1992
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                                   STRANDEDNESS:
                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                       NAME: Bencen, Gerard H
REGISTRATION NUMBER: 3
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                        nucleic acid
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21 N.W. 41st Street, Suite A-1
                                     single
DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/07/991.867P
FILING DATE: 12-DFC-100
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Best Local :
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                                                                                                                 TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 8457 base pair
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus
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                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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nes 99; Conserv
                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Gainesville
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UF114.C3
                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                     TELEPHONE:
                                              : 8457 base pairs
                                                                                                                                                                                                                                Saliwanchik, David R
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DNA (genomic)
                                      double
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1888 TACGGATTCCAAGGACAATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAA 1947

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Query Match
Best Local Similarity
"~+~hes 96; Conserv
                                                                                          ; LOCATION: 69..126; OTHER INFORMATION: PCT-US93-10520-1
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                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9310520 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/752,764
FILING DATE: 30-AUG-1991
PRIOR APPLICATION NUMBER: US 07/753,059
FILING DATE: 30-AUG-1991
                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                          FEATURE:
                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 07/752,857
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CLASSIFICATION:
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STATE: MA
                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                     TELEPHONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US93/10520
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                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                 nucleic acid
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                                                                                                                         CDS
69..1268
                                                                                                                                                                                                                                  1674 base pairs
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                Conservative
                                                                                                                                                                                       S: single
linear
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                                                                                                                                                                       protein
                           1.2%;
                                                                                                          /note= "mOP3-PP"
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             Score 39.6; DB 5;
Pred. No. 0.45;
0; Mismatches 94;
                                             Length 1674;
                Indels
              0;
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              0;
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RESULT 11
US-07-991-867B-41
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US-07-991-867B-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41,
                                                                                                                                     TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07.
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07.
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: WO 92/14818
FILING DATE: 12-FEB-1992
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Moyer, Richard W. APPLICANT: Hall, Richard L. APPLICANT: Gruidl, Michael E.
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CITY: Gainesville
                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07 FILING DATE: 12-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 32606
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5476781
                                                                      nucleic acid
                                                                                                                                                                                                                                                        Saliwanchik, David R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
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Query Match 1.3
Best Local Similarity 50.0
Matches 99; Conservative

1.2%;

Score 39.6; DB Pred. No. 0.45; 0; Mismatches

DB 1; 99;

Length 1689;

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1888 TACGGATTCCAAGGACAATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAA 1947

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; OTHER INFORMATION:
US-08-901-200A-1
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                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (508) 435-6951 INFORMATION FOR SEQ ID NO:
                                                                                                          1372 CACATTCACAGTCTTGGCCCTCTCTGTTCTTTTTGCCAAGGCTGAGAAGATGGTCCTAGT 1431
                                                                                                                                              1768 CATATGTTCAGCCATGACCAGCTCTTCTCTCTATTAAAAATCACGGTTGATGCTGATGTT 1827
1888 TACGGATTCCAAGGACAATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAA 1947
                                     1432 TATAACCCTGGTGACCTCAGTAGCCCGATCTCTCATCTCCCCAAACTCCCCAATGCAGCC 1491
                                                                       1828 GATACTAACGTTGACATCAGCAGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAA 1887
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MEDIUM TYPE: Floppy
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LENGTH: 1674 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: MEYERS, THOMAS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 69..1265
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                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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PANG, ROY H.L.
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                                                                                                                                                                                    Conservative
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OZKAYNAK, ENGIN
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                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                Matches
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                1828 GATACTAACGTTGACATCAGCAGCCTTATCCCTGTTCCTGAGGATCCTAATTCAGAA 1887
                                                                1372
                                                                                              1768 CATATGTTCAGCCATGACCAGCTCTTCTCTCTATTAAAAATCACGGTTGATGCTGATGTT 1827
1432 TATAACCCTGGTGACCTCAGTAGCCCGATCTCTCTCTCCCCAAACTCCCCAATGCAGCC 1491
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 28-JUL-1997 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
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                                                                                                                              Local Similarity
nes 96; Conserv
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                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 69..1265
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MEYERS, THOMAS C
                                                                                                                                                                                                                                                                                                                                                      ENGTH:
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OZKAYNAK, ENGIN
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28-JUL-1997
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                                                                                                                                             Score 39.6; DB Pred. No. 0.45;
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                                                                                                          Matches
                                                                                                                   Query Match
Best Local Similarity
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Patent No. 56521
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 248-71 INFORMATION FOR SEQ ID NO:
                                  1372 CACATTCACAGTCTTGGCCCTCTCTGTTCTTTTTGCCAAGGCTGAGAAGATGGTCCTAGT 1431
                                                        1768 CATATGTTCAGCCATGACCAGCTCTTCTCTCTATAAAAATCACGGTTGATGTGATGTT 1827
                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sir
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,528A
FILING DATE: 07.JUN-1995
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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1828 GATACTAACGTTGACATCAGCAGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAA 1887
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                           LOCATION: 69..1265
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: FENTON ESq., GILLIAN M. REGISTRATION NUMBER: 36,508
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                                                                                                          96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPPERMANN, HERMANN
                                                                                                          Conservative
                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KUBERASAMPATH,
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50.5%;
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                                                                                                                     Score 39.6; DB Pred. No. 0.45;
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; LOCATION: 69..1265
; OTHER INFORMATION:
US-08-479-666-1
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                                                                                                                                        Matches
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                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (508) 435-695
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                              1828 GATACTAACGTTGACATCAGCAGCCTTATCCCTGTTCCTGAGGATCCTAATTCAGAA 1887
                                                                                                   1768 CATATGTTCAGCCATGACCAGCTCTTCTCTCTATTAAAAATCACGGTTGATGCTGATGTT 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                    1372 CACATTCACAGTCTTGGCCCTCTCTGTTCTTTTTGCCAAGGCTGAGAAGATGGTCCTAGT 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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1432 TATAACCCTGGTGACCTCAGTAGCCCGATCTCTCATCTCCCCAAACTCCCCCAATGCAGCC 1491
                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                1674 base pairs
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                                                                                                                                      Conservative
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KUBERASAMPATH, THANGAVEL
                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                      1.2%;
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                                                                                                                                                      Score 39.6; DB Pred. No. 0.45;
                                                                                                                                        Mismatches
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INFORMATION FOR SEQ

(216)241 0816 DR SEQ ID NO:

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TELEFAX:

SEQUENCE CHARACTERISTICS:

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US-08-731-722-4
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                                                                                     TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 base pairs
TYPE: nucleic acid
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1i
                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                  TOPOLOGY:
                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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ZIP: 32606-6669
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STRANDEDNESS: single
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               NDIVIDUAL ISOLATE:
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2421 N.W. 41st Street, Suite A-1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biocontrol of Fungal Soilborne Pathogens by Pythium oligandrum
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Pred. No. 0.16;
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Query Match
Best Local Similarity
Thes 88; Conserve
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Best Local Similarity
                                                                                                                                                                                                                                             TELEFAX: (415) 576-3300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                         FEATURE:
                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                             NAME: Quine, Jonathan A. REGISTRATION NUMBER: P-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 13-OCT
                                                                                                                                            NAME/KEY:
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                                                                                                                            LOCATION:
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                                                                                                                                                                                                                              nucleic acid
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SYSTEM: PC-DOS/MS-DOS
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US-08-946-617-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08911320A Patent No. 5869633 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
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APPLICANT: Yang, Jian
TITLE OF INVENTION: Nucleotide Integrase Preparation
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 6-JUN-1995
ATORREY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0041-1 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: INCYTE PHARMACEUTICALS, INC. TITLE OF INVENTION: THROMBIN RECEPTOR HOMOLOG
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APPLICATION NUMBER: 08/467,125
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                                                                                                            COUNTRY:
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                   OPERATING SYSTEM:
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             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Zimmerly, Steven
PatentIn
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Release #1.0, Version #1.30
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & (
STREET: 800 Superior Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1326
                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zimmerly, St APPLICANT: Guo, Huatao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                  TELECOMMUNICATION INFORMATION:
                               NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24671/00105
                                                                                                                                                                                                                                                                                                                    STREET: 800 Sup
CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Golrick, Mary E
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                      FILING DATE
                                                                                                                                          APPLICATION NUMBER:
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TELEPHONE:
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(216)622-8416
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1: /cgn2_6/ptodata/2/
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Copyright (c) 1993 - 2000
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         /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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Matches 88; Conservative
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Query Match Best Local Similarity 59.5 Matches 88; Conservative	RESULT 1  US-08-526-964-1/c  Sequence 1, Application US/085269; Sequence 1, Application US/085269; Sequence 1, Application US/085269; Sequence 1, Application US/085269; Patent No. 5698421; GENERAL INFORMATION: Alan MAPLICANT: Lambowitz, Alan MAPLICANT: Zimmerly, Steven APPLICANT: Yang, Jian  TITLE OF INVENTION: Nucleotide NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSEE: Calfee, Halter & STREET: 800 Superior Avenue CITY: Cleveland STATE: Ohio COUNTRY: USA ZIP: 4114 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: Patentin Release operation NUMBER: US/08/5; FILLING DATE: CLASSIFICATION NUMBER: US/08/5; FILLING DATE: CLASSIFICATION NUMBER: 34,829 REFERENCE/DOCKET NUMBER: 34,829 REFERENCE/DOCKET NUMBER: 32,721 TELEOMMUNICATION INFORMATION: TELEPHONE: (216) 241-0816 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2483 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO US-08-526-964-1		C 28 37 1.2 724 C 29 37 1.2 732 C 30 37 1.2 782 C 31 37 1.2 827 C 32 37 1.2 827 C 33 37 1.2 827 C 34 37 1.2 834 C 35 36.8 1.1 1850 C 36 36 1.1 2656 C 39 36.6 1.1 2656 C 39 36.6 1.1 8700 C 40 36.6 1.1 8700 C 41 36.6 1.1 8700 C 42 36.4 1.1 8700 C 43 36.2 1.1 934 C 44 36.2 1.1 935 C 45 36 1.1 2251
%; Score 41.6; DB 1; Length %; Pred. No. 0.16; 0; Mismatches 59; Indel	Alan M Steven  O Uncleotide Integrase Preparation 17 Halter & Griswold r Avenue  C-DOS/MS-DOS TRelease #1.0, Version #1.30 TA: US/08/526,964 US/08/526,964 US/08/526,964  TION: E E E E C-BER 22727/00127 RRMATION: CS: CS: CS: CS: CS: CS: CS: CS: CS: CS	ALIGNMENTS	4 US-08-998-416-683 4 US-08-998-416-1336 4 US-08-998-416-224 4 US-08-998-416-535 4 US-08-998-416-538 4 US-08-998-416-538 4 US-08-998-416-305 3 US-08-617-860B-32 2 US-08-605-106-4 4 US-09-117-257-7 2 US-08-917-257-7 2 US-08-645-193B-18 1 US-08-645-193B-18 1 US-08-645-193B-18 1 US-08-731-722-6 2 US-08-731-722-6 5 5231168-1 4 US-08-991-677-11
ch 2483; els 1; Gaps 1			Sequence 683, App Sequence 1036, Ap Sequence 272, App Sequence 234, App Sequence 535, App Sequence 305, App Sequence 305, Appli Sequence 4, Appli Sequence 7, Appli Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli

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DEFINITION
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                                                                                                                                                                                                                                                                                                                      - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 964)
                                                                                                                                                                                                                                    d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - BP 191 91006 EVRY cedex - FRANCE (E-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope.
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
80 a 100 c 132 g 281 t
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/clone_lib="DrosBAC"
/clone="BACN37015"
                                                           /db_xref="taxon:7227"
                                                                                       /organism="Drosophila
/plasmid="pBeloBAC11"
                                                                                                                                                                               Location/Qualifiers
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Pred. No. 0.
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                                                                                                                   melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  segref@genoscope.cns.fr
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FEATURES

Query Match

1.5%;

Score 48;

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Length 1101;

COMMENT

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JOURNAL

TITLE AUTHORS SOURCE KEYWORDS

ORGANISM

VERSION ACCESSION

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SOURCE
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TITLE
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                                                                                                                                                                                                      AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr -
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                           ø
                                                                                        /organism="Drosophila
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                   /clone="BACR05N11"
/note="end : TET3"
7 c 28 g
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                                                                                                                                                                                                                  TYYTTTTTTYAT 861
                                                                                                                                                                                                                                                                                       CTTAYTATTAATATATTTTAAAHYAYYTAATWTTTNAHCAAAAAMAWTAAAAAYYATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                     C23700 Dictyostelium discoideum FC (H.Urushihara) Dictyostelium
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 999)
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Drosophila melanogaster genome survey sequence T7 end of BAC
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/clone="BACN17C05"
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/plasmid="pBeloBAC11"
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                                                                                                                                                         Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Email: d402hu@sakura.cc.tsukuba.ac.jp. Location/Qualifiers
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Shimizu, H. and Urushihara, H. Sexual-cDNA in CSM Unpublished (1997)
                                                                Seq primer: M13-Reverse
Class: shotgun
                                                                                                                        Email: bjloftus@tigr.org Clones are derived from the
                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                               1 (bases 1 to 893)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
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              quality sequence stop: 811.
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/clone="FC-AB19"
/clone_11b="Dictyostelium discoideum
/clone_110 c 79 g 231 t
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/strain="KAX3"
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                                                 TTTATTTTAAAAAACAGTTAAATAATTAATAGACAATAATCTATTCTTATTGACTTCTTTT 3198
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
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/clone_lib="RPCI-98"
/clone="BACR27A24"
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                                                                                                                                                                                                      Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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/note="Genoscope sequence ID : COAG215CF11SP1-end PUC-Ori"
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/db_xref="taxon:99883"
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                                                                                                Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
7225K13 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 723)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS; genome survey sequence. Tetraodon nigroviridis.
                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                  Genoscope.
                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis
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                                                                                                                                                                                                                     (bases 1 to 723)
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/db_xref="taxon:99883"
/clone="225K13"
/clone_lib="G"
                                                                                      Location/Qualifiers
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16.6%; Pred. No. 0.05;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence
BACN15E09 of Drosophila
BACN15E09 of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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/plasmid="pBeLoBACI1"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACNI5E09"
/clone="BACNI5E09"
/note="end: T77"
/note="end: T77"
a 179 c 151 g 370 t 186 ot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                BP 191 91006 EVRY cedex - FRANCE (E-mail : Web : www.genoscope.cns fr)
                                                                                                                                                                                                          Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1017)
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15P11 of DrosBAC library from Drosophila melanogaster (from BacN15P11)
                                                                                                                                                                                                                                                         Genoscope
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/note="Genoscope sequence ID : COAG222CF06LP1-end : T7"
/note="Genoscope sequence ID : COAG222CF06LP1-end : T7"
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/db_xref="taxon:99883"
/clone="222111"
Location/Qualifiers
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                                                                                                                                                                                                                                                                             Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BBGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                СААМИМТААААААААААААААААААААААНТТТТТТАҮССАТТТТТТТҮ 988
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                                                                                                                                                                                                               and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="apc1-98"
/clone="BACR08K10"
                   /note="end : 64 c
                                                                                                                                                                                      Location/Qualifiers
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/note="end : T7"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                            CNS0167M 1201 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15M24 of DrosBAC library from Drosophila melanogaster (fr
                                                                                Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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AL106396.1

    Web : www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as

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Direct
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1 (bases 1 to 1201)
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1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29P01"
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Pred. No. 0.0044;
4; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNS020K7 1092 bp DNA GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 222L11 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part
collaboration with the European Drosophila Genome Project (EDC
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fi
              Human gene number estimate
Tetraodon nigroviridis DNA
                                                       Bernot, A., Fizames, C., Wincl
Saurin, W. and Weissenbach, J
                                                                                               2 (bases 1 to 1092)
Roest-Crollius, H., Jaillon, O.,
                                                                                                                                      Unpublished
                                                                                                                                                                                                                    Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot
                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis
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Tetraodon nigroviridis.
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                                                                                                                                                                                                   Weissenbach, J
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/plasmid="pBeloBAC11"
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/clone="BACN15M24"
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9; Mismatches
                                                                                                                                                           Tetraodon nigroviridis
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                                                                              Wincker, P., Brottier, P.,
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                                                                                             Dasilva, C.,
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                                                                                                 Bouneau, L., Fisher, C.,
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                                      wide analysis using
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AL069797
                                                            Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR29L15 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ALO69797
        Genoscope
                   Pterygota; Neoptera; Endopterygota; Diptera; Muscomorpha; Ephydroidea; Drosophilidae; Dros
                             Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                GSS.
    Direct Submission
                                                      AL069797.1
                                           fruit fly
              (bases 1 to 1101)
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CNS0177R
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                         Brachycera;
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ALU62726 Drosophil
C92840 C92840 Dict
C92114 C92114 Dict
ALU77933 Drosophil
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AL107364 Drosophil
C23700 C23700 Dict
AZ535391 ENTBO88TR
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AL105023 Drosophil
AV680925 AV680925
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AL106572
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AL053618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AATTCTTACTTGCGTCATATAAAATAGAAAACTCAGAGAGTCAAGATAAAAATTCTTGAC
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CNSODEO7 1101 bp DNA GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29PO1 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ALD69440
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Perfect score:
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polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae C;Speckes: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: C86546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, 'Mucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA A;Residues: 1-936 <STO> A;Cross-references: GB:BA000008; NID:g8978817; PIDN:BAA98653.1; GSPDB:GN00142 A;Experimental source: strain J138 C;Genetics: A;Gene: pmp_7
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                                                                             AFNKSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMAY 886
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Search completed: October 2, 2001, 03:29:09 Job time: 1326 sec

CWL029

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Pmp_3 [imported] - Chlamydophila pneumoniae (strain J138)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: H86492
R:Shiral, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
A:Accession: H86492
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-772 <STO>
A:Cross-references: GB:BA000008; NID:g8978389; PIDN:BAA98226.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_3_2
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KTESLPPPPPTLSTDHTSWGGYVWAGELGTR--VAVENTSGRGFFREYTPFVKVQAVYSR
                                                                         NQGTVYGGTLYYQHNETYISLPC-----KLRPCSLSYVPTEIPVLFSGNLSYTHTDNDL
                                                                                                        FWCAGLSNFFHKDSTKTRRGFRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAK 544
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A; Molecule type: DNA
A; Residues: 1-936 <ARN>
A; Residues: 1-936 <ARN>
A; Cross-references: GB: AE001627; GB: AE001363; NID: g4376721; PIDN: AAD18589.1;
A; Cross-references: Strain CWL029
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polymorphic membrane protein G family CP0306 [imported] - Chlamydophila pneu C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: B72077; B81592 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; GNature Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206806
                                                    A;Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:AAD18591.1; PID: A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Schen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; H., C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Sa Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
                  A; Reference number: A81500; MUID: 20150255
A; Accession: B81592
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A;Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38163.1; PID:g718
A;Experimental source: strain AR39, HL cells
C;GenetLos:
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                                               TLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTS
                                                                   AISRDFSDSHLYNLAIPLGIKLEK--RFAEQYYHVVAMYSPDVCRSNPKCTTTLLSNQGS
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                                                                                                                 -- KGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIKVEASYIHQDSFKERNT
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376 KLIMDLGTSLVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDES	QY 316 NKEYTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANS 375 :: : :	QY 258 IGATGTVSHSAIDLGTSAKITALRAAQGHTIYEYDPITVTGSTSVADALNINSPDTGD 315         ::  : :           :       :       :   Db 348 IVATTPQTTKRNSIDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLNKADAGN 407	QY 205 HTKNLTLSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNT 257 :	Qy 148 INVKGNLSLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTRGGAI 204       ::   :     :   :	Query Match  32.6%; Score 1400.5; DB 2; Length 928; Best Local Similarity 34.3%; Pred. No. 4.7e-73; Matches 330; Conservative 161; Mismatches 315; Indels 157; Gaps 23;  Qy 1 MKIPLRELLI-SLYPILSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYV 59	RESULT 10 GB1591 polymorphic membrane protein G family CP0303 [imported] - Chlamydophila pneumoniae (stra C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C; Species: Chlamydophila pneumoniae C; Species: Chlamydophila pneumoniae R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000 A, Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A; Reference number: A81500; MUID:20150255 A; Accession: G81591 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-928 (REA> A; Cross-references: GB.AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38160.1; PID:g718923 A; Experimental source: strain AR39, HL cells C; Genetics: A; Gene: CP0303	Qy 722 QDSFVELGAISRDFSDSHLYNLAIPLGIKLEKRFAEQYYHVVAMYSPDVCRSNPKCT 778
170	Qy 118 AANKTYTLSGFSALSFLKSPASTYTNGLGAINVKGNLSLLDNDKVLIQDNES 169	QY 58 YVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNELGGGFSFTFSNIDATTASGAAIGSE 117	Qy 1 MKIPLRFLLISLVPTLSMSNLLGAATTE-ELSASNSFDGTTSTTSFSSKTSSATDGTN 57      :          :       :       :    :	Query Match 32.0%; Score 1376.5; DB 2; Length 928; Best Local Similarity 36.6%; Pred. No. 1.1e-71; Matches 349; Conservative 125; Mismatches 341; Indels 139; Gaps 23;	RESULT 11 E86546  polymorphic outer membrane protein G/I family [imported] - Chlamydophila pneumoniae ( C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: E86546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Rss. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349 A;Accession: E86546 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-928 (570> A;Cross-references: GB:BA000008; NID:98978819; PIDN:BAA98655.1; GSPDB:GN00142 A;Experimental source: strain J138 C;Genetics: A;Gene: pmp_9	Qy 608 TYAGSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGOLSYGHTDHRMKTES 667     :	Qy 436 FYQNGFLNEDHSYDGILELDAGKDIVISADSRSINAVQSPYGYQGKWTINWSTD 489

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polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: G86546
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                                                                                                                                    NFKESGAEARAFDDGDLVNCSIPVGIRLEKISEDEKNNFEISLAYIGDVYRKNPRSRTSL
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A; Molecule type: DNA
A; Residues: 1-928 <STO>
A; Cross references: GB:BJ
A; Experimental source: st
C; Genetics:
A; Gene: pmp_10
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A;Title: Comparison of whole genome sequences of chlamydia | A;Reference number: A86491; MUID:20330349
A;Accession: C86546
                                                                                                                                                          GISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNTNFAK
                                                                                                                                                                                                                                                                                                                                                                                           MKIPLRFLLI-SLYPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYV 59
                                                                                    TYAGSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGQLSYGHTDHRMKTES
                                                                                                                                 GVANFLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENLISFAFCQLFGSDKDFLVAKNHTD
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LPPPPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGF-----FREYTPFVKVQAVYSR 721
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                                             TYAGAFYIQHITECSGFIGCLLDK------LPGSWSHKPLVLEGQLAYSHVSNDLKTKY
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30; Conservative
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ce: strain J138
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A;Status: preliminary
A;Molecule type: DNA
A;Rosiduss: 1-330 <ARN>
A;Cross-references: GB:AE001627; GB:AE001363; NID:g4376721; PIDN:AAD18590.1; PID:g43767:
A;Experimental source: strain CWL029
C;Genetics:
C;Genetics:
A;Gene: pmp_8
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AITTKTLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQLVFMNNKGETGGGALG
                                                                       TADKALTFTGFSNLSFIAAPGTTVASGKSTLSSAGALNLTDNGTILFSQNVSNEANNNGG
                                                                                                                                                                YVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSE 117
                                                                                                                                                                                                                                                         MKIPLRFLLISLVPTLSMSNLLGAAT --- TEELSASNSFDGTTSTTSFSSKTSSATDGTN 57
                                                                                                        AANKTVTLSGFSALSFLKSPASTVTNGLGAINVKGNLSLLDNDKVLIQDNFS-----
                                                                                                                                                                                                                       MKIPLHKLLIS -- STLVTPILLSIATYGADASLSPTDSFDGAGGST -FTPKSTADANGTN
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                                                                                                                                             YVLSGNYYINDAGK-GTALTGCCFTE--TTGDLTFTGKGYSFSFNTVDAGSNAGAA-AST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTRYTSYPEA-----QGSWTNNSGALELGGSLALYLPKEAPFFQGYFPFLKFQAVYSRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KATVSWAKQSFNPTAEQEAPLVPNLLWGSFIDVRPFQNFIELGTEGAPYEKRFWVAGISN 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTESLPPPPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGFFREYTPFVKVQAVYSRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLRLQHDASLYSVVSILLGEGGLREILLPYVS-----KTLPCSFYGQLSYGHTDHRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGFLNEDHSYDGIL--ELDAGKDIVISADSRSINAVQSP---YGYQGKWTINW--STDDK 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MQPGTKLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTITLTSPLVFQDSSGNFYE
                                                                                                                                                                                                                                                                                             Conservative 124;
                                                                                                                                                                                                                                                                                                                32.9%;
37.0%;
                                                                                                                                                                                                                                                                                             Score 1413.5; DB 2;
Pred. No. 8.4e-74;
4; Mismatches 332;
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                   LSNQGSWKTKGSNLARQAGIVQASGFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF
                                                                      NEKESGAEARAFDDGDLVNCSIPVGIRLEKISEDEKNNFEISLAYIGDVYRKNPRSRTSL
                                                                                                       SFVELGAISRDFSDSHLYNLAIPLGIKLEKRFAEQ--YYHVVAMYSPDVCRSNPKCTTTL
                                                                                                                                                                                 KTESLPPPPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGFFREYTPFVKVQAVYSRQD
                                                                                                                                                                                                                                                                                            FFHKDKSGTNQAFRHKSYGYIVGGSAEDFSENIFSVAFCQLFGKDKDLFIVENTSHNYLA
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                                                                                                                                             DTRYTSYPEA-----QGSWTNNSGALELGGSLALYLPKEAPFFQGYFPFLKFQAVYSRQQ
                                                                                                                                                                                                                                                      SLRLQHDASLYSVVSILLGEGGLREILLPYVS----KTLPCSFYGQLSYGHTDHRM
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RESULT A81591

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, C Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumc A;Reference number: A81500; MUID:20150255 polymorphic membrane protein G family CP0307 [imported] - Chlamydophila pnei C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000 C;Accession: A81591 pneumoniae 0 **Hicke** ŝ

Chlamydia pneumoniae

AR39

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Salzbe

A; Status: preliminary

A;Molecule type: DNA A;Residues: 1-930 <REA> A;Residues: 1-930 <REA> A;Cross-references: GB:AE002193; GB:AE002161; NID:g7189234; PIDN:AAF38164.1; PID:g718 A;Experimental source: strain AR39, HL cells C;Genetics: A;Gene: CP0307

Query Match Best Local Similarity 32 37 .9%; Score Pred. 1413.5; DB No. 8.4e-74; <u>ب</u> Length

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R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; SNucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae A;Reference number: A81500; MUID:20150255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-949 < REA>
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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Best Local Similarity
Matches 339; Conserv
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                                                                                                  KQSFNPTAEQEAPLVPNLLWGSFIDVRPFQNFIELGTEGAPYEKRFWVAGISNVLHRSGR
                                                                                                                                                       F-SLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTATNTKEATATWT
                                                                                                                                                                                                                                     TAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHMFSHDQL
                                                                                                                                                                                                                                                           NTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDESFYQNGFLNEDHS
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ENRKGFRHTSGGYVIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNNSRTYGGTLFFKHS
                                    ENORKFRHVSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNTNFAKTYAGSLRLOHD
                                                                                                                                                                                          YDGILELDAGKDIVISADSRSINAV-----QSPYGYQGKWTINWSTD----DKKATVSWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNLTFSGFSLLSFDSSPSTTVTTGQGTLSSAGGVNLENIRKLVVAGNFSTADGGAIKGAS 192
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                                                                           KTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGD
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35.8%; Pred. No. 1e-74;
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae A;Reference number: A86491; MUID:20330349
A;Accession: D86546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: D86546
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A;Residues: 1-930 <570.
A;Cross-references: GB:BA000008; NID:g8978818;
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_8
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YTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLI 378
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RESULT 4 D72077 D72077  D72077  A D72077  D72077  C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (strain C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C; Accession: D72077 C; Accession: D72077 R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grim Nature Genet. 21, 385-389, 1999 A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A; Reference number: A72000; MUID:99206606 A; Accession: D72077 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-928 <arn> A; Residues: 1-928 <arn> A; Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:AAD18593.1; PI</arn></arn>	Qy 737 DSHLYNLAIPLGIK-LEKRFAEQY-YHVVAMYSPDVCRSNPKCTTTLLSNQGSWKTKGSN 794	:	Qy 559 ENQRKFRHVSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNTNFAKTYAGSLRLQHD 618   ::  :  :  : -:	Qy 499 KQSFNPTAEQEAPLVPNLLMGSFIDVRPFQNFIELGTBGAPYEKRFWVAGISNVLHRSGR 558           : : :             :   : :       : :       : :	Qy 448 YDGILELDAGKDIVISADSRSINAVQSPYGYQGKWTINWSTDDKKATVSWA 498 : : ::  :    :       :  :  :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :	Qy 388 NTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDESFYQNGFLNEDHS 447	Qy 328 EKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDLGTSLVA 387	Qy 268 AIDLGTSAKITALRAAQGHTIYFYDDITVTGSTSVADALNINSPDTGDNKEYTGTIVFSG 327	Qy 211 LSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATGTVSHS 267	QY 181SLKIANNKSLSFIGNSSSTRGGAIHTKNLT 210       :	Qy 181 180  Db 172 FLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSI 231	Qy 121 KTVTLSGFSALSFLKSPASTVTNGLGAINVKGNLSLLDNDKVLIQDNFSTGDGGAINCAG 180   :
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RESULT 2
E86492
polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae (str: Cspecies: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: E86492
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Accession: E86492
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-712 <STO>
A;Cross-references: GB:BA000008; NID:g8978386; PIDN:BAA98223.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genet: pmp_2_1
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A;Title: Comparison of whole genome sequences of chlamydia p A;Reference number: A86491; MUID:20330349
A;Accession: H86546
                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-928 <STO>
A;Cross-references: GB:BA000008; NID:g8978822; PIDN:BAA98658.1;
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_11
                                                                                                                                                                                                                                                                                              polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: H86546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba,
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                       KDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSEAAN 120
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                                              MKTSIPWVLVSSVLAFS-CHLQSLANEELLSPDDSFNGNIDSGTFTPKTSA----TTYSL
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35.8%; Pred. No. 1e-74;
tive 147; Mismatches 3
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Scoring table: BLO	Perfect score: 4298 Sequence: 1 MK	Title: US	Run on: Oct	OM protein - protei	Q
BLOSUM62	4298 1 MKIPLRFLLISLVPTLSMSNFEWRGSSRSYNVDAGSKIKF 841	US-09-446-677B-8	October 2, 2001, 03:29:00; search time 76.79 Seconds (without alignments) 834.260 Million cell updates/sec	OM protein - protein search, using sw model	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Searched: BLOSUM62
Gapop 10.0 , Gapext 0.5 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	5	4	ω	N	1	Result No.
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## ALIGNMENTS

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ISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLG 588 : : ::   :    :   :      ::  NANITTKTGDINGKVESSSGSVTLVATGATLAVG 1036	DDKKATVSWAKOSFNPTAEQEAPLVPNILLWGSFIDVRPFQNFIELGTEGAPYEKRFWVAG 548	ESFYONGFLNEDHSYDGILÈLDAGKDIVISADSRSINAVQSPYGYQGKWTINWST 488	GTSLVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISD 433	VFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDL 381	VSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKBYTGTI 323 :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : :   : : :   : : :   : : :   : : :   : : :   : : :   : : : :   : : :   : : :   : : : :   : : : :   : : : : :   : : : : : : : : : : : : : : : : : : : :	IHTKNLTLSSGGETLFOGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATGT 263       :  :  :	QDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTRGGA 203 :               :   :	SEAANKTVTLSGFSALSFLKSPASTVTNGLGAINVKGNLSLLDNDKVLI 164      :    :	NVPKTGETØSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIG 115	SLYPTLSMSNLLGAATTEELSASNSFDGTTŠTTSFSSKTSSATDGTNYVFKDSVVIE 67   ::

Search completed: October 2, 2001, 03:27:47 Job time: 7229 sec

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APPLICATION NUMBER: US PCT/US

FILING DATE: 16-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 920570

FILING DATE: 16-MAR-1992

ATTORNEY_AGENT INFORMATION:

NAME: Berkstresser, Jerry W

REGISTRATION NUMBER: 22,651

PREFERENCE COCCUMENT NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 415-08: INFORMATION FOR SEQ ID NO:
    1275
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LENGTH: 1536 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1038-625
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                               1097 HSKVETSGSNNNTEDSSDNNAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTIN 1156
                                                                                                                                                                                                                                                                                                                                                        1037 LKLTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTL 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                  10 ISLVPTLSMSNLLGAATTEE-----LSASNSFDGTTS-TTSFS----SKTSS----- 51
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AL INFORMATION:
                                         GGAI--HTKNLTLSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTI 258
                                                                                                                                                                         ATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGS 1216
                                                                                      TIKGTESVTTSS--QSGDIGGTISGGTVEVKATESLTTQSNSKIKATTGEANVTSATGTI 1274
                                                                                                                                                                                                   FTFSNIDATTASGAAIGS-EAANKTVTLS---GFSALSFLKSPASTVTNGLGAINVKGNL 154
                                                                                                                                                                                                                                                                                                           ----ATDGTNYVFKDS------VVIENVPKTGETQSTSCFKNDAAAGDLNF-LGGGFS 98
GGTISGNTVNVTANAGDLTV--GNGAEINATEGAATLTTSSGKLTTEASS----
                                                                                                                               SLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNS-----STR 200
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23.3%; Pred. No. 2.3e-08;
ative 74; Mismatches 185; Indels 13
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; TOPOLOGY: US-08-728-470-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08728470 Patent No. 5928651
                                                                                                            TELEFAX: (703) 415-08
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                 NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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                                                                       LENGTH:
                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                     1338 amino acids
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                                                                                                                                 (703)
                   linear
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                (703) 415-0810
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16-MAR-1992
                                    single
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High Molecular Weight Surface Proteins
of No. 5928651-Typeable Haemophilus
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Query Match
Best Local Similarity Matches 141;

Conservative

4.7%; Score 200.5; DB ( 22.0%; Pred. No. 4.5e-08 Live 99; Mismatches 260

DB 2; 269;

Length 1338; Indels

131;

Gaps

27;

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RESULT 13
US-08-617-697-2
; Sequence 2, Application US/08617697
; Patent No. 5977336
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                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                  APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
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CORRESPONDENCE ADDRESS:
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                                                               ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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  MEDIUM TYPE:
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                                              22202-0286
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Floppy disk
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Best Local Similarity
Matches 118; Conserv
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FILING DATE: 05-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US P
FILING DATE: 16-MAR-1993
1443 VKYIQPGIASVDEVIEAKRILEKVKDL 1469
                                                                                                                                                                                                                                                       1326 SAKGQVNLSAQDGSVAGSINAANVT------LNTTGTLTTVKGSNINAT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1037 LKLTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKYTFNQVKDSKISADGHKYTL 1096
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LENGTH: 1536 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                          1217 TIKGTESVTTSS--QSGDIGGTISGGTVEVKATESLTTQSNSKIKATTGEANVTSATGTI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              201 GGAI--HTKNLTLSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTI 258
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SOFTWARE: Patentin Balantin
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STRANDEDNESS: sin
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REGISTRATION NUMBER: 22,651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                       ESFYONGFLNEDHSYDGILELDAGKDI 460
                                                                                   ---SGSVIATTSSRVNITGDLITINGLNIISKNGINTVL----LKGVKI---
                                                                                                                          MDLGTSLVANTES-IELTNLEINIDSL----RNGKKIKLSAATAQKDIRIDRPVVLAISD 433
                                                                                                                                                                      -SGTLVIN-----AKDAE-----LNGAALGNHTVV--
                                                                                                                                                                                                                                                                                             GATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKE 318
                                                                                                                                                                                                                                                                                                                                        GGTISGNTVNVTANAGDLTV--GNGAEINATEGAATLTTSSGKLTTEASS------HIT 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNS------SSTR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTFSNIDATTASGAAIGS-EAANKTVTLS---GFSALSFLKSPASTVTNGLGAINVKGNL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ATDGTNYVFKDS------VVIENVPKTGETQSTSCFKNDAAAGDLNF-LGGGFS
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16-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/302,832
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                                                                                                                                                                      -NATNANG
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RESULT 14 US-08-719-641-2

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                                                                                                                                                                                               ; MOLECULE TYPE: DNA (genomic) US-08-469-880-2
                                                                                     Query Match 4.8
Best Local Similarity 23.3
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US PCT/US93/02:
FILING DATE: 16-MAR-1993
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                             -08-469-880-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quence 2, Application US/08469880 tent No. 5876733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1443 VKYIOPGIASVDEVIEAKRILEKVKDL 1469
1037 LKLTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTL 1096
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1369 -SGTLVIN-----AKDAE-----LNGAALGNHTVV----NATNANG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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                                          10 ISLVPTLSMSNLLGAATTEE-----LSASNSFDGTTS-TTSFS----SKTSS----- 51
                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                         TOPOLOGY:
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STREET: Bldg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTGTIVFSGEKLTEAEAKDEKNRTSKLLONVAFKNGTVVLKGDVVLSANGFSODANSKLI 378
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                 (703) 415-0810
(703) 415-0813
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                                                                                                                                                                                                                                                           single
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                                                                                4.8%; Score 205; DB 2; I
23.3%; Pred. No. 2.3e-08;
tive 74; Mismatches 185;
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                                                                                                                           Length 1536;
                                                                                   Indels 130;
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FILING DATE: CLASSIFICATION: 424 PROR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PILING DATE: 16-MAR-1993 PRIOR APPLICATION NUMBER: US PCT/US93/02166 PILING DATE: 16-MAR-1993 PRIOR APPLICATION NUMBER: US PCT/US93/02166 PILING DATE: 16-MAR-1993 PRIOR APPLICATION NUMBER: GB 9205704.1 PILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION: NAME: Berkstresser, Jerry W REGISTRATION NUMBER: 22,651 REFERENCE/DOCKET NUMBER: 1038-633	pplication US 28651 Barenkamp, NVENTION: Hi NVENTION: Hi SEQUENCES: 1 SEQUENCES: 1 SEQUENCES: 1 SECONT ADDRESS: ENCE ADDRESS: Flopy IN 18 PC COMM SYPE: Floppy IN 18 PC COMM SYSTEM: PC PATENTION DATA TON NUMBER:	Oy 319 YTGTIVESGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKANGFSQDANSKLI 378	Db 1157 ATTGNVEITAQTĠSILĠGIESSGGSVTLTATEĠALAVŚNISGNTVTVTANSGALTTLAGS 1216  Qy 155 SLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTR 200  :: :	52ATDGTNYVFKDSVVLENVPKTGETQSTSCFKNDAAGGLNF-LGGGFS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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1443 VKYIQPGIASVDEVIEAKRILEKVKDL 1469
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ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
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PRIOR APPLICATION NIMBER: GB 9205704.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1097 HSKVETSGSNNNTEDSSDNNAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTIN 1156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/302,832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202-0286
                                       ESFYQNGFLNEDHSYDGILELDAGKDI 460
                                                                                                                                                                                                                                                                                              GATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKE 318
                                                                                                                                                                                                                                                                                                                                                                                                                           TIKGTESVTTSS--QSGDIGGTISGGTVEVKATESLTTQSNSKIKATTGEANVTSATGTI 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNS-----STR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ATDGTNYVFKDS------VVIENVPKTGETQSTSCFKNDAAAGDLNF-LGGGFS 98
                                                                                  ---SGSVIATTSSRVNITGDLITINGLNIISKNGINTVL----LKGVKI-----D 1442
                                                                                                                       MDLGTSLVANTES-IELTNLEINIDSL----RNGKKIKLSAATAQKDIRIDRPVVLAISD 433
                                                                                                                                                                    -SGTLVIN-----AKDAE-----LNGAALGNHTVV----NATNANG-----
                                                                                                                                                                                                            YTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLI 378
                                                                                                                                                                                                                                                        SAKGQVNLSAQDGSVAGSINAANVT - -
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                                                                                                                                                                                                                                                                                                                                                                                GGAI--HTKNLTLSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTI 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTFSNIDATTASGAAIGS-EAANKTVTLS---GFSALSFLKSPASTVTNGLGAINVKGNL 154
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16-MAR-1993
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                                                                                                                                                                                                                                                        -----LNTTGTLTTVKGSNINAT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO:
1326 SAKGQVNLSAQDGSVAGSINAANVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: JW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,198
FILING DATE: 13-DEC-1995
                                                                                                                                                                                    1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1037 LKLTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTL 1096
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APPLICANT: ST. GEME III, JOSEDH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             155 SLLDNDKYLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNS-----STR 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2001 Je:
STREET: Bldg. 1
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 ISLVPTLSMSNLLGAATTEE-----LSASNSFDGTTS-TTSFS----SKTSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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                                 GATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKE 318
                                                                                      GGTISGNTVNVTANAGDLTV--GNGAEINATEGAATLTTSSGKLTTEASS------HIT 1325
                                                                                                                                  GGAI--HTKNLTLSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTI 258
                                                                                                                                                                                    TIKGTESVTTSS--QSGDIGGTISGGTVEVKATESLTTQSNSKIKATTGEANVTSATGTI 1274
                                                                                                                                                                                                                                                                           ATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGS 1216
                                                                                                                                                                                                                                                                                                                      FTFSNIDATTASGAAIGS-EAANKTVTLS---GFSALSFLKSPASTVTNGLGAINVKGNL 154
                                                                                                                                                                                                                                                                                                                                                                      HSKVETSGSNNNTEDSSDNNAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTIN 1156
                                                                                                                                                                                                                                                                                                                                                                                                                  ----ATDGTNYVFKDS------VVIENVPKTGETQSTSCFKNDAAAGDLNF-LGGGFS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1536 amino acids
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.8%; Score 205; DB 2;
23.3%; Pred. No. 2.3e-08;
ative 74; Mismatches 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2:
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---LNTTGTLTTVKGSNINAT----- 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1536;
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us-08-038-682-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08038682 Patent No. 5549897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1161
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1106
                                                 SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1190 LTTKSG-----SKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGD-LTVG 1235
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1056 TAKDGRDLTIGNSNDGNSG------AEAKTVTFNNVKDSKISADGHNVTLNSKVKT 1105
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       731
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                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                              CITY: Arlington
STATE: Virginia
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             APPLICATION NUMBER: US/08/038,682 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                        STREET: 2001 Je
STREET: Bldg. 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAIDLGT----SAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDN-KEYT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTLGGQ------NSSSSITG-----NITIEKAANVTLEANNAPNQQNIRDRVI 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTIVFSGEK-----LTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISIL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCAGSLKIANNKSLSFIGNSSSTRGGAIHTKNLTLSSGGETLFQGNTAPTAAG----- 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGTEGAPYEKRFWVAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMP--GGDTLSLG 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSSNGGRESNSDNDTGLTIT----AKNVEVNKDITSLKTVNITASEKVTTTAGS-TINAT 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-----CFKNDAAAGD------LNFLGGGFSFTFSNIDATTASGAAIGSEA-----
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                                                                                                                                                                                                                                                                                             E: Shoemaker and Mattare, Ltd
                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS
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US-08-302-832-2
; Sequence 2, Application US/08302832
; Patent No. 5603938
; GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
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Best Local Similarity 23.3

Matches 118; Conservative
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                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                   APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Su
TITLE OF INVENTION: of No. 5603938-Typeable
NUMBER OF SEQUENCES: 8
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LENGTH: 1536 amino aci
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NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                  1443 VKYIQPGIASVDEVIEAKRILEKVKDL 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                      1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1037 LKLTQDLNISGFNKAEITAKDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTL 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1097 HSKVETSGSNNNTEDSSDNNAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTIN 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 SLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNS------SSTR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAI--HTKNLTLSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGS 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTFSNIDATTASGAAIGS-EAANKTVTLS---GFSALSFLKSPASTVTNGLGAINVKGNL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ATDGTNYVFKDS------VVIENVPKTGETQSTSCFKNDAAAGDLNF-LGGGFS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SGSVIATTSSRVNITGDLITINGLNIISKNGINTVL----LKGVKI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDLGTSLVANTES-IELTNLEINIDSL----RNGKKIKLSAATAQKDIRIDRPVVLAISD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLI 378
                     Arlington
  Virginia
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415-0813
NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74;
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                                                                                                                                                                                                                                                                                                                                                                                             460
                                                                                                                                                                  Surface Proteins
                                                                                                                                             Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING LANCE 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
APPLICATION DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 415-08: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/617,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1477 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                         321
                                                                                                                                                                                                                                                  836
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                                                                936 GVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKE 995
                                                                                                                                                                                                      230
                                                                                                                                                                                                                                                                                                                                      791 KINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISIL-------GGN 835
                                                                                                                                                                                                                                                                                                                                                                                                                             731
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 SNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGETQST 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
GTIVFSGEK-----LTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGF-----
                                                                                                           SAIDLGT-----SAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDN-KEYT
                                                                                                                                                                                                                                                                                                                                                                             -ANKTVTLSGFSALSFLKSPASTVTNGL--GAINVKGNLSLLDNDKVLIQDNFSTGDGGA 175
                                                                                                                                                      KLGSLLV--NGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINITQ 935
                                                                                                                                                                                                  KGGAIAIADSGTLSISGDSGDI------IFEG---NTIGATG-----TVSH
                                                                                                                                                                                                                                                  VTLGGQ--
                                                                                                                                                                                                                                                                                         INCAGSLKIANNKSLSFIGNSSSTRGGAIHTKNLTLSSGGETLFQGNTAPTAAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNSKGLTTQYRSSAGVNFNGVNGNMSFNLK-----EGAKVNFK-----LKPNENMNT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-----CFKNDAAAGD------LNFLGGGFSFTFSNIDATTASGAAIGSEA----- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.8%; Score 205; DB 2; Length 1477; 20.7%; Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88; Mismatches
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Query Match 4.8%; Subset Local Similarity 20.7%; P. Matches 136; Conservative 88;

Score 205; DB 4; Length 1477; Pred. No. 2.2e-08; B; Mismatches' 240; Indels 19:

Indels 194;

Gaps

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US-08-719-641-4
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                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0/
FILING DATE: 16-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1190 LTTKSG-----SKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGD-LTVG 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
STATE: Virginia
                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2001
STREET: Bldg.
                                                                                                                                                                         TELEPHONE:
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                       (7<del>0</del>3)
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                      linear
                                                                                                                                                                       (703) 415-0810
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                                        single
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High Molecular Weight Surface Proteins
of No. 6218141-Typeable Haemophilus
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                                                                                                                                                                                           ZIP: 22202-0286

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPUTER:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHTIR Release #1.0, V.

CURRENT APPLICATION DATA:
                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1190 LTTKSG-----
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                                       PRIOR APPLICATION DATA:
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                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2001 Je
STREET: Bldg. 1
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                  APPLICATION NUMBER:
                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNLTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEI 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKE 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISIL-------GN 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAATAQKDIRIDRPVYLAISDESFYQNGFLNEDHSYDGILELDAGKDIVISADSRSINAV 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTIVFSGEK-----LTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTLGGQ-----NSSSSITG-----NITIEKAANVTLEANNAPNQQNIRDRVI 877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-----CFKNDAAAGD------LNFLGGGFSFTFSNIDATTASGAAIGSEA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Shoemaker and Mattare, Ltd.
2001 Jefferson Davis Hwy., 1203 Crystal Plaza
16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGD-LTVG
                  US PCT/US93/02166
                                                                                                                                                                         US/08/728,470
                                                                                                                                                                                                                     Version
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US-08-728-470-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1477 amino acids
  1190
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                1056 TAKDGRDLTIGNSNDGNSG------AEAKTVTFNNVKDSKISADGHNVTLNSKVKT 1105
                                           533 LGTEGAPYEKRFWVAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMP--GGDTLSLG 588
                                                                                                                                  473
                                                                                                                                                                                                                     413
                                                                                                                                                                                                                                                                                                                                                        996 GNLTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEI 1055
                                                                                                                                                                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 KGGAIAIADSGTLSISGDSGDI------IFEG---NTIGATG-----TVSH 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 4.8%; Score 205; DB 2; 1 Local Similarity 20.7%; Pred. No. 2.2e-08; hes 136; Conservative 88; Mismatches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 SNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGETQST 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAIDLGT-----SAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDN-KEYT 320
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LTTKSG-----
                                                                                       ----NGKASITTKTGDISGTISGNTVSVSAT--
                                                                                                                                                                            SSSNGGRESNSDNDTGLTIT----AKNVEVNKDITSLKTVNITASEKVTTTAGS-TINAT 1160
                                                                                                                                                                                                   SAATAQKDIRIDRPVVLAISDESFYQNGFLNEDHSYDGILELDAGKDIVISADSRSINAV 472
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                                                                                                                                QSPYGYQGKWTINWSTDDKKATVSWAKQSFNPTAEQEAPLVPNLLWGSFIDVRPFQNFIE 532
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                                                                                                                                                                                                                                                                                                        ------SQDANSKLIMDLGTSLVANTESIELTNL---EINID--SLRNGKKIKL 412
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  SKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGD-LTVG 1235
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RESULT 6
US-08-617-697-4
; Sequence 4, Application
; Patent No. 5977336

US/08617697

GENERAL INFORMATION:

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Best Local Similarity
1056 TAKDGRDLTIGNSNDGNSG-----
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1477 amino acids
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APPLICATION TUMBER: US/08/530
FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
ATTORNEY_AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: JV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                           176
                                                                                                                                                                                                                             267 SAIDLGT-----SAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDN-KEYT 320
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STATE: Virginia
COUNTRY: U.S.A.
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STREET: Bldg.
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                                                                                                                                                                                      GVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKE 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGETQST 78
                                                                                                     GNLTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEI 1055
                                                                                                                                            GTIVFSGEK-----LTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGF----
                                                                                                                                                                                                                                                                                                                     KGGAIAIADSGTLSISGDSGDI------IFEG---NTIGATG-----TVSH 266
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    Shoemaker and Mattare, Ltd
    Jefferson Davis Hwy., 1203 Crystal Plaza

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VENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
VENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                      SQDANSKLIMDLGTSLVANTESIELTNL---EINID--SLRNGKKIKL 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.8%; Score 205; DB 2;
20.7%; Pred. No. 2.2e-08;
ative 88; Mismatches 240
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               -- AEAKTVTFNNVKDSKISADGHNVTLNSKVKT 1105
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                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4.15-0813
INFORMATION FOR SEQ ID NO: 4.
SEQUENCE CHARACTERISTICS:
LENGTH: 1477 ami-
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Patent No. 5876733
GENERAL INFORMATION:
                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US POFILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 LGTEGAPYEKRFWVAGISNVLHRSGRENORKFRHVSGGAVVGASTRMP--GGDTLSLG 588
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                                     19 SNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGETQST 78
                                                                                           Local Similarity
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                             STRANDEDNESS:
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STATE: Virginia
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STREET: Bldg.
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                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
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 SNSKGLTTQYRSSAGVNFNGVNGNMSFNLK-----EGAKVNFK-----LKPNENMNT 730
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                                                                                                                                                                                         linear
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01 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                                                                                       single
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                                                                         4.8%; Score 205; DB 2;
20.7%; Pred. No. 2.2e-08;
Live 88; Mismatches 240;
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RESULT 2
US-08-302-832-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1106
                                                                PRIOR APPLICATION DATA:
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5603938-Typeable Haemophilus
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                 STREET: 2001 Jeff
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 16-SEP-1994
                   APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992
                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGGAIAIADSGTLSISGDSGDI------IFEG---NTIGATG-----TVSH 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSSNGGRESNSDNDTGLTIT----AKNVEVNKDITSLKTVNITASEKVTTTAGS-TINAT 1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSPYGYQGKWTINWSTDDKKATVSWAKQSFNPTAEQEAPLVPNLLWGSFIDVRPFQNFIE 532
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APPLICATION DATA:
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                        US/08/302,832
                                                                                                                                                                                       #1.30
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RESULT 3
US-08-530-198-4
US-08-530-198-4
Sequence 4, Application US/08530198
Patent No. 5869065
GENERAL INFORMATION:
APPLICANT: BARENKAMP, STEPHEN J
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US-08-302-832-4
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                                                                                                                                                                                                                                1190
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LENGTH: 1477 amino acids
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                                                                                                                                                                                                                                                                          533 LGTEGAPYEKRFWVAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMP--GGDTLSLG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 KGGAIAIADSGTLSISGDSGDI------IFEG---NTIGATG-----TVSH 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        791 KINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISIL-------GN 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 4.8%; Score 205; DB 1; Local Similarity 20.7%; Pred. No. 2.2e-08; nes 136; Conservative 88; Mismatches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 10
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US-08-618-685-467-4
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Sequence 7, Appli Sequence 7, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli	Query Match 4.8%; Score 205; DB-1; Length 1 Best Local Similarity 20.7%; Pred. No. 2.2e-08; Matches 136; Conservative 88; Mismatches 240; Indels	US-08-038-682-4  US-08-038-682-4  Sequence 4, Application US/08038682  Patent No. 5540897  GENERAL INFORMATION: APPLICANT: BARENKAMP, STEPHEN J APPLICANT: ST. GEME III, JOSEPH W TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS NUMBER OF SEQUENCES: RUDBERS SEE: Shoemaker and Mattare, Ltd STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaz. STREET: Bidg. 1  CITY: Allington STATE: Virginia COUNTRY: U.S.A. ZIP: 2202-0268 COMPUTER READABLE FORM: COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25  CURRENT APPLICATION NUMBER: US/08/038,682  FILING DATE: 16-MAR-1993  CLASSIFICATION NUMBER: 22,651  REFERENCE/DOCKET NUMBER: 23,651  REFERENCE/DOCKET NUMBER: 1038-293  TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810  TELEPHONE: (703) 415-0810  TELEPAX: (703) 415-0813  INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LEGGH: 1477 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: protein US-08-038-682-4	28 178.5 4.2 1026 2 US-08-614-377A-7 29 178.5 4.2 1026 4 US-09-142-648B-7 30 176.5 4.1 1026 1 US-08-194-290-7 31 171 4.0 1248 2 US-08-465-956-17 32 171 4.0 1248 3 US-08-465-966-17 34 165.5 3.9 1287 1 US-08-200-232-2 35 165.5 3.9 1287 5 PCT-US95-02219A-2 36 165.5 3.9 1287 5 PCT-US95-02219A-2 37 163 3.8 1222 2 US-08-682-517-15 38 163 3.8 1222 2 US-08-682-517-15 39 161.5 3.8 1296 3 US-08-682-517-15 41 161.5 3.8 1296 3 US-08-682-517-260-3 42 161 3.7 674 1 US-08-317-522A-3 43 161 3.7 674 2 US-08-738-975-3 45 161 3.7 674 2 US-08-738-975-3
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Best Local Similarity Matches 334; Conserv Query Match Best Local in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae. Sequence 534 619 592 499 474 385 414 325 357 177 117 118 265 297 209 237 156 60 58 LVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDESFYQNGFLNE 444 HLYNLAIPLGIKLEKREAEQYYHVVAMYSPDVCRSNPKCTTTLLSNQGSWKTKGSNLARQ 798 DHSYDGILELDAGKDIVIS--ADSRSINAVQSPYGYQGKWTINWSTD----DKKATVSWA 498 LTLSSG-GETLFOGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATG---TV LLDNDKVLIQDNFSTGDGGAINC--AGS-----LKIANNKSLSFIGNSSSTRGGAIHTKN 208 kgswgndafgiecggaipvvasgrrswvdthtpflnlemiyahqndfkengtegrsfqse 815 HTSWGGYVWAGELGTRVAVENTSGRGFFREYTPFVKVQAVYSRQDSFVELGAISRDFSDS 738 gngrsyrhssagyalgggfftasenffnfafcqlfgydkdhlvaknhthvyagamsyrhl ENORKFRHVSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNTNFAKTYAGSLRLQHD 618 qqvfp-lielsaqgtmtttd1pdtp1lntt-nhygyqgtg11vwvddataktknat1twt 591 SHSAIDLGTSAKITALRAAQGHTIYEYDPITVTGSTSVADALNINSPDTGDNKEYTGTIV 324  ${\tt lvlssgrggvlfsnnka} a natpkgga {\tt iaildsgeisisadlgniifegnttsttgspasv}$ lsltgstrfvaflgnsssqqggaiyasgdsvisenagilsfgnnsattsggaisaegnlv 236 gesktlakilsgn-----sdslpfvfnarfayghtdnnmttkytgyspv---feasaegvtlnglainidsldgtnkaiikataaskdvalsgpimlvdaggnyyehhnlsg FSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDLGTS 384 AANKTVTLSGFSALSFLKSPAST-----VTNGL------145 YVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSE 117 mrssfslllissslafpllmsvsadaadl-tlgsrdsyngdtstteftpkaatsdasgtt 59 MKIPLRFLLI--SLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSK-TSSATDGTN 57 fsgeklseeelkkpdnlkstftqavelaagalvlkdgvtvvantitqvegskvvmdggtt 473 yildgdvsisqagkq-tslttscfsn--tagnltflgngfslhfdniisstvagvvvsnt 116 918 AA; 32.4%; Score 1394.5; DB 20; Length 918; Ilarity 35.4%; Pred. No. 1.1e-85; Conservative 139; Mismatches 343; Indels 127; Gaps ------GAINVKGNLS 155 of. 711 413 356 755 264 18;

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Search completed: October 2, 2001, 03:26:41 Job time: 30233 sec

Claim

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English

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AAX06817) isolated from a C. pneumoniae expression library. The C invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid sequences encoding them (see C AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
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This polypeptide comprises the novel 96.7 kDa surface exposed protein Omp9 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAX06821) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAX068417-28), and nucleic acid sequences encoding them (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
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CHRISTIANSEN G.
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Best Local S
Matches 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid sequences encoding them (see AAW06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide comprises the novel 97.6 kDa surface exposed protein ompli of the human respiratory pathogen Chlamydia prevente. Its amino acid sequence was deduced from DNA (see AAX06823) isolated from a C. pneumoniae expression library. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
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N-PSDB; AAX06823.
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Mygind P;
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YTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLI 378
                                                                                             {\tt gaicahgldlsaagptlfsnnrcgntaagkggaiaiadsgslslsanggditflgntlts}
                                                                                                              GAIHTKNLTLSSGGETLFQGN-TAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGA
                                                                                                                                                                                                                                                                                                                                                                                                                         MKIPLRFLLISLVPTLSMSNLLGAAT---TEELSASNSFDGTTSTTSFSSKTSSATDGTN 57
                                                               TG--TVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKE
                                                                                                                                                               feasssitqnsslffsgntatdaagkggaiycektgetptltisgnksltfaenssvtqg
                                                                                                                                                                                                                                                                                                                                                               yvlsgnvyindagk-gtaltgccfte--ttgdltftgkgysfsfntvdagsnagaa-ast 113
                                                                                                                                                                                                                                                                                                                                                                                               YVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSE 117
                               tsaptstrnaiylgssakitnlraaqgqsiyfydpi-asnttgasdvltinqpdsnspld
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Pred. No. 2.4e-
24; Mismatches
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                                                                                                                                                                                                                                                           Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae surface exposed protein
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CHRISTIANSEN G.
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Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding

these proteins

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                                                                                                                                                                                                                                                                                                    This sequence is a Chlamydia antigen of the invention, designated CPN100639. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, addult-onset asthma and acute exacerbations of asthma in adults.
                                                                                                                                                                                                                              Query Match
Best Local Similarity
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01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquired pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia antigen; diagnosis; infection; community acquired pneumonia; therapy; upper respiratory tract disease; bronchitis; sinusitis; asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma
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                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                     MKIPLRFLLISLVPTLSMSNLLGAAT --- TEELSASNSFDGTTSTTSFSSKTSSATDGTN 57
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DB; AAA30853, AAA30854.
{\tt tadkaliftgfsnlsfiaapgttvasgkstlssagalnltdngtilfsqnvsneannngg}
                                AANKTVTLSGFSALSFLKSPASTVTNGLGAINVKGNLSLLDNDKVLIQDNFS-----
                                                                                                 YVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSE 117
                                                                    yvlsgnvyindagk-gtaltgccfte--ttgdltftgkgysfsfntvdagsnagaa-ast 113
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                                                                                                                                                                                                            32.7%; Score 1407.5; DB 2: nilarity 36.9%; Pred. No. 1.5e-86; Conservative 124; Mismatches 333;
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98US-0110340.
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19-JUN-1998; 30-DEC-1998

98WO-DK00266.

Chlamydia

pneumoniae

outer membrane protein 11; surface exposed protein; n; infection; diagnosis; vaccine; atherosclerosis; a

asthma

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AAW88424
ID AAW8
XX
AC AAW8
XX
DT 26-J
XX
Chla
XX
KW Omp.
KW antt
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Query Match
Best Local Similarity
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20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
27-AUG-1998;
                                                                                                                                        AAY69362-69 represent Chlamydia pneumoniae polypeptides. The polypeptides are present in the bacterial membrane structure, in the external vicinity of the membrane structure, in the inclusion membrane structure, in the external vicinity of the inclusion membrane structure, and in the cytoplasm of the infected cell. The polypeptides may be used to prevent, treat and detect the presence of Chlamydia infection and/or the presence of Chlamydia in a sample. The polypeptides may also be used to induce an immune response in a mammal. Antibodies directed against the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia in the polypeptides may also be used the prevent and the polypeptides may also be used to prevent and the polypeptides may also be used to prevent the polypeptides may also be used the polypeptides may also be used the polypeptides may a
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antigens and corresponding DNA molecules that can be used to prevent, treat and diagnose disease caused by Chlamydia infection : mammals, especially humans -
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                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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allvragnhhafasnfevfsqfevelrgssrsyaidlggrfgf 918
                                                         dlfnlavpvgikfekfsdkstydlsiayvpdvirndpgctttlmvsgdswstcgtslsrg
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                                                                                                                      kgswgndafgiecggaipvvasgrrswvdthtpflnlemiyahqndfkengtegrsfqse
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Page 940-942; Disclosure; 1912pp; English.
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bronchitis; heart disease; sarcoidosis;
a; erythema nodosum; pharyngitis;
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AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.

Query Match . 33.3%; Score 1429.5; DB 20; Best Local Similarity 35.8%; Pred. No. 5.2e-88; Matches 339; Conservative 147; Mismatches 336; 336; Indels Length 125; 949; Gaps 15;

AIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKEYTGTIVFSG tgdvffye-pgkgtplsdscfkq--ttdnltflgnghsltfgfidagthagaa-asttan KTVTLSGFSALSFLKSPASTVTNGLGAINVKGNLSLLDNDKVLIQDNFSTGDGGAINCAG KDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSEAAN 120 mktsipwvlvssvlafs-chlqslaneellspddsfngnidsgtftpktsa----ttysl 76 MKIPLRFLLISLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVF LSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTI---GATGTVSHS  ${\tt lsnnkflyfegnaakttggaicntkasgspeliisnnktlifasnvaetsggaihakkla}$ lssggfteflrnnvssatpkggaisidasgelslsaetgnitfvrntltttgstdtpkrn flltgtsgdalfsnnssstkggaiattagarianntgxvrflsniastsggaiddegtsi -----SLKIANNKSLSFIGNSSSTRGGAIHTKNLT 60 327 180 312

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Query Match 33.3 Best Local Similarity 35.8 Matches 339; Conservative

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                                                     This sequence is a Chlamydia antigen of the invention, designated CC CPN100634. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of infections. Chlamydia is a pathogen implicated in the development of disease (especially bronchitis and sinusitis, asthmatic bronchitis, asthmatic bronchitis,
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                                              syd-ilelkasgtvtstavtpdpimgekfhygyggtwgpivwgtgasttatfnwtktgyi
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Its amino acid sequence was deduced from DN
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39.0%;
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(see AAW88417-28), and nucleic acid sequences encoding them (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer

these outer

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ARESULT AAW88417
ID AAW88417
ID AAW8
XX AAW8
AC AAW8
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                                                                                                                This polypeptide comprises the novel 98.9 kDa surface exposed protein Omp4 of the human respiratory pathogen Chlamydia pneumoniae. Its maino acid sequence was deduced from DNA (see AAXO6816) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Omp4-Omp15
                                                                                                                                                                                                                                                                                                                                    Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birkelund S,
Mygind P;
                                                                                                                                                                                                                                                                    Claim 7; Page 40-42; 115pp; English
                                                                                                                                                                                                                                                                                                                     these proteins
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(CHRI/)
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CHRISTIANSEN G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae. The genomic sequence was amplified using two PCR primers. The 5' primer contains a Notl restriction site, a ribosome binding site, an initiation codon and a sequence close to the 5' end of the 98kba putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BsrGl restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame C-terminal fusion with the Histidine tag. The PCR product was cloned into a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with Notl and BamHl and performing a ligation reaction. This expression vector was injected intramuscularly and intranasally into mice, which were subsequently incoulated with Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice were lower than those of the controls. Thus the 98kDa putative outer membrane protein can be used as a vaccine to provide protection against The present polypeptide may also be administered orally to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1998;
01-MAR-1999;
27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the 98kDa putative outer membrane protein from
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gltlfsrnsvnggtap----kggaiaiedsgelslsadsgdivflgntvtsttpgt-nrs
                GETLF-----QGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGAT--GTVSHS
                                                                                                                                                                                                                                         KSPASTVTNGLGAINVK-GNLSLLDNDKVLIQDNFSTGDGGAINC------
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                                                                                                                                                                                                                                                                                                                TQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSEAANKTYTLSGFSALSFL 134
                                                                     vtgasssttgdmsggaicayktstdtkvtltgnqmllfsnntsttaggaiyvkklelasg
                                                                                                                                             entsskkggaiqtsdaltitgnggevsfsdntssdsgaaifteasvtisnnakvsfidnk
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99US-0122066.
99US-0428122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 kDa putative outer membrane protein antigen, used and protection against Chlamydia infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                     36.4%; Score 1564; DB 21; 39.2%; Pred. No. 4.3e-97; tive 121; Mismatches 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; diagnosis;
                                                                                                                                                                                                         (BIRK/) BIRKELUND S.
(CHRI/) CHRISTIANSEN
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tion; diagnosis; vaccine; atherosclerosis; asthma.
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            Chlamydia
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Pred. No. 1.6e-160;
3; Mismatches 1;
                                    infection; outer
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                                                                                                                                                                                                                                                                                                                                                                                                             the presence of Chlamydia nucleic acids in samples (and therefore diagnose infections) and the proteins may be used as antigens for production of antibodies that may be used to detect Chlamydia protin samples (e.g. via enzyme linked immunosorbant assay (ELISA)).
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                                              rqdsfvelgaisrdfsdshlynlaiplgiklekrfaeqyyhvvamyspdvcrsnpkcttt
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Matches 532; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae, a human respiratory pathogen. The invention provides a new species specific test for identifying mammals (including humans) infected with C. pneumoniae. The test comprises detecting antibodies specific for surface exposed proteins Omp4-Omp15 (see AAW88417-28) or detecting nucleic acid fragments encoding them (see AAW88417-28) or preumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide is described as a subsequence of the claimed novel surface exposed protein Omp7 (see AAW88420) of Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the membrane proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae or nucleic acids encode the proteins of C. pneumoniae o
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diagnosis;
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; vaccine; a
                                                                                                                                                                                                                                                                       60.5%; Score 2600; DB 20; 71.5%; Pred. No. 3.5e-167; Live 21; Mismatches 51;
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compensation of the human respiratory pathogen Chlamydia
compensation and sequence was deduced from DNA (see
compensation provides 12 novel surface exposed proteins, Omp4-Omp15
compensation provides 12 novel surface exposed proteins, Omp4-Omp15
compensation provides 12 novel surface exposed proteins, Omp4-Omp15
companies of compensation of them (see
companies of the test comprises detecting antibodies specific for
comp4-Omp15 or detecting nucleic acid fragments are also used
comp4-Omp15 or detecting nucleic acid fragments are also used
comp4-Omp15 or detecting nucleic acid fragments are also used
comp4-Omp15 or detecting nucleic acid fragments are also used
companies proteins, especially by PCR. The proteins are also used
concleic acids and proteins can also be used in the immunization of
companies for effecting in vivo expression of antigens. The
covaccines for effecting in vivo expression of antigens. The
covaccines may also prevent atherosclerosis and bronchial asthma,
covaccines may also prevent atherosclerosis and bronchial asthma.
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                            MNTNFAKTYAGSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGQLSYGHTD
                                                                       EKRFWVAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYF
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02-NOV-1998;
The nucleic acids may be used for the recombinant production of the Chlamydia polypeptides (either in vivo or in vitro) according to standard recombinant DNA methodologies. The polypeptides may then be used to vaccinate against Chlamydia infections in mammals. Chlamydia, such as C. pneumoniae, are pathogens responsible for upper respiratory tract infections such as community acquired pneumonia, acute respiratory disease and bronchitis and may be implicated in atherosclerotic changes and asthma. The nucleic acids may also be used as probes for detecting
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2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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1407.5     32.7     930     21     hAyy90240     Chlamydia       1400.5     32.7     930     20     hAw88424     Chlamydia       1400.5     32.6     928     20     hAw88428     Chlamydia       1394.5     32.4     918     20     hAw88422     Chlamydia       1374.5     32.0     928     20     hAw88423     Chlamydia       1369.5     31.7     928     21     hAy90239     Chlamydia       1364.5     31.7     928     21     hAy90239     Chlamydia       1346.5     31.3     914     20     hAx88429     Chlamydia       1330.5     30.9     927     20     hAx99842     Chlamydia       1315.5     30.6     925     21     hAx99843     Chlamydia       1316.5     27.6     945     21     hAx99843     Chlamydia       1186.5     27.6     945     21     hAx99843     Mature Chl       1164.5     27.1     945     21     hAx96936     Mature Chl       1164.5     27.1     945     21     hAx96936     Chlamydia       1164.5     27.1     945     21     hAx96936     Chlamydia       1164.5     27.2     948     20 <td></td> <td>AAY34611</td> <td>20</td> <td>597</td> <td></td> <td>tπ</td> <td>31</td>		AAY34611	20	597		tπ	31
1407.5     32.7     930     21     AAW90240     Chlamydia       1404.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88428     Chlamydia       1394.5     32.4     918     20     AAW88423     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia       1364.5     31.9     928     21     AAY90239     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1329.5     30.9     936     21     AAY35054     Chlamydia       1315.5     30.9     936     21     AAY99842     Chlamydia       1315.5     30.4     885     21     AAY99843     Chlamydia       1186.5     27.6     945     21     AAY90238     Amture Chl       1186.5     27.1     945     21     AAY90238     Amture Chl       1186.5     27.1     945     21     AAY86274     Chlamydia       1104     26.6     643     20     AAY35056     Chlamydia       1108     25.2     973     21		AAW88419	20	922		996	30
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1407.5     32.7     930     21     AAY90240     Chlamydia       1400.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88418     Chlamydia       1394.5     32.4     918     20     AAW88422     Chlamydia       137.5     32.0     928     20     AAW88423     Chlamydia       1369.5     31.7     928     21     AAY90239     Chlamydia       1364.5     31.7     928     21     AAY90237     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1330     30.9     927     20     AAY35054     Chlamydia       1315.5     30.6     925     21     AAY99842     Chlamydia       1366.5     27.6     945     21     AAY99368     Chlamydia       1186.5     27.1     945     21     AAY90238     Mature Chlamydia       1186.5     27.1     945     20     AAW88428     Chlamydia       1144     26.6     643     20     AAY35056     Chlamydia	•	AAY96274	21	973			27
1407.5     32.7     930     21     hAY90240     Chlamydia       1404.5     32.7     930     20     hAW88424     Chlamydia       1400.5     32.6     928     20     hAW88428     Chlamydia       1394.5     32.4     918     20     hAW88422     Chlamydia       1374.5     32.0     928     20     hAW88423     Chlamydia       1369.5     31.9     928     21     hAY90239     Chlamydia       1364.5     31.7     928     21     hAY90237     Chlamydia       1346.5     31.3     914     20     hAW88429     Chlamydia       1329.5     30.9     927     20     hAY90237     Chlamydia       1329.5     30.9     936     21     hAY99842     Chlamydia       1315.5     30.6     925     21     hAY99843     Chlamydia       1186.5     30.4     885     21     hAY99843     Chlamydia       1186.5     30.4     885     21     hAY99368     Amature Chlamydia       1186.5     30.4     885     21     hAY99368     Amature Chlamydia       1186.5     27.1     945     20     hAW88428     Amature Chlamydia       1186.5     27.1     94		AAY35056	20	643	•	1144	26
1407.5     32.7     930     21     AAY90240     Chlamydia       1407.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.7     930     20     AAW88424     Chlamydia       1394.5     32.4     918     20     AAW88422     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia       1369.5     31.9     928     21     AAY90239     Chlamydia       1364.5     31.7     928     21     AAY90237     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1330     30.9     927     20     AAY89842     Chlamydia       1315.5     30.6     925     21     AAY99843     Chlamydia       1308     30.4     885     21     AAY99843     Chlamydia       1186.5     27.6     945     21     AAY69368     Mature Chl	Chlamydia pneur	AAW88428	20	945		1164.5	25
1407.5     32.7     930     21     AAY90240     Chlamydia       1404.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88428     Chlamydia       1394.5     32.4     918     20     AAW88422     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia       1369.5     31.9     928     21     AAY90239     Chlamydia       1364.5     31.7     928     21     AAY90237     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1346.5     31.3     91.4     20     AAW88429     Chlamydia       1350.5     30.9     927     20     AAY35054     Chlamydia       1315.5     30.6     925     21     AAY99843     Chlamydia       1315.6     30.4     885     21     AAY90238     Mature Chlamydia       1315.8     30.4     885     21     AAY90238     Mature Chlamydia		AAY69368	21	945		1186.5	24
1407.5     32.7     930     21     AAY90240     Chlamydia       1404.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88428     Chlamydia       1394.5     32.4     918     20     AAW88422     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia       1364.5     31.9     928     21     AAY90237     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1329.5     30.9     927     20     AAY90237     Chlamydia       1329.5     30.9     927     20     AAY9034     Chlamydia       1329.5     30.9     927     21     AAY99843     Chlamydia       1315.5     30.6     925     21     AAY99843     Chlamydia	Ch1	AAY90238	21	885		1308	23
1407.5     32.7     930     21     AAY90240     Chlamydia       1404.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88428     Chlamydia       1394.5     32.4     918     20     AAW88422     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia       1369.5     31.9     928     21     AAY90239     Chlamydia       1364.5     31.7     928     21     AAY90237     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1390     30.9     927     20     AAY8964     Chlamydia       1329.5     30.9     936     21     AAY99842     Chlamydia		AAY99843	21	925		1315.5	22
1407.5 32.7 930 21 AAY90240 1404.5 32.7 930 20 AAW88424 1400.5 32.6 928 20 AAW88428 1394.5 32.4 918 20 AAW88422 1374.5 32.0 928 20 AAW88422 1376.5 31.9 928 20 AAW88423 1369.5 31.9 928 21 AAY90237 1364.5 31.7 928 21 AAY90237 1364.5 31.7 928 21 AAY90237 1364.5 31.7 928 21 AAY90237 1369.5 31.3 914 20 AAW88429 1390.5 31.3 914 20 AAW88429		AAY99842	21	936		1329.5	21
1407.5     32.7     930     21     AAY90240     Chlamydia       1404.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88428     Chlamydia       1394.5     32.4     918     20     AAW88422     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia       1364.5     31.9     928     21     AAY90239     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia       1346.5     31.3     914     20     AAW88429     Chlamydia		AAY35054	20	927			20
1407.5     32.7     930     21     AAY90240     Chlamydia       1404.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88418     Chlamydia       1394.5     32.4     918     20     AAW88422     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia       1369.5     31.9     928     21     AAY90239     Chlamydia       1364.5     31.7     928     21     AAY90237     Chlamydia		AAW88429	20	914			19
1407.5     32.7     930     21     AAY90240     Chlamydia       1404.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88418     Chlamydia       1394.5     32.4     918     20     AAW88422     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia       1369.5     31.9     928     20     AAW88423     Chlamydia       1369.5     31.9     928     21     AAY90239     Chlamydia	-	w	21	928		1.1	18
1407.5     32.7     930     21     AAY90240     Chlamydia       1404.5     32.7     930     20     AAW88424     Chlamydia       1400.5     32.6     928     20     AAW88428     Chlamydia       1394.5     32.4     918     20     AAW88423     Chlamydia       1374.5     32.0     928     20     AAW88423     Chlamydia	-	w	21	928		1.5	17
1407.5       32.7       930       21       AAY90240       Chlamydia         1404.5       32.7       930       20       AAW88424       Chlamydia         1400.5       32.6       928       20       AAW88418       Chlamydia         1394.5       32.4       918       20       AAW88422       Chlamydia	-	AAW88423	20	928		1.1	16
1407.5 32.7 930 21 AAY90240 Chlamydia 1404.5 32.7 930 20 AAW88424 Chlamydia 1400.5 32.6 928 20 AAW88418 Chlamydia	•	AAW88422	20	918	٠	4.1	15
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1407.5 32.7 930 21 AAY90240 Chlamydia		842	20	930		-	13
		024	21	930		•	12

## ALIGNMENTS

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AAW88420
ID AAW8
  RESULT
Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for
                               N-PSDB; AAX06819
                                         WPI; 1999-105610/09.
                                                                       Birkelund S, Christiansen
                                                                                                                         23-ЈИМ-1997;
                                                                                                                                              19-JUN-1998;
                                                                                                                                                                   30-DEC-1998.
                                                                                                                                                                                       WO9858953-A2.
                                                                                                                                                                                                          Chlamydia pneumoniae.
                                                                                                                                                                                                                             Omp7; outer membrane protein 7; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma.
                                                                                                                                                                                                                                                             Chlamydia pneumoniae surface exposed protein Omp7
                                                                                                                                                                                                                                                                                26-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                      AAW88420;
                                                                                                                                                                                                                                                                                                                         AAW88420 standard; Protein; 841
                                                                                           (BIRK/) BIRKELUND S.
(CHRI/) CHRISTIANSEN G.
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                                                                                                                          97DK-0000744.
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                                                                       Knudsen K,
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541 GACGTTACCATCTTAACTAATGAATATCCTATCACCCTAATTTTTTCTAAAAGAAA 596

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ORGANISM
Search completed: October Job time: 51664 sec
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Best Local Similarity 53.6%;
Matches 81; Conservative
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                                                                                                                                                                1248 AGCTCAGAAAGATATTCGTATAGATCGTCCT 1278
                                                                                                                                                                                                                                                                                    1188 TTTGGAAATTAATATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCAC 1247
                                                                                                                                                                                                                                                                                                                                                                                             1128 GTTGATTATGGATTTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAA 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                        62 GTTTATTGATTATTTTCTCACTTCGCCGTTTGGGAATCACAAAGGGTTTCCTTTTGCCAC 121
                                                                                                                                 AGCAGAGGGAGATATTAATGTTGATCATCCT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 363.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 451) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NRI-CGAP institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW085457 451 bp mRNA EST 14-OCT-1999 wy65d10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553427 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW085457.1 GI:6040609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //note="Morgan: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 333208-325895 Soares NbHSP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002-150407, 151176-152327 Soares NbHRP apool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 733720-726407, 39080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                        2001, 03:06:46
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 111; Length 451; Pred. No. 4.9; 0; Mismatches 70; Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1173 TATCGAGTTAACGAATTTGGAAATTAATATAGACTCTCTCAGGAAACGGGAAAAAGATAAA 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
927 GDWKRGTDWRTWKRTWKGWGRKGDKGRKTAGRAGDGKDKKKGKDKDRTDDAKATDGKDTW
                                                                                                                                                                                                                                                                                                                                                                                                                                687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DAC strain used for the BDGP's pl and EST libraries. A more detailed description of the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTCAGTGCTGCCACAGCTCAGAAAGATATTCGTATAGATCGTCCTGTTGTACTGGCAAT 1292
                                                 GTTAGTTCCTAATCTTCTTTGGGGGTTCTTTTATAGATGTTCGTCCCTTCCAAAATTTTAT
                                                                                                                                                   GAAAGCTACGGTTTCTTGGGCAAAGCAAAGTTTTAATCCCACTGCTGAGCAGGAGGCTCC
                                                                                                                                                                                                                                                            TCTTGAGTTAGATGCTGGGAAAGACATCGTGATTTCTGCAGATTCTCGCAGTATAAATGC 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGCGATGAGAGTTTTTATCAAAATGGCTTTTTGAATGAGGACCATTCCTATGATGGGAT 1352
                                                                                                     RWRRDRKDRRGRRDRWRRWRGADKKWKWDDDDTAKDDWTKKDTDWTAGATAGWDDDKAKD
                                                                                                                                                                                                             GGGDRDRDARARRARWDTKDTRGAKDKADKKKAGRKRKWWTRKTWKRDTADWKAWAAWRW
                                                                                                                                                                                                                                                                                                                  KATAGAWDWDDARRGRGGRWGDKRRTGARGDKDKTGKKKKTGDKRDKGGGDGDRGDGGA
                                                                                                                                                                                                                                                                                                                                                                                                                          AWKGAKGAGARGKATAKARAKKRWKDDKDTKKKKTKTTATKKKTTTTKRAATDKWKWRKK 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHAGTWWTKKDTKKKKKKKKKKWGKAKRAATDDTAWTATTWKKTAKKDAGKAAKWKADRTK 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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Matches 113; Conserv
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751 ATTATCTTTGAAGGCAATACGATAGGAGCTACAGGAACCGTCTCTCATAGTGCTATTGAT 810
                                                                TAATTTTTGGTTATGTTAACAAAAATTACCTCTAAAGAGGATGTTCAAAAAAATAGCAAT
                                                                                                         TATGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGATGCTCTCAATATTAATAGC
                                                                                                                                                      ACACTAAAAAAAAATAAAATGCTCTATATATTTTCTTAGTTGGGACATTTCGTTTCAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10037 row: a column: 09
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 870)
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BF979823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602288333T1 NIH_MGC_97
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pBluescript KS+); Site_1: BamHI; Site_2: Sal1-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

158 c 148 g 266 t
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/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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47.9%;
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Pred. No. 5.3;
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Homo sapiens cDNA clone IMAGE:4374032 3',
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                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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TATYTTTTTTTTATAAAATRAAAATATAAATTTKGGAGMAAWAKGKGCMAHDGGAAGTK 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                      /organism="Drosophila m
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR30019"
/note="end : T7"
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Neoptera; Endopterygota; Diptera; Brachycera;
a; Ephydroidea; Drosophilldae; Drosophila.
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                                                                                                                                         TATTTTGAAGGCAAAAGGTTCTTATGGGGATGCAATTAAAAGTTTAGTGCTGTATTTACA
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                                                                                 ACTTTTATGGCGGATCATGATGCATGGTTGGAGTTAGCAGAACTCTACATTAA
                                                                                                                                                                                                TTATAAAGAACTGGAGAAAGAAGACCCCACTAATGCGGCAATACGTAAAAGGAAAATTGT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGTTTGCAACATGCTCGCCACATAAAATAYTTCATCAGGGGGCGAAGGGAAACMAGTTC 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAGGGTAATAAAATTGTWA-TTGGTTAATTTGTTGARGKTAWTTTTTTTTTTTTTCCC
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AV675196 Nori Satoh u
cDNA clone citb1113 5
AV675196
CNS000D1
Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                                                        179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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/db_xref="taxon:7719"
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TET3 end of BA
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CTTTCACATTTAGCAATATCGATGCAACCACGGCTTCTGGAGCTGCTATTGGAAGTGAAG 352
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                                                   CTGTGTCTTTTAAAAATGATGATGAAGATGGAGAATCTGAATCAAAAGAAACAAGAACTC 87
                                                                                 CTAGTTGTTTTAAAAATGACGCTGCAGCTGGAGATCTAAATTTCTTAGGAGGGGGATTTT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKKRTKTGRAWWAAGTRTTWDAATAWKTKRAAAAAGRRAAAWAKDRGTKRGKGRKKRGT
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                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW682810 580 bp mRNA EST 27-APR-2000
SWYDZ5CAU13D06SK Brugia malayi young adult day 25 cDNA
(SAW99MLW-BmYD25) Brugia malayi cDNA clone SWYD25CAU13D06 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          College, Northampton, Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes expressed in young adult Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brugia malayi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams,S.A.
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                                                                                                                                    Similarity
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    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome@smith.edu
                                                                                                                                                                                                                                              RNA I; Lymphatic filarial nematode parasite of humans.

MRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds on day 25 after infection and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 6.2 x 105 independent recombinants and the average insert size is approx.1101bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email:
                                                                                                                                                                                                                                     genome@neal.smith.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="young adult, /lab_host="XL1-Blue MRF/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Brugia malayi young adult day 25 cDNA
(SAW99MLW-BmYD25)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Brugia malayi"
/db_xref="taxon:6279"
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CCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGCACCCTATCCATT 732
                                                                            CATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAGGGGAATACAGCG
                                                                                                                                                                          GCTAAAACTACTACTGCTACTGCAGCTRCTACTACTACTGCTACWATTKCWGCTGCT 467
                                                                                                                                                                                                                        GCAAACAATAAGTCCCTTTCTTTATTGGAAATAGTTCTTCAACACGTGGCGGAGCGATT 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis genome survey sequence T7 end of clone 123M05 of library G from Tetraodon nigroviridis, genomic surve sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius, H., Jaillon, O., Dasilva, C., Bound Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 735)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="123M05"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Genoscope sequence
45 c 223 g 197
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                                                                                                                                                                                                                                                                                                  Score 39.8;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAGAGTATACGGGAACCATAGTCTTTTCTGGAGAAGCTCACGGAGGCAGAAGCTAA 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTTGRAAAGCTTTTTTTGAAWAAAR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCAGCAGCTACCAARAAACCAGCCCCTGAAAARAAGCCTGMARAGAAGAAAACCTAMWAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTTTTAAAAGGTGATGTCGTTTTAAG 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE187133 450 bp mRNA EST 22
NXNV_159_D05_F Nsf Xylem Normal wood Vertical Pinus
clone NXNV_159_D05 5', mRNA sequence.
BE187133
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                                                                                                                                                                                                                                                                                                                                        Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                               Molecular Basis of Wood Formation Unpublished (2000)
Contact: Johnson, Arthur North Carolina State University Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Stre
Spermatophyta; Coniferopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinus taeda
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//clone lib="ITI NPIOS PL2"
//clone lib="ITI NPIOS PL2"
//tissue_type="placenta"
//note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
//note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
//note="Vector: pCMVSPORT 6; Site_1: NotI and
enriched, double-stranded cDNA was digested with Not I and
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
//rechnologies. Contmatized. Library was constructed by
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Lib
/organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="RXV_159_D05"
/clone_lib="Nsf Xylem Normal wood Vertical"
/rote="Vector: BlueScript SK; Site_1: Eco RI; The
/sequences contain a 'cDNA adapter' between the Eco
and the start of the EST. The adapter sequence is
'AATTCGGCACGAG'."
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/clone="CL0BB003ZA04"
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Pred. No. 0.31;
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ida; Coniferales; Pinaceae; Pinus; Pinus.
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                                                                                                      TTTTATCAAAATGGCTTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGAT 1365
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RGDGRAGRAKRRDDRRGDRGRRRRRRRTRKWRWWRRAAWWTAWTTWWWGTTKGAWWTKTR
                                GCTGGGAAAGACATCGTGATTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCG 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGTTTTAAAAAT 249
                                                                      TTATADDTWKRTTGTKTRTWKWKWWARRAAKWRDWWRDTDWWDKWDTKWKDDRWTKRWAT 963
                                                                                                                                            64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end Sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37F10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                   pBeloBAC11.
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                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila
/plasmid="pBeloBAC11"
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                                                                                                                                          ; Score 41.4; D
; Pred. No. 1.3;
87; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                           262 GGAGATCTAAATTTCTTAGGAGGGGGATTTTCTTTCACATTTAGCAATA 310
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            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                  CNS005UJ 1178 bp DNA GSS DIOSOPHILA melanogaster genome survey sequence TET3 end of BAC #BACR12E18 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7
Class: BAC ends
High con-
                                                                                                                       GSS.
                                                                                                                                                         AL060808
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                         AL060808.1
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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E-Coli DH10B"
158 c 109 g 294 t 3 others
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/clone="Plate=3133 Col=4
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NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                               AL514531
AL514531
                                       Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                            prime, mRNA sequence.
AL514531
AL514531.1 GI:12778025
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                    Email: segref@genoscope.cns.fr,
                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 778)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR12E18"
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Pred. No. 0.
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Catarrhini; Hominidae
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                       Web : www.genoscope.cns.fr
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RESULT 3
CNS016E2/c
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Plasmid Trosophila melanogaster
Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
                                                                                                                                                       fly), ger
AL106628
                                                                                                                                                                      CNS016E2 1204 bp DNA GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN15Al2 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                 AL106628.1
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR08K10"
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DEFINITION

CIT Approved Human Genomic one Plate=3133 Col=4 Row=0,

Sperm Library DNA sequence.

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                                                                                                                                    TKGAAAATACMWAAAGRAWAGWATATGWATRGAAGAWACGGGWAGAGG
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                                                                                                                                                                                                                                                                                                                                                                 KAAAKKKDKKKDAADKKAAKDAAKKKKDKAAKAADKDAAKKWDKKKKAGGAARAAAKKGK 831
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP). http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
AQ896240 805 bp
HS_3133_A2_H02_T7C CI3
sapiens genomic clone
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1 (bases 1 to 1204)
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/clone="BACN15A12"
/note="end : T7"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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167; Mismatches 226; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 400)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                           AQ567666 400 bp DNA GSS 01-JUN-1999

HS_2118_B2_C03_T7C CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone Plate=2118 Col=6 Row=F, DNA sequence.

AQ567666
       Sequence-tagged connectors: A sequence approach to
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AQ516936
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CNS0039G
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                                         Smith,K., Swartzell,S., g,J., Young,J., Zhao,S.,
                                                                                               Hominidae;
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Best Local Similarity
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and haron Mammoser in Pieter de Jong's laboratory in the Department o
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insepterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
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Proc. Natl. Acad. Sci. U. S. A. 96
99380589
Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 2118 _row: F column: 6
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Tel: (206) 616-3618
Fax: (206) 616-3887
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phila melanogaster genome survey sequence TET3 end of BAC #
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KEYWORDS SOURCE ORGANISM

Homo sapiens

VERSION

AQ567666.1

GI:4961157

ACCESSION

REFERENCE

AUTHORS

TITLE

RESULT AQ567666

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DEFINITION

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em_gss_vrt3:
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sp_gss5:
sp_gss6:
sp_gss11:
sp_gss21:
sp_gss22:
sp_gss26:
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9b_est16:*
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em_esthum4:*
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gb_est211:*
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gb_est23:*
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gb_est33:*
gb_est34:*
gb_est35:*
gb_est36:*
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2318.115 Million cell updates/sec
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Search completed: October 2, 2001, 03:46:39 Job time:  $51392 \ \text{sec}$ 

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CALCIUM AND TEMPERATÜRE

NUMBER OF SEQUENCES: 28

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/354,988

FILING DATE: 19-MAY-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 282,880

FILING DATE: 05-DEC-1988

APPLICATION NUMBER: 690,951
                                                      Query Match
Best Local Similarity
"~+~hes 96; Conserve
                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Brassica napus US-08-821-994-86
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Sequence 86, Application US/08821994A
Patent No. 6228643
GENERAL INFORMATION:
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LENGTH: 1102
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FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER FILING DATE: 1997-03-18
                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEO ID NOS: 89
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
                      1357 GAGTTAGATGCTGGGAAAGACATCGTGATTTCTGCAGATTCTCGCAGTATAAATGCTGTA 1416
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550 GTGTTTAATCCGCCGTTTTTCATTATGAATTGAAAAGCATAATCCATTAGACCGCCGTTA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 01-JAN-1985
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                                                                            Conservative
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ION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
                                                                                          1.3%; Score 32.4; DB 4;
47.5%; Pred. No. 6.2;
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Pred. No. 13;
0; Mismatches
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                                                                          Mismatches
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                                                                                                                                                                                                  Query Match 1.3%;
Best Local Similarity 44.7%;
                                                                                                                                                                             Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/15266:
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: US 663897
FILING DATE: 14-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION UNMBER: 16773
REFERENCE/DOCKET NUMBER: PNK/55-
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APPLICANT: BURNIE Mr., Ja
APPLICANT: MATTHEWS Ms.,
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                              1030 AAATTACTTCAAAATGTTGCTTTTAAAAATGGGGACTGTAGTTTTAAAAGGTGATGTCGTT 1089
                                       1090 TTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGATTTAGGGACG 1149
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: FUNGAL STRESS PROTEINS NUMBER OF SEQUENCES: 10
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                                                                                      493 AAAGCCGTTGAAAAATCACCATTCTTGGATGCCTTGAAAGCTAAGAACTTTGAAGTCTTG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 TCTCCTGTTACGATCTTGTTTATACCTTCTACTGCTGCAGCTGTTGAAAACGCCCAACAA 371
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553 TTCATGGTGGATCCAATCGATGAATATGCCATGACTCAATTGAAGGAATTTGAAGACAAG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 CTTCCGCAAGTTCCTTGGTCTT 349
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RESULT 12
US-08-441-139-12
; Sequence 12, Ap
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Best Local :
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Patent No. 6214971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                2602 TTTAACGAAGTGTAATATGTAAAA 2625
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nes 97; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                            TGTGTAAATGTAAAGGTAGATAACATTGAGAAAAGAATTTGGAAAATTATGTAAAATAA 2601
                                                                                                                                                                                                               TCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAATATAGACTCT 1209
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  Application US/08441139
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(206)682-6031
(206)682-10:
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Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 107;
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; NAME/KEY:
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US-08-441-139-12
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                                                                    FEATURE:
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NAME: Digiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                 FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 400 Garden City
                                                    LOCATION:
                                                                    NAME/KEY
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2878..3115
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2378..2764
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Matches Query Match Best Local

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Conservative

1.3%;

Score 32.6; D Pred. No. 13; 0; Mismatches

DB 1; 34;

Length 5470; Indels

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2026 TCGACGGATCATACTTCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTT 2085

2998 TAGTGCAAATAATTCATTATCTCTTACATTAGTTGAAACTGGTGCTAATACAGGTGTATT 3057

TGCTACAACTGTTCAAGCTGGTACATTATCTTCTTTAACTGCTGGTACATTAACAGTTAC 3117

84 A8 A8

306 CAATATCGATGCAACCACGGCTTCTGGAGCTGCT 339

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                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
1102
                            1771 CAGCTCTTTGCGCGTGACAAAGACTACTTTATGAATACCAATTTCGCAAAGACCTACGCA 1830
                                                                                         1711 GCTGTAGGTAGGTGCTAGCACGAGGATGCCGGGTGGTGATACCTTGTCTCTGGGTTTTGCT 1770
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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APPLICATION NUMBER:
FILING DATE:
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ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                         Conservative 178;
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Pred. No. 5.
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Best Local
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                                                                                                                                                                                                                                                                                                                   TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
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                                 1090 TTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGATTTAGGGACG 1149
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                   1030 AAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGTGATGTCGTT 1089
2482 ACTCGTAAAAATGAATATGAGCATAAAGAATTAGCAAGAATACATTGTAATGAAGAAAAA 2541
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/845,258 FILING DATE: 24-APR-1997
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                                                                   AAATATACTAAGAATGGTATTAATTGTTATGAATATGTACTTCGTAAATGCAGTTCTTAT
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97; Conserv
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                                                                                                                                     Conservative
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Michael J.
                                                                                                                                                   1.38;
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Pred. No. 9.
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                                                                                                                                                                     DB 4;
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US-08-682-517-7
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; LOCATION:
US-08-682-517-14
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                                    Matches
                                                                   Query Match
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CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 4197 base pairs
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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LENGTH: 3666 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2934 TTATGCAGATGCTAAAAATGCTGCAGGTGTTGCT 2967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 124; Conserv
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
66 AGGAGCTGCTACCGAAGAGCTATCGGCTAGCAATAGCTTCGATGGAACTACATCAAC 125
                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/682,517
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                                                 Score 34; DB 2;
Pred. No. 4.2;
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                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   of surface layer proteins
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US-08-682-517-8
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                                                                                                                                                                                                                                             Query Match 1.3%;
Best Local Similarity 45.3%;
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,517
                                                                                                                                              2878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 4197 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3118 TTATGCAGATGCTAAAAATGCTGCAGGTGTTGCT 3151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2998
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                                                            2938 TGATGCAGATCTTAATGTAAGTGCAACAACTGTTGATACTGCAACTGTTTCATTAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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NAME/KEY:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3058 TGCTACAACTGTTCAAGCTGGTACATTATCTTCTTTAACTGCTGGTACATTAACAGTTAC 3117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 CAATATCGATGCAACCACGGCTTCTGGAGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                  66 AGGAGCTGCTACCACGAAGAGCTATCGGCTAGCAATAGCTTCGATGGAACTACATCAAC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bacillus sphaericus INDIVIDUAL ISOLATE: P-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
TTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTAGTTGTTTTAA 245
                                                                                                                                            AGCAGCTGGTGGTTTAGTTGATTTAACAACTGCAACTAACACTTTAGGAATTTCATTAGC 2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTTAAAGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAGCTGGTGGTTTAGTTGATTTAACAACTGCAACTAACACTTTAGGAATTTCATTAGC
                                                                                                    AACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTTAAAGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGTGCAAATAATTCATTATCTCTTACATTAGTTGAAACTGGTGCTAATACAGGTGTATT 3057
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                                                                                                                                                                                                                          Conservative
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95..3850
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95..184
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185..3850
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                                                                                                                                                                                                                        Score 34; DB 2; Length 4197; Pred. No. 4.2; 0; Mismatches 150; Indels
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                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2052 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                   184
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: MISROCK, S. LESLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                      212
                                                                                    124 ACAACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTTAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                    Local Similarity
les 81; Conserv
                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/630,916A FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AGTACCTACGCTTTCTATGTCGAATTTATTAGGAGCTGCTACTACCGAAGAGCTATCGGC 95
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
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GATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGTTTT 243
                                                   ACTCCAGTAGTGTCTGAAGAAATGCCTTGTCTCCAAATTGCACTAGTACTACTGTTGAA 271
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Fowlkes, Dana M.
                                                                                                                                                                                                                                                                                                                                            (212) 896-8864/9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                    Score 35.4; DB Pred. No. 1.1; 0; Mismatches
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                                                                                                                                                     DB 3;
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US-08-682-517-13
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Best Local Similarity 45.3%;
Matches 124; Conservative
                                                                                                                                                                                              Sequence 14, Application US/08682517 Patent No. 5874267
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TITLE OF INVENTION: Expression of surnymber of sequences: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
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SEQUENCE CHARACTERISTICS:
LENGTH: 3666 base pairs
TYPE: nucleic acid
                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                              2874 TGCTACAACTGTTCAAGCTGGTACATTATCTTCTTTAACTGCTGGTACATTAACAGTTAC 2933
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                                                                                                                                                                                                                                                                                                                                                      306 CAATATCGATGCAACCACGGCTTCTGGAGCTGCT 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                 244 AAAAATGACGCTGCAGCTGGAGATCTAAATTTCTTAG 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGTTTTAA
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                                                                                                                     Expression of surface 25
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                        Version
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                        #1.30 (EPO)
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RESULT 2
US-08-370-975B-6
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                                                                                       NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2089
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1636
TELEFAX: (716)263-1600
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08370975B Patent No. 5622851
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APPLICANT: Maley,
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 20303 base pai
                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/370,975B FILING DATE: 10-JAN-1995
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1293 TAGCGATGAGAG 1304
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1053 TAAAAATGGGACTGTAGTTTTAAAAGGTGATGTCGTTTTAAGTGCGAACGGTTTCTCTCA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human Deoxycytidylate Deaminase
OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933 TGATACTGGAGATAACAAAGAGTATACGGGAACCATAGTCTTTCTGGAGAGAAGCTCAC 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    993 GGAGGCAGAAGCTAAAGATGAGAAGAACCGCACTTCTAAATTACTTCAAAATGTTGCTTT 1052
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                TOPOLOGY:
                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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: New York
                                            nucleic acid
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Clinton Square,
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Weiner, Karen X.B.
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                  linear
                                                                                                                                                                                                                                                                                                                                 Floppy disk
DNA (genomic)
                             single
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quare, P.O. Box 1051
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1.3%; Pred. No. 0.35;
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Best Local
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08370975B
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                                                                                                                                                                                                           TELEPHONE: (716)263-1636
TELEPAX: (716)263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26764 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13871 AATATATCCTGTTAAATTTGTCAAACTTCTAGAGAACCGCCTACATGAGACAGTAAGGATT 13930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13991 TCCATGGTCCAAGGTTAATGCAGTTCTGAATTCTGACAGTTAGTAATAGAAAAGAAAAAA 14050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13931 AATCAAGCCCTACTAAGAGAGAATTTGAAAAATACAGTTTTCTAATTATACAGTCTCTTC 13990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14051 AAAAAAACCAAAGCATATGAATTGTCTTATAATT 14084
                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timlan, Susan J.
REGISTRATION NUMBER: 34,103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POSITION IN GENOME:
                                                                                                                    MOLECULE TYPE: DNA POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 TACAGATGGCACCAATTATGTTTTTAAAGATTCTGTAGTTATAGAAAATGTACCCAAAAC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 AGGGGAAACTCAGTCTACTAGTTGTTTTAAAAAT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 TAGCAATAGCTTCGATGGAACTACATCAACAACAAGCTTTTCTAGTAAAACATCATCGGC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 AGTACCTACGCTTTCTATGTCGAATTTATTAGGAGCTGCTACTACCGAAGAGCTATCGGC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 1.5%;
Local Similarity 48.6%;
hes 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 14603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rochester
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                                                                                                CHROMOSOME/SEGMENT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Nixon, Hargrave, Devans & Doyle Clinton Square, P.O. Box 1051
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                                                                                                                                                          linear
                                                                                                                                    DNA (genomic)
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Pred. No. 0.61;
0; Mismatches 110; Indels
  Score 38; Pred. No.
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    DB 1;
0.71;
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                      Length 26764;
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Result
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Maximum Match 100%
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Maximum DB
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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31.8
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.sed:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.sed:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           October 2, 2001, 03:44:51; Search time 268.88 Seconds (without alignments) 1778.488 Million cell updates/sec
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2526
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/Backfiles1.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                            Length
DB
                     US-08-357-264-2
US-08-672-514-2
US-08-672-514-2
US-08-809-326A-8
US-08-809-326A-13
US-08-568-459A-3
US-08-633-993A-12
US-08-844-188-12
US-08-844-188-39
US-08-844-188-39
                                                                                                                                                        US-08-630-916A-45
US-08-682-517-13
US-08-682-517-7
US-08-682-517-8
US-08-682-517-8
US-08-845-258-10
US-08-845-258-10
US-08-8441-139-12
519523-5
US-08-821-994-86
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US-08-370-975B-6
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Sequence 1, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 7, Appli
Sequence 14, Appli
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Sequence
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                     8, Appli
13, Appli
3, Appli
3, Appli
12, Appl
12, Appl
12, Appl
42, Appl
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ALIGNMENTS

## RESULT 1 US-08-232-463-14/c Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION: APPLICATION NUMBER: EP 91 114 300.6 FILLING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REFERENCE/DOCKET NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECAX: (703)838-4109 TELECAX: (703)883-4109 TELEFAX: (703)683-410: TELEX: 899149 INFORMATION FOR SEQ ID NO: NERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: SCHELFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS COUNTRY: USA ZIP: 22313-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatil TOPOLOGY: line IMMEDIATE SOURCE: CLONE: pTZgpt-COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardner SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: U FILING DATE: STREET: 1800 Dia CITY: Alexandria STATE: VA APPLICATION NUMBER: FILING DATE: STRANDEDNESS: 1800 Diagonal Road, Suite 500 linear single US/08/232,463 us/07/935,313 14: Version #1.25

US-08-232-463-14 PTZgpt-F1s

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AGATGCGGGTAGCAAAATCAAATTTTA 2525 	AGCAGAGCTTTTCGGGAACTTTGGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGT 2498	GAACTTAGCAAGACAGGCTGGTATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGC 2438	TAACCCCAAATGTACGACTACCTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTC 2378	ACGGTTTGCAGAGCAATATTATCATGTTGTAGCGATGTATTCTCCAGATGTTTTGTCGTAG 2318	TGATTTTAGTGATTCGCATCTTTATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAA 2258 	AAAAGTCCAAGCTGTTTACTCGCGCCAAGATAGCTTTGTTGAACTAGGAGCTATCAGTCG 2198	TCGAGTTGCTGTTGAAAATACCAGCGGCAGAGGAATTTTTCCGAGAGTACACTCCATTTGT 2138 agctatcccggtagttgcttcaggacgtcggtcttgggtggatacccacacgccatttct 2369	GACGCTCTCGACGGATCATACTTCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAAC 2078	GCTTAGCTACGGCCATACGGATCATCGCATGAAGACCGAGTCTCTACCCCCCCC	ACTCCGCGAGATCCTGTTGCCTTATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCA 1958	ACGTTTGCAGCACGATGCTTCCCTATACTCTGTGGTGAGTATCCTTTTAGGAGAGGGAGG	TGCGCGTGACAAAGACTACTTTATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTT 1838 

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                                                                                                                                                                                                                                                                                                                       was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding comp4-0mp15 proteins (see AA806817-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: comp12,11,10,5,4,13 and 14 in one cluster and omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89,6-100,3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for comp4-0mp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
                                                                                                                                                                                                                            Query Match
Best Local
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Mygind P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encocouter membrane proteins of C.
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                                                                                                                                                                                                                                                                                                Sequence
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                                                                                     CGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGT----GGGGAAACTCTATTTCA 659
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DB; AAW06822.
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taacaacaaagctgcgaatgctactcctaaaggaggggcaattgcgattctagattctgg
                                                                   aggtgcgatttataccaaaaaattggtgttatcctcaggacgaggaggagtgttattttc
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CHRISTIANSEN
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                         AAZ61502-09 encode Chlamydia pneumoniae polypeptides. The polypeptides are present in the bacterial membrane structure, in the external vicinity of the membrane structure, in the inclusion membrane structure, in the external vicinity of the inclusion membrane structure, and in the cytoplasm of the infected cell. The polypeptides may be used to prevent, treat and detect the presence of Chlamydia infection and/or the presence of Chlamydia in a sample. The polypeptides may also be used to induce an immune response in a mammal. Antibodies directed against the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia infection.
                                                                                                                                                                Novel antigens and corresponding DNA molecules that can prevent, treat and diagnose disease caused by Chlamydia mammals, especially humans -
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Sequence 2957
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DB; AAY69369.
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                                                                                                                                  TACGGTTTCTTGGGCAAAGCAAAGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGT
                                                                                                                                                                                   gtatcaagggaactggaatattgtttgggtcgacgatgcaactgcaaaaaacaaaaatgc
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Pred. No. 5.9e-80;
0; Mismatches 951; Indels
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                           GACAGGCTGGTATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGCAGAGCTTT
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Chlamydia pneumoniae. By generating antibodies against C.

Chamydia pneumoniae. By generating antibodies against C.

pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)

was obtained which reacted with outer membrane proteins. The

cantibody was used to identify the genes (see AAX06816-27) encoding

comp4-Omp15 proteins (see AAW88417-28) in an expression library of

C. pneumoniae DNA. The genes are situated in 2 gene clusters:

comp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in

the other, and encode polypeptides of about 89,6-100.3 kDa and

comptactifying mammals (including humans) infected with Chlamydia

pneumoniae. The test comprises detecting antibodies specific for

comp4-Omp15 or detecting nucleic acid fragments encoding these outer

membrane proteins, especially by PCR. The proteins are also used

This DNA sequence codes for the novel 97.2 kDa surface exposed protein Omp5 (see AAW88418) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C.

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                                                                                                                                                                                            Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
                                                                                                                                                                                                                                      WPI; 1999-105610/09
P-PSDB; AAW88418.
                                                                                                                                                                 Claim 6;
                                                                                                                                                                                                                                                                     Birkelund S, 
Mygind P;
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                                                                                                                                                                                    these proteins
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                                                                                                                                                                                                                                                                                                  (BIRK/) BIRKELUND S. (CHRI/) CHRISTIANSEN
                                                                                                                                                                                                                                                                                                                                 23-JUN-1997;
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infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
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This invention describes a novel nucleic acid (N1) encoding a Chlamydi pneumoniae protein (P1), given in the specification. The isolated nucl acid is useful for diagnostic and analytical methods, such as, hybridization-based assays or amplification-based assays. The protein be used for diagnostic purposes, for their enzymatic or structural activity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizing fragment of N1; (2) an isolated nucleic acid
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                                                                                                                                                                                                                                                                                           Isolated nucleic acid for use in diagnostic encodes genomic sequence of Chlamydia pneumo
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08-APR-1999;
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Matches 1030; Conser
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                                                                                                                                                                                       1095
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                   GAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGATATTCGTATAGATCG
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                                                                                                                                                                1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
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                                       CTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAACCGCACTTCTAA 1031
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                                                                                                                                                           aaatcatacaattttcttctatgatcccatcacttcagaaggaacctcat----caga
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polypeptide antigens from Chlamydia useful and treating diseases such as community acc sinusitis and asthmatic bronchitis, adult-
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Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
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Mygind P;
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                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-1998;
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Pf these proteins

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Claim 6; Page 52-53; 115pp; English.

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CThis DNA sequence codes for the novel 90.0 kDa surface exposed CC protein Omp8 (see AAW88421) of the human respiratory pathogen CC Chlamydia pneumoniae. By generating antibodies against C. C pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) CC was obtained which reacted with outer membrane proteins. The CC cantibody was used to identify the genes (see AAX06816-27) encoding CC cantibody was used to identify the genes (see AAX06816-27) encoding CC cantibody was used to identify the genes (see AAX06816-27) encoding CC cantibody was used to identify the genes (see AAX06816-27) encoding CC cantibody was used to identify the genes (see AAX06816-27) encoding CC pneumoniae DNA. The genes are situated in 2 gene clusters:

CC comp4-comp15 proteins (see AAX88417-28) in an expression library of comp12,11,10,5,4,13 and 14 in one cluster and omp6,7,8,9 and 15 in CC the other, and encode polypeptides of about 89,6-100.3 kDa and CC cantibody and the code polypeptides of about 89,6-100.3 kDa and code polypeptides of about 89,6-100.3 kDa and CC captures of the test comprises detecting antibodies specific test for identifying mammals (including humans) infected with Chlamydia CC omp4-omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used CC in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids being particularly useful as DNA cc vaccines may also prevent atherosclerosis and bronchial asthma, CC vaccines may also prevent atherosclerosis and bronchial asthma, CC vaccines may also prevent atherosclerosis and bronchial asthma, CC which are possibly associated with C. pneumoniae.

SQ Sequence 2787 BP; 811 A; 583 C; 598 G; 795 T; 0 other;

Ouery Match are possibly associated with C. pneumoniae. The capture of the company of the co
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                                           AGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGATTTAGGGACGTCG 1152
                                                                                                                              TTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGTGATGTCGTTTTA 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C PCR primers. The 5' primer contains a NotI restriction site, a ribosome the 98kDa putative outer membrane protein coding sequence close to the 5' end of the 98kDa putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BsrGl restriction site. The stop codon was c excluded and an additional nucleotide was inserted to obtain an in-frame C terminal fusion with the Histidine tag. The PCR product was closed cinto a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with NotI and BamHl and performing a Cliqution reaction. This expression vector was injected intramuscularly a chamydia pneumoniae. The chlamydial lung titers of the immunised mitce were lower than those of the controls. Thus the 98kDa putative outer common protein can be used as a vaccine to provide protection against C Chlamydia infections, especially Chlamydia pneumoniae infections. C C The polypeptide may also be administered orally to treat Chlamydia construction of attenuated Chlamydia starins that can over-express the construction of attenuated Chlamydia starins that can over-express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 273254 BP;
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08-APR-1999;
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CAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCTACAGGAACCGTCTCT-----
                                                   AACTCCTAAGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGA
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                                                                     TGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGCACCCTATCCATTTCTGGAGA 740
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                                                                                                                                                                                                                                                                                                                               chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding Comp4-omp15 proteins (see AAX0881417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Comp12,11,10,5/4,13 and 14 in one cluster and omp6,7,8,9 and 15 in the other, and encode polypeptides of about 96-100.3 kDa and Cabout 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for omp4-omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines may also prevent atherosclerosis and bronchial asthma,
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Best Local Similarity
                              1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This DNA sequence codes for the novel 98.9 kDa surface exposed protein Omp4 (see AAW88417) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encocuter membrane proteins of C.
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(CHRI/) CHRISTIANSEN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1997;
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 AAACCTCACACTATCTTGGTGGGGAAACTCTATTTCAGGGGAATACAGCGCCTACGGC 680
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DB; AAW88417.
                           TAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGTGGCGGAGCGATTCATACCAA 620
                                                                                tggcggtgcgatctgcaacaccaaggcgagtggatctcctgaactgataatctctaacaa
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                                                                                                                                        cacgtcgatactatcgaacaacaaatttctatattttgaagggaatgcagcgaaaactac
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                                                                                                                                                                                                                                                                                                                                                         possibly associated with C. pneumoniae.
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Location/Qualifiers
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 Location/Qualifiers 101..2887
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                                                                                                                                                                                                                                                                                                                                                             This sequence encodes a Chlamydia antigen of the invention, designated CC CPN100634. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate encode according to standard recombinant DNA methodologies. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The infections. Chlamydia is a pathogen implicated in the development of infections. Chlamydia is a pathogen implicated in the development of disease (especially bronchitis and sinusitis, asthmatic bronchitis, adults.
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1095; Conser
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and treating diseases such as community acquired
sinusitis and asthmatic bronchitis, adult-onset
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Pred. No. 3.5e-89;
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Mygind P;
                                                                                                                                                                                                                          Chlamydia
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          WPI; 1999-105610/09.
P-PSDB; AAW88431.
                                                                                                23-JUN-1997;
                                                                                                                   19-JUN-1998;
                                                                                                                                                                           Chlamydia
                                                                                                                                                                                              infection;
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vaccine; atherosclerosis; asthma;
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(see AAW88431) of Chlamydia pneumoniae, a human respiratory pathogen. It is described as a subsequence of a claimed nucleic acid fragment (see AAX06819) encoding Omp7 (see AAW88420). The invention provides a new species specific test for identifying mammals (including humans) infected with C. pneumoniae. The test comprises detecting antibodies specific for surface exposed proteins Omp4 Omp15 (see AAX06817-28) or detecting nucleic acid fragments encoding them (see AAX06816-27), especially by PCR. The proteins are also used in the claim proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encountermembrane proteins of S. pneumoniae or nucleic acids encountermembrane proteins of S. pneumoniae
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AAW88431) of
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proteins
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Score 1425 Pred. No. (

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;
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920 TTATGTTTCCAAGAC	860 CCTATACTCTGTGGTO	800 TATGAATACCAATTTO	740 GGGTGGTGATACCTTGT	680 TCAAAGGAAATTCCGTC 	620 CGAAAAGAGATTTTGG 	560 TTTTATAGATGTTCG	500 AAGTTTTAATCCCACT	440 AAAGTGGACAATCAAT               389 aaagtggacgatcaat	380 CGTGATTTCTGCAG <i>I</i> 	320 CTTTTTGAATGAGGA 	260 TATTCGTATAGATCG	200 TATAGACTCTCTCAG	140 TTTAGGGACGTCGTT 	080 TGATGTCGTTTTAAG 	021 CGCACTTCTAAATT 	961 GGAACCATAGTCTTT 	901 TCTGTTGCTGATGC
TCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGA	GAGTATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCC	CGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTC	GTCTOTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTT	TCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCC	GGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAA	;TCCCTTCCAAAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTA	TGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTC	NTTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCAAAGCA	NTTCTCGCAGTATAAATGCTGTACAATCTCCGTATGGCTATCAGGG	\CCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACAT	;TCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGG	3GAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGA	GGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAA	]TGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGA	ACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTT-AAAAGG	TTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC	TCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG
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                                                         CATCGCATGAAGACCGAGTCTCTACCCCCCCCCCCCCGACGCTCTCGACGGATCATACT
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The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins ANY3458+Y35879. C. pneumoniae cau respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusiti
                                                                    Griffais
                                                                                             04-NOV-1998;
21-NOV-1997;
                                                                                                                                                    Chlamydia
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               The nucleic acids may be used for the recombinant production of the Chlamydia polypeptides (either in vivo or in vitro) according to standar recombinant DNA methodologies. The polypeptides may then be used to vaccinate against Chlamydia infections in mammals. Chlamydia, such as C. pneumoniae, are pathogens responsible for upper respiratory tract infections such as community acquired pneumonia, acute respiratory disease and bronchitis and may be implicated in atherosclerotic changes and asthma. The nucleic acids may also be used as probes for detecting the presence of Chlamydia nucleic acids in samples (and therefore diagnose infections) and the proteins may be used as antigens for the production of antibodies that may be used to detect Chlamydia proteins
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4	CTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTTAGCAAGACAGGCTGGT	2341	Qγ
2340	catgttgtagcgatgtattctccagatgtttgtcgtagtaaccccaaatgtacgactacc	2281	뫄
2340	CATGTTGTAGCGATGTATTCTCCCAGATGTTTGTCGTAGTAACCCCCAAATGTACGACTAC	2281	Qy
2280	tataaccttgcgattcctcttggaatcaagttagagaaacggtttgcagagcaat	2221	ДĎ
2280	TATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTA	2221	Qy
2220	cgccaagatagctttgtagaactaggagctatcagtcgtgattttagtg	2161	Db
2220	CGCCAAGATAGCTTTGTTGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTT	2161	Qy
2160	agcggcagaggatttttccaagagtacactccatttgtaaaagtccaagctgtttacgct	2101	Дb
2160	AGCGGCAGAGGATTTTTCCGAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACTC	2101	Qy
2100	tcttggggaggatatgtctgggctggagagctgggaactcgagttgc	2041	ДĎ
2100	TCTTGGGGAGATATGTCTGGGCTGGAGAGCTGGGGAACTCGAGTTGCTGTTGAAAATACC	2041	Qy
2040	catcgcatgaagaccgagtctctaccccccccccccccc	1981	ФФ
2040	CATCGCATGAAGACCGAGTCTCTACCCCCCCCCCCCCCGACGCTCTCGACGGATCATACT	1981	Qy
1980		1921	Db
1980	TATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGG	1921	Qy
1920	ctatactctgtggtgagtatccttttaggagaggaggactccgcga	1861	Дb
1920	CTATACTCTGTGGGGAGTATCCTTTTAGGAGGAGGAGGACTCCGCGAGATCCTGTTGCC	1861	Qy
1860	atgaataccaatttcgcaaagacctacgcaggatctttacgtttgcagcacgatgcttcc	1801	ДЬ
80	ATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTCC	1801	Qy
1800	ggtggtgataccttgtctctgggttttgctcagctctttgcgcgt	1741	DЬ
1800	GGTGGTGATACCTTGTCTCTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACT	1741	Qy
7	caaaggaaattccgtcatgtgagtggaggtgctgtagtaggtgctagcacgaggatgccg	1681	DЬ
1740	CAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCCG	1681	Qy
1680	gaaaagagattttgggttgcaggcatttccaatgttttgcataggagcggtcgtgaaaat	1621	Db
1680	GAAAAGAATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAA	1621	Qy
1620	tttatagat	1561	Db
1620	TTTATAGATGTTCGTCCCTTCCAAAATTTTTATAGAGCTAGGTACTGAAGGTGCTCCTT	1561	Оу
1560	agttttaatcccactgctgagcaggaggctccgttagttcctaatcttctttggggttct	1501	Дb
	TTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTCT	1501	Qy
1500	ggacgatcaattggtctactgatgataagaaagctacggtttcttgggcgaagcag	4	ДĎ
1500	AAGTGGACAATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCAAAGCAA	1441	Qy
1440	gtgatttctgcagattctcgcagtatagatgctgtacaatctccgtatggctatcaggga	38	DЬ
1440	TTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCGTATGGCTATCAGGG	w	Qγ

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                              The nucleic acids may be used for the recombinant production of the Chlamydia polypeptides (either in vivo or in vitro) according to standa: recombinant DNA methodologies. The polypeptides may then be used to vaccinate against Chlamydia infections in mammals. Chlamydia, such as C. pneumoniae, are pathogens responsible for upper respiratory tract infections such as community acquired pneumonia, acute respiratory disease and bronchitis and may be implicated in atherosclerotic changes and asthma. The nucleic acids may also be used as probes for detecting the presence of Chlamydia nucleic acids in samples (and therefore diagnose infections) and the proteins may be used as antigens for the production of antibodies that may be used to detect Chlamydia proteins
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Sequence
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Matches 2515; Conser 181 121 61 61 ۳ ATGAAGATTCCACTCCGCTTTTTATTGATAGTACTTAGTACCTACGCTTTCTATGTCGAAT **AAAGATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGT** TCAACAACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTT ttattaggagctgctactaccgaagagttatcggctagcaatagcttcgatggaactaca TTATTAGGAGCTGCTACCAAAGAGCTATCGGCTAGCAATAGCTTCGATGGAACTACA 120 atgaagattccactccgctttttattgatatcattagtacctacgctttctatgtcgaat tcaacaacaagcttttctagtaaaacatcatcggctacagatggcaccaattatgttttt Conservative 99.3**%**; 99.6**%**; Score 2508.4; Pred. No. 0; O; Mismatches 0; B 11; 21; Indels Length 2526; 0,

Gaps

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anti-arteriosclerotic; vaccine;

Antigen; anti-inflammatory; respiratory; antibacterial;

anti-asthmatic;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antiquens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
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1320	ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGC	1261	Qy
1320		1261	Db
1260	ATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGAT	1201	Qy
1260		1201	Db
1200 1200	TTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT	1141 1141	pb Qy
1140	.5 = 5.	1081	Qy
1140		1081	Db
1080	CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGT	1021 1021	Qy Db
1020	GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC	961 961	ОУ
960	TCTGTTGCTGATGCTCTAATAATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG	901	D Qy
900	CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA	841 841	Db .
840	ACAGGAACCGTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA	781	
840		781	Qy
780	ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT	721	Qy
780		721	Db
720	GGGAATACAGCGCCTACGGCTGCTGGTAAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC :	661	Qy
720		661	Db
660	GCCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG ( 	601	Qy Db

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Result
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Maximum Match 100%
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Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for
                   P-PSDB; AAW88420
                        WPI; 1999-105610/09.
                                    Birkelund S, Mygind P;
                                                                       23-JUN-1997;
                                                       (BIRK/) BIRKELUND S.
(CHRI/) CHRISTIANSEN G.
                                          Christiansen G,
                                                                         97DK-0000744.
                                           Knudsen K,
                                            Madsen
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Search completed: October 2, 2001, 01:09:34 Job time: 44847 sec

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Query Match
Best Local Similarity
Matches 1030; Conser
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GAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGGGTLSAGGVNLENIRKLYVAGNFS
TADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIAS
TSGGAIDDEGTSILSNNKFLYEGNAKTTGGAICNTKASGSPELLISNNKTLIFASN
VAETSGGAILHAKKLALSSGGFTEFLNNVSSATFRGAISDASGESLSLSAETGNITF
VRNYLTTTGSTDFFKRNAINIGSNGKFTEFLERAKNHTIFFYDFTTSGGTSSDYLKINN
GSAGALNPYQGTILFSGFTLTADELKVADNLKSSFTQPVSLTAKGASNKVIVSGK
LNLLDIEGNIYESHMFSHDQLFSLKITTVDADVDTNVDISSLTPVPAEDPNSEYGFQG
QWNVNWTTDTAINTKEATATWTTGFVPSPERKSALVCNTLWGFSAITFKDLLFTAFCHL
FARDBCCFIAHNNSRTYGGTLFKTGDENRKGFRHTSGGYVIGGSAHTPKDDLFTFAFCHL
FARDBCCFIAHNNSRTYGGTLFFKHSHTQDNVLTKLGKAFSESAIEKFFEDOM
KVEMYVYSQNSFFESSSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSD
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99206606
                Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S. Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
                                                                                           Chlamydophila pneumoniae CWL029.
Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Madsen,A. and Birkelund,S.
NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
PATENT: WO 9858953-A 9 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
Location/Qualifiers
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                                                                 GGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGAT
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/db_xref="GI:4376275"
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RVLLCQALFGHPEALLLDEPTNHLDLYSIMLGHEKALFGNUVVSHDHFPLNTITT
HIADIDYDTIIIYPGNYDDMVEMKTASSEQEKADIKSSEKVVLSLEATTKDYGHQVIH
SQVQSBLREIKLDPOELKKSNIQRPYIRFPLSDKSSGKVVLSLEATTKDYGHQVIH
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KDPQALIFLNRFGRRISTRSIDSSFQEYLRRSGLSGHITPHTIRHTIATHWLESGMDLK
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/gene="xerC"
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LADCGQETLFEWLRNRKTGINDQEIRSVLGKMLFGGDDAFKQIQALSGGETARLLMAG
MMLENHNVLILDEANNHLDLESVSALSWAINDYKGTAIFVSHDRGLIQDCATKLLIFD
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Kalman,S., Mitchell,W.,
Grimwood,J., Davis,R.W.
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Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                           Submitted (01-DEC-1998) Program in Infectious Diseases, of California, 235 Earl Warren Hall, Berkeley, CA 94720,
                                                                                                                                                                                                                                                                                                                                                                                              Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S. Comparative genomes of Chlamydia pneumoniae and C. trachomatis nat. Genet. 21 (4), 385-389 (1999)
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                                                                                                      /organism="Chlamydophila
/strain="CWL029"
/db_xref="taxon:115713"
172. 2957
                                                              /note="Polymorphic Outer
contains frame shift"
    /gene="pmp_3.1"
/note="Cpn0014"
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QAMETADPLQQLLVLSAVSGHLGKTSDDLLFKALASPYPVIRLEAAYRLANLKNTKVI
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DSCLLTNGRFAMYPWFLGGSMITLTPEFIVIRGY ISTSEGFKDLCLISGDYLEYSSD
SLLSIGKTTLRYCRIPILELPFFSIMPMEIPKPINFRGTGGFLGSYLGMSYSPISR
KHFSSTFFLDSFFKHGYGMGFNLHCSGXQVPENPINFRGFTGFLGSYLGMSYSPISR
KHFSSTFFLDSFFKHGYGMGFNLHCSGXQVPENPINFRGFTGFLGSYLGMSYSPISR
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HGDFCFTHKHVNFSGEYHLSDSWETVADIFPNNFMLKNTGFTROCTWINDNYFEGYLT
SSYKVNSFQNANQELPYLTLRQYPISITNTGYVLENIYECGYLMFAFSDHIVGBNFSS
LRLAARPKLHKTYPLFIGTLSSTLGSSLIYYSDVPEISSRHSQLSAKLGUDYRFLLHK
SYIQRHHILEBFTFFITETRFLAKNEDHYIFSJQDAFHSLNLLKAGIDTSVLSKTNPR
FPRIHAKLMTTHILSNTESKPTFFKTACELSLFFGKKNTVSJDAEMINKKHCMDHMI
                                                                                                      complement(13172.
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                                                                                                                                                                                                                                                   LLELGCDTPKLLEY ITERLYQPHYNETLALSFSKGRTLQNWKRVNI IYPQDPQERERL
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FQAAKLPGEPIIRAYADLAIYNLTKDPEKKRSLHDYAKKLIQETLLFVDTENQRPHPS
                                                                                                                                                                                                                                                                                                             DHLHSFIHKLPEEIQCLSAAIFLRLETEESDAYIRDLLAAKKSAIRSATALQIGEYQQ
KRFLPTLRNLLTSASPQDQEAILYALGKLKDGQSYYNIKKQLQKPDVDVTLAAAQALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFLKLDKPKKPPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RWEWIGNDNVAMTLESCHRSKYSLIKCDRENFILDVSRPIDQLLDSPLSDHRNLILGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="pmp_3.2"
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                                                                                                                                               /note="CPn0022"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(11484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(11484. .13190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Predicted OMP [leader peptide:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CPn0020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(9380.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="pmp_5.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Polymorphic Outer Membrane Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MKRCFLFLASFVLMGSSADALTHQEAVKKKNSYLSHFKSVSGIV"
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                                                                                                                                                                                      .13762)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Family;
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Matches 1095;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208676 CACGTCGATACTATCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208616 TTATGTTAGATTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 TITTCTTAAATCCCCAGCAAGTACAGTGACTAATGGATTGGGAGCTATCAATGTTAAAGG
                                                                                                                                                                                                                                                                                                                                                                  CAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCTACAGGAACCGTCTCT-----
TGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACGGGAACCATAGT
                                                                                                                                                                                                TAAACGTAATGCGATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGCACCCTATCCATTTCTGGAGA
                                                                AAATCATACAATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCAT-----CAGA
                                                                                                                         AGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGA
                                                                                                                                                                                                                                                                                                                                GACAGGAAACATTACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGATACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTCCTAAGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAGGGGAATACAGCGCCTACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAGTCCCTTTCTTTATTGGAAATAGTTCTTCAACACGTGGCGGAGCGATTCATACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCGGTGCGATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCGGAGCAATT------AATTGTGCAGGCTCCTTGAAGATCGCAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAATTTAAGCCTATTGGATAATGATAAGGTATTGATTCAGGACAATTTCTCAACAGGAGA
                                                                                                                                                                                                                                                                -CATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTACGTGCTGCGCA
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PLQYVGSVSDRQGTEIVFYDDKIFSTCTFDRSILMKKLRELAFLNRGITIVFEDDRDV
SFDKYTFFYEGGIOSFYSLMQNKESLFSEPIYICGTRVGDDGEIEFEAALQMNSGYS
ELVYSYANNIPTRQGGTHLTGFSTALTRVINTYIKAHNLAKNNKLALTGEDIREGLTA
VISVKYPNPQFEGQTKOKLGNSDVSSVAQQVVGEALTIFFERMYIVEGDSGGSAKQRTV
QAREAKKARELITLKKSALDSARLGKKLIDCLEKDPEKCHMYIVEGDSGGSAKQRTO
RRFQAILPIRGKILNVEKARLQKIFQNQEIGTIIAALGCGIGADNFNLSKLRYRRIII
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SYLLMLGTNESSILFKSTERELRGEALESFINVILDVESFIRTLEKKAIPFSEFLEMY
KEGIGYPLYYLAPATGMOGGRYLYSDBEKEEBALAQEETHKFKIIELYKVAAVFYDIQNQ
LKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCYTLEEVINVLKNLGRKGIEIQRYKG
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VVDNSIDEAMAGYCSRIDVRILEDGGIVIVDNGRGIPIEVHERESAKQGREVSALEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="DNA gyrase subunit B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHVQIREIQFLLG"
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50.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 1015; Indels
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FEATURES
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On Sep 15, 2000 this sequence version replaced gi:6172290 gi:6172294 gi:6172294 gi:6172296 gi:6172336 gi:6172338 gi:6172332 gi:6172334 gi:6172334 gi:6172338 gi:6172338 gi:6172384 gi:6172386 gi:6172388 gi:6172390 gi:6172392 gi:6172394 gi:6172384 gi:6172386 gi:6172398 gi:6172390 gi:6172392 gi:6172394 gi:6174666 gi:6174668 gi:6635174 gi:6635176 gi:6635178 gi:6635180 gi:8547433 gi:8547438 gi:8978640.

AB033782-AB033785, AB033800-AB033815: Submitted (14-Feb-2000) AB038348-AB03882: Submitted (14-Dec-2000).
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                                                                                                                                                                                                                                                                                AEAHPVLNQLIHRIFSKGKAESILSSRAEKFLKQVIVEQVNPKITDVKL
complement(2487. .3347)
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                                                                                                                                                                                                                        complement(2487. .3347)
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/gene="CPj0269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIATLMILTTGVIVLLAMGSPGLSVLVSTIIGTSVTTIGTALFIIĞLVKLIKKSLAWI
QYĞKTEQEVVKÖKYBEFSIFKBDNYHKLTSCLPSPLDIESPSPBASTPVSKLRIACSG
VAIVLGVTLLIGAVVSVFCTGYLDLALCVGFACLGTALFVGGLAGLRTHSLIAQGIM
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                                                                                                                                                                                                                                                                                                                                                            {\tt KGVIGLNLVRSYVGDSLGDLEKHVLHAENLGILSSIVLGSDFFYANEDENFFFNECSS}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="synonym:Chlamydia pneumoniae (strain J138)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPj0267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPj0268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2472)
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                                CDS
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KKYSLDAFSNPRKKGIRALEIDEGDELIAACHIVSDEEKVMLFTHLGMAVRFPHEKVR
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CYWLKVWQLPEGERRAKGKPIINFLEGIRPGEELAAILNIKNFDNAGFLFLATKRGVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5871. .8375)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MFIVIEGGEGSGKSSLAKALGDQLVAQDRKVLLTREPGGCLIGE
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GIAEGLGADFVADLCSKVVGPTPFLPNFVLLLDIPADIGLQRKHRQKVFDKFEKKPLS
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/gene="dnax_2"
complement(4359.
                                                                    KEGDALVSMEKLSSNENDDEVLSGSEEECSDTVSLR*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5871.
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YIIHEADRWTLAAISAFLKVFEEPPKHAVIILTTAKVQRLPKTIISRSLSIFIERGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHEIPSVVFQKMQVTVPNWIDPARG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVSLQYKEKELVSVSPGQDLSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLNLGLKASALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELFDVDLETPKEALEELILNLNRPYNEIIIGGFSQGAILATHLVLTSQNPYAGALIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILCSKETFSYLFRYAQCEIPVTEVSQIIKESSETDKQVLRDKVQRFMEVLLELYRDRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CPj0271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPFLSPYYIE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8375)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5866)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5255)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5866)
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complement(8391.

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12872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1092
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                                                                                                                                                                                                                                                                                                              CGGTCGTGAAAATCAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAG
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                                                     CAMAGATTGTTTATCGCTCACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAA
                                                                                                                                                                  TGCTCACACTCCTAAAGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGA
                                                                                                                                                                                                                                                                                   TGGAGATGAAAATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTGCTCCTTACGAAAAGAGATTTTTGGGTTTGCAGGCATTTTCCAATGTTTTTGCATAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTATGGGGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTTGGGGTTCTTTTATAGATGTTCGTCCCTTCCAAAATTTTTATAGAGCTAGGTACTGA 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGACCAAAACAGGATTTGTTCCCAGCCCCGAAAGAAATCTGCGTTAGTATGCAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGGGCAAAGCAAAGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCAGCAGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAGACATCGTGATTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCGTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACCAGCTCTTCTCTCTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGA 13171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGTCTTAAGCAGCCCGTCAGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGATTTAGGGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGTGATGTCGTTTT
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                                                                                                    Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Shiba,T., Ishi,K., Hattori,M., Kuhara,S. and Nakazawa,T Comparison of whole genome sequences of Chlamydia pneumo from Japan and CWLI029 from USA Nucleic Acids Res. 28 (12), 2311-2314 (2000)
Direct Submission
Submitted (04-JUL-2000)
                                                                                                                                                                                                                                  Chlamydophila pneumoniae J138 (strain:J138) DNA
Chlamydophila pneumoniae J138
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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VTFSCROAVANGGAIYAKKLTLASGGGGGISFSNIVLQATAGAGGAISILAAGECSL
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LEGGLAVSHSNDLTKKYTAYPEVKGSWGNNAFNMALGASSSHSPELHCETTYAPYI
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AANNGGAIYTEASSFISSNKAISFINNSVTATSATGGAIYCSTSAFKEVLTLSDNGE
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PIHMGYQGNMALSWQEDTATKSKAATLTWTKTGYNPNEERRGTLVANTLWGSFVDVRS
TQQLVATKVRQSQETRGIWCEGISNFFKDSTKINKGFRHISACVVGATTTLASDNL
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TYTPKNTTTGIDYTLTGDITLONLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKF
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KQDYCEENGGAISTKNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPT
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Edaairnlikkqteaglifftdegrrxswdddemwgfhgvdrrdskudeigvylkd
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Liddivfyyrqviqdlyaaggrnlqlddcamcrlldirapswygvdshdrlqeileqf
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DAGANCTFTNTAANKLLSFSGFSYLSLIQTTNATTGTGAIKSTGACSIQSNYSCYFGQ
/product="outer membrane protein 4"
/protein_id="CAB37072.1"
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/protein_id="CAB37071.1"
/db_xref="01:4455886"
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DDKYSGGAEPLAYVSGEKHVCLGLISSNHSCIEDRDAVVSRIYEAASYIPLERLSLSP
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/protein_id="CAB37070.1"
/db_xref="GI:4455885"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYRKNPDCTTALLINNTSWKTTGTNLSRQAG IGRAG I FYAFSPNLEVTSNLSME I RGS
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AQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIK
                                                                                 /codon_start=1
/transl_table=11
                                                                                                                                                          /gene="omp4"
                                                                                                                                                                                                     /gene="omp4"
11535. .14321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIRNDPKCTTALVISGASWETYANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:Q92897"
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GACAGGAAACATTACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGATACTCC 12577
                                                             CAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCTACAGGAACCGTCTCT---- 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACGTCGATACTATCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTAC 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTATGTTAGATTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGG 12217
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                                                                                                                                                                                                                                                             AAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGC 12457
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                                                                                                                              AACTCCTAAGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGA 12517
                                                                                                                                                                                            TGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGCACCCTATCCATTTCTGGAGA 740
                                                                                                                                                                                                                                                                                               AAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAGGGGAATACAGCGCCTACGGC 680
                                                                                                                                                                                                                                                                                                                                                                                               TAAGTCCCTTTCTTTATTGGAAATAGTTCTTCAACACGTGGCGGAGCGATTCATACCAA 620
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EITSTP"
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ITCYPEGTSY1FLDDVRISNVKHDQEDAGVFINKSGNLFFMGNKOKFTFHNLLMTEGFG
AAISNRVGDTTLTLSNFSYLAFTSAPLLPQGQAAIYSLGSVMLENSEEVFTGCNYSSW
SGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYGGAISTHNLTLTTRGPSCFE
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14579. .14644
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FARDKDCFIAHNNSRTYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIPLAL
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QWNVNWTTDTATNTKEATATWTKTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIG
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FSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGK
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/protein_id="CAB37073.1"
/db_xref="GI:4455888"
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14579. .16123
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14579. .16123
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Pred. No. 6.8e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTGAAAATACCAGCGGCAGAGGATTTTTCCGAGAGTACACTCCATTTGTAAAAGTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACGAGGATGCCGGGTGATACCTTGTCTCTGGGTTTTGCCTCAGCTCTTTGCGCGTGA 1787
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                                                                                                                                                                                                   CPN133034 17280 bp DNA E Chlamydia pneumoniae GGAI-protein family (partial), omp11, omp10, omp5, omp4, omp1 ORF1, strain VR1310.
Chlamydophila pneumoniae.
Chlamydophila pneumoniae
Bacteria; Chlamydiales; Chlamydophila.
                                                                                         protein; outer membrane protein 11; outer membrane protein outer membrane protein 14; outer membrane protein 4; outer
                                                                                                                hypothetical protein; omp10 gene; omp11 gene; omp12 gene; omgene; omp14 gene; omp4 gene; omp5 gene; ORF1; outer membrane protein; outer membrane protein 11; outer membrane protein 1:
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3827. .6613
                                                                                                                                                                                                                                                  GSAHIYNVDCGLRYSF"
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L., Hjerno,K
                                                                                           note="putative"
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ITAAFCOLFGKDRDHF IKNRASAYAASLHLOHLATLSSPSLLRYLPGSESEQPVTEG
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LNFIGNTAITSGGAIYTDNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLSA
LGGDITFEGNTVVKGASSSQTTTRNSINIGNTNAKIVQLRASQGNTIYFYDPITTSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               */translation="MKSSLHHFLISSSLALPLSLNFSAFAAVVEINLGPTNSFSGPGT
YTPPAQTTNADGT!YNLTGDVSITNAGSTPALTASCFERTTGNLSFQGHGYQFLLQNI
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NFSNDNGGALQGSSISLSLNPNLTFAKNKATQKGGALYSTGGITINNTLNSASFSENT
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/gene="CP0306"
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/gene="CP0306"
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8329. .9444
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Glimmer2; putative"
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/protein_id="AAF38163.1"
/db_xref="GI:7189233"
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/protein_id="AAF38162.1"
/db_xref="GI:7189232"
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CGGTCGTGAAAATCAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAG ACAATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAAC **AACTCCTAAGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGA** CTAT----CAGGGAAAGTGGACAATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTC CTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAACCGCACTTCTAA 1031 TAAACGTAATGCGATCAACATAGGAAGTAACGGGAAATTCACGGGAATTACGGGCTGCTAA CAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCTACAGGAACCGTCTCT----AGGTGCTCCTTACGAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAG 1667 CCTATGGGGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAAC TCTTTGGGGTTCTTTTATAGATGTTCGTCCCTTCCAAAATTTTATAGAGCTAGGTACTGA 1607 TTGGACCAAAACAGGATTTGTTCCCAGCCCCGAAAGAAATCTGCGTTAGTATGCAATAC TTGGGCAAAGCAAAGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCT 1547 CATCAGCAGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGG GAAAGACATCGTGATTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCGTATGG 1430 AGGTCTTAAGCAGCCCGTCAGCCTAACAGCAAAAAGGTGCTTCAAATAAAGTGATCGTATC CAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGATATTCGTATAGA 1271 ATTATCAACTACAGCTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTT GTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAATATAGACTCTCT 1211 ATTCACGCAGCCAGTCTCCCTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTT ATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGTGATGTCGTTTT 1091 ATTTTCTGGAGAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTC CGTATTGAAGATAAATAACGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCT TGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACGGGAACCATAGT 971 AAATCATACAATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCAT-----CAGA AGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGA 911 TGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGCACCCTATCCATTTCTGGAGA TGGAGATGAAAATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAG TGGTATGGAACACAAACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGAC TGACCAGCTCTTCTCTCTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGA TGGGAAGCTCAACCTGATTGATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCA TCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGCTTTTTGAATGA 1331 **AAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGATTTAGGGACGTC** -CATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTACGTGCTGCGCA -----ATGATGGGATTCTTGAGTTAGATGCTGG 1370 1487 3761 3821 2867 3287 3467 1151 3881 3047 3107 3407 3527 3707 851 3167 3647

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AE002192 AE002161
AE002192.2 GI:816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M. Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Chlamydophila pneumoniae
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1, 2000 this sequence version replaced gi:7189226
Location/Qualifiers
                                                                  /product="polymorphic membrane protein G family"
/protein_id="AAF38158.1"
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/TTCYPEGTSYIFLDDVRISNVKHDQEDAGVFINRSGNLFFMGNRCNFTFHNLMTEGFG
                                                                                                                                                                                                                 similarity; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                           complement(275. .1819)
/gene="CP0301"
                                                                                                                                                                                                                                                                                                                                         /translation="MFTSLGRSAIFYFTGSLKHLRLGEFLEIFQK"
complement(275. .1819)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein; identified by Glimmer2;
putative"
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/gene="CP0300"
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/gene="CP0300"
NNHAYHDVNSNGGATATAPGGSTSTSVKSGDLTFKGNTASQDGNTTHNSTHLQSGAQF
                                           AAISNRVGDTTLTLSNFSYLAFTSAPLLPQGQGAIYSLGSVMIENSEEVTFCGNYSSW
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/db_xref="GI:7189227"
                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Utterback, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      KASGSPELIISNNKTLIFASNVAETSGGAIHAKKLALSSGGFTEFLRNNVSSATPKGG
AISIDASGELSLSAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGKFTELRAAKNHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {	t TAGARIANNTGYVRFLSNIASTSGGAIDDEGTSILSNNKFLYFEGNAAKTTGGAICNT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2077. .4926)
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ρ γ	456 8496	GAATTTAAGCCTATTGGATAATGATAAGGTATTGATTCAGGACAATTTCTCAACAGGAGA 515 	
å Š	516 8556	TGGCGGAGCAATTAATTGTGCAGGCTCCTTGAAGATCGCAAACAA 560	
D Q	561 8616	TAAGTCCCTTTCTTTATTGGAAATAGTTCTTCAACACGTGGCGGAGCGATTCATACCAA 620	
₽ <b>Ş</b>	621 8676	AAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAGGGGAATACAGCGCCTACGGC 680	
P V	681 8736	TGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGCACCCTATCCATTTCTGGAGA 740	
D Qy	741 8796	CAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCTACAGGAACCGTCTCT 795	
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β δ	852 8916	AGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGA 911	
B 64	912 8970	TGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACGGGAACCATAGT 971	
д <b>2</b>	972 9030	CTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAGCACCTCTAA 1031 	
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ρ <sub>0</sub> γ	1092 9150	AAGTGCGAACGGTTTCTCCAGGATGCAAACTCTAAGTTGATTATGGATTTAGGGACGTC 1151	
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유 성	1272 9330	TCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTTATCAAAATGGCTTTTTGAATGA 1331 	
Ф	1332 9390	GGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGG 1370	
Qy	1371	GAAAGACATCGTGATTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCGTATGG 1430	

ρ δÃ ₽ Š γ В Qy В Q 밁 QУ 밁 δÃ Š δã 밁 Ş õ Вр Qy δÃ В Q Qγ 밁 Qy B Ωy B 밁 밁 밁 B 망 В В 10395 10335 10275 10215 10155 10101 10050 CAGCCATTCAGACAACCGTATGGAAACGCACTATACCTCATTGCCAGAATC-----2208 1968 9990 1908 9930 1848 9810 1728 9750 1668 9690 1608 9630 1548 9570 1488 9510 1431 9450 CATCAGCAGCCTTATCCCTGTTCCTGCTGAGGGATCCTAATTCAGAATACGGATTCCAAGG 2442 AGAGCTTTTCGGGAACTTTGGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGTAGA 2501 9870 CAAAGATTGTTTTATCGCTCACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAA CCCCAAATGTACGACTACCCTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAA 2381 CAAAGACTACTTTATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCA CACGAGGATGCCGGGTGATACCTTGTCTCTGGGTTTTTGCTCAGCTCTTTGCGCGGTGA AGGTGCTCCTTACGAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAG 1667 ACAATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAAC CTTAGCAAGACAGGCTGGTATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGC .2441 GACGGATCATACTTCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGC 2087 TGCTCACACTCCTAAAGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGA CGGTCGTGAAAATCAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGGTAGTAGGTGCTAG 1727 TTGGGCAAAGCAAAGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCT 1547 CTAT---CAGGGAAAGTGGACAATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTC CGGAGATTCCTACACCTATGATCTCTCAGGATTCTTTGTTTTCCGATGTCTATCGTAACAA 10394 AGAGCAATA-----TTATCATGTTGTAGCGATGTTATCTCCAGATGTTTGTCGTAGTAA 2321 TGATTCGCATCTTTATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGC 2267 **AATGGTTTATGTATCACAAAATAGCTTCTTCGAAAGCTCTAGTGATGGCCCGTGGTTTTAG** TGTTGAAAATACCAGCGGCAGAGGATTTTTCCGAGAGTACACTCCATTTGTAAAAGTCCA 2147 GATCCTGTTGCCTTATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTA 1967 TGGAGATGAAAATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAG TCTTTGGGGTTCTTTATAGATGTTCGTCCCTTCCAAAATTTTATAGAGCTAGGTACTGA 1607 TCTTTCAAGACAGGCATTTTTACTGAGGGGTAGCAACAACTACGTCTACAACTCCAATTG 10514 TATTGGAAGGCTGCTTAACCTCTCGATTCCTGTGGGTGCGAAATTCGTGCAGGGGGATAT 10334 AGCTGTTTACTCGCGCCAAGATAGCTTTGTTGAACTAGGAGCTATCAGTCGTGATTTTAG 2207 TITTGTTCTTTCCAACCCACATCCTCTTTTCAAGACCTTCATTCCACAGATGAAAGTCGA 10214 GCACTCTCATACCCTACAACCCCAAAACTATTTGAGATTAGGAAGAGCAAAGTTTTCTGA 9989 CCTATGGGGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAAC 9689 TTGGACCAAAACAGGATTTGTTCCCAGCCCCGAAAGAAATCTGCGTTAGTATGCAATAC TCCCCAATCTACAGCGACTCTTGTGATGAGCCCAGACTCTTGGAAAATTCGCGGTGGCAA -----CGAAGGTTCTTGGAGCAACGAGTGTATAGCTGGTGGTATCGGCCTAGACCTTCC ATCAGCTATAGAAAAATTCCCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTT 10049 TGGTATGGAACACAAACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGAC Ξ 9749 9569 1487 10274 9629 9509 10454 9929 1787 10154 10100 1847 9869

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTTCAAGACAGGCATTTTTACTGAGGGGTAGCAACAACTACGTCTACAACTCCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGATTCCTACACCTATGATCTCTCTAGGATTCTTTGTTTCCGATGTCTATCGTAACAA 5486
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Ralman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.

Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydophila pneumoniae CWL029.
Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                   Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 10757)
Kalman,S., Mitchell,W.,
Grimwood,J., Davis,R.W.
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Chlamydia pneumoniae section
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                                                                                                                                                                                                                                                                                                                                         Marathe, R., Lammel, C., and Stephens, R.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCT 01-DEC-2000 44 of 103 of the complete genome.
                                                                                                                                                                                                                                   pneumoniae CWL029'
                                                  Protein G/I Family"
                                                                                                                                                                                                                                                                                                                                                            Fan, J., Olinger, L.,
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                              VYRNNPQSTATLYMSPDSWKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
SRNYNVDVGTKLRF"
                                                                                                                                                                                                                                                    TSGGAIDDEGTSILSNNKFLIFEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASN VAETSGAIDDEGTSILSNETGTFERNAKTTGGAICNTKASGSPELIISNETGTTF VARTSGAIHAKKLALSSGGFTEFLRNUVSSATPKGAISIDASGELSLSAETGNITF VRNTLITTGSTDTPKRABINIGSNGKFTELRAAKNHTIFFYDDITSEGTSDVLKINN GSAGALNPYQGTILFSGETLTADELKVADNLKSSETQPVSLSGGKLLLQKGVTLESTS FSQEAGLLGHDSGTTLSTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGK LNLLDIEGNITSGHREFNDQLFSLKATVDANDTNVDISSLIPVPAEDPNSEYGFQG QWNVNWTTDTATNTKEATATWTKTGFVPSPERKSALVCNTLMGVFTDIRSLQQLVEIG
                                                                                                   ATGMEHKQGFWVSSMTNFLHKTGDENRKGFRHTSGGYVIGGSAHTPKDDLFTFARCHL
FARDKOET JAHNNSRTYGGTLFFKHSHTJQFWVLLLGKRKSESA IEKFPREI PLAL
DVQVSFSHSDNRMETHYTSLPESEGSMSNECLAGGIGLDLPFVLSNPHPLFKTFI PQM
KVEMVYVSQNSFFESSSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTF TPKTSATTYSLTGDVFFYEPGKGTPLSDSTFGYTDLSTAGGVHLENIRKLVVAGNTS GAAASTTANKLTFSGFSLLSFDSSFSTTVTTGQGTLSAGGVHLENIRKLVVAGNTS TADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....e= rolymorphic Outer Membrane Protein G Family;
contains frame shift"
complement/car.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="pmp_10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKDKISVSKHPFIEHFEFVKTFEKGNAKAKQTIPSPSQFFHEMIFAPNLKNTRKFYPT
NQELIDDIVFYYRQVIQDLYAAGCRNLQLDDCAWCRLLDIRAPSWYGVDSHDRLQEIL
EQFLWIHNLVMKDRPEDLFVSLHVCRGDYQAEFFSRRAYDSIEEPLFAKTDVDSYHYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEMMSPFQQPEQCHFDVVGSFLRPESLTRARSDFEEGRIVYEQM
RVVEDAAIRNLIKKQTEAGLIFFTDGEFRRYSWDFDFWWGFHGVDRRRDSNDPEIGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AALSDALNILNGPDLAGNPAYQGTIVFSGEKLSEAEAAEADNIKSTIQQPLTLAGGQLS
LKSGYVTLVAKSFSQSFGSTLLMDAGTTLFTAGGIINUVLNVDSLKETKKATLKATQ
ASQTYVTLKGSLSLVDPSGNYVEDVSRNNPQVFSCLTIJADDPANIHTTDLAADPLEKN
PIHWGYQGNWALSWQEDTATKSKAATLTWTKTGYNPNEERRGTLVANTLWGSFVDVRS
TQJLVATKVRQSQETRGIWCEGISNFFKDSTKINKGFRHISAGYVVGATTTLASDNL
ITAAFCQLFGOKDRDHFIKKNRASAYAASLHLQHLATLASPSLLRXLPGSESEQPVLFB
AQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Polymorphic Outer Membrane Protein
/protein_id="AAD18593.1"
/db_xref="G1:4376733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="CPn0449"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WALDDKYSGGAEPLAYVSGEKHVCLGLISSNHSCIEDRDAVVSRIYEAASYIPLERLS
LSPQCGFASCEGDHRMIEEEQWKKIAFVKEIAKEIWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Hypothetical Protein"
/protein_id="AAD18592.1"
/db_xref="GI:4376732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3233. .4348)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEASYIHQDSFKERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNFIGNTAITSGGAIYTDNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLSA
LGGDITFEGNTVVKGASSSQTTTRNSINIGNTNAKIVQLRASQGNTIYFYDPITTSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {	t aanng} {	t Gaiy} {	t Tassfis} nacytatsa{	t TgGaiy} {	t Csstsapk} {	t Pvltlsdnge}
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NFSNDNGGALQGSSISLSLNPNLTFAKNKATQKGGALYSTGGITINNTLNSASFSENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="pmp_11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="pmp_11"
/note="CPn0451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="CPn0450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYRKNPDCTTALLINNTSWKTTGTNLSRQAGIGRAGIFYAFSPNLEVTSNLSMEIRGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11
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Best Local Similarity 50.1%;
Matches 1095; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3888
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                                                                                                 4062
                                                                                                                                                                                                                                                                                                                                  3948 TAAACGTAATGCGATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAA 4007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3588 CACGTCGATACTATCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3528 TTATGTTAGATTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGG 3587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stem_loop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3828 AACTCCTAAGGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGA 3887
                                   972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     741 CAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCTACAGGAACCGTCTCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621 AAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAGGGGAATACAGCGCCTACGGC 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAGTCCCTTTCTTTATTGGAAATAGTTCTTCAACACGTGGCGGAGCGATTCATACCAA 620
                                CTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAACCGCACTTCTAA 1031
                                                                                                                                                     TGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACGGGAACCATAGT 971
                                                                                                                                                                                                                                                    AGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGA 911
                                                                                                                                                                                                                                                                                                                                                                               ----CATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTACGTGCTGCGCA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAGGAAACATTACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGGATACTCC 3947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTGGTAAAGGAGGTGCTATCGCGGATTGCAGACTCTGGCACCCTATCCATTTCTGGAGA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATTTAAGCCTATTGGATAATGATAAGGTATTGATTCAGGACAATTTCTCAACAGGAGA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTCTTAAATCCCCAGCAAGTACAGTGACTAATGGATTGGGAGCTATCAATGTTAAAGG 455
                                                                                              CGTATTGAAGATAAATAACGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCT 4121
                                                                                                                                                                                                                   AAATCATACAATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCAT-----CAGA 4061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCGGTGCGATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAA 3707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCGGAGCAATT------AATTGTGCAGGCTCCTTGAAGATCGCAAACAA 560
1760 a
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GSAGALMPYGGTIFSGTTABEKKYADNIKSSTOPVSLSGKLLLOKGVTLESTS
FSQEAGSLLGWDSGTTISTTAGSITITNLGINVDSLGLKQPVSLTAKGASKKYIVSGK
FSQEAGSLCHWDSGTTISTTAKSITITNLGINVDSLGLKQPVSLTAKGASKKYIVSGK
LULIDLENIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVFABDPNSEYGFQG
QMNVMTTDTAINTKEATATWFKTGFVFSPERKSALVCNTLWGYSTDIRSLQQLVEIG
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FARDDDCFIAHNNSFTYGGTLFFKHSHTLQPQNYLRLGFRAFFSESAIEKFPREIPLAL
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TADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIAS
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VAETSGGAITAKKLLALSSGGFTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITF
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KVEMVYVSQNSFFESSSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSD
VYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="omp4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1341 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 341; DB 2; Length 6030; Pred. No. 6.5e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 1015; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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8 GGCCATTACGGATCATGGCATGAAGACGAGTCTCTACCCCCCCC	Qy 196 Db 514	
2 ATCAGCTATAGAAAAATTCCCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTT 5141	Db 508	
8	Qy 190	
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8	Оу 184	
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88 CAAAGACTACTTTATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCA 1847	Qy 178	
12 TGCTCACACTCTAAAGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGA 4961	Db 490	
28 CACGAGGATGCCGGGTGGTGATACCTTGTCTCTGGGTTTTGCTCAGCTCTTTTGCGCGTGA 1787	Qy 172	
2 TGGAGATGAAAATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAG 4901	84	
AGTGGAGGTGCTGTAGTAGGTGC	Qy 166	
12 TGGTATGGAACACAAACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGAC 4841	Db 478	
08 AGGTGCTCCTTACGAAAAGAGATTTTGGGTTGCAGGCATTTTCCAATGTTTTGCATAGGAG 1667	QY 160	
22 CCTATGGGGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAAC 4781	Db 472	
48 TCTTTGGGGTTCTTTTATAGATGTTCGTCCCTTCCAAAATTTTATAGAGCTAGGTACTGA 1607	Qy 154	
	Db 4662	
	Оу 1488	
	Db 4602	
	Qy 1431	
42 CATCAGCAGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGG 4601	4.5	
1 6	Qy 137	
	Db 448	
	Qy 1332	
2 TGGGAAGCTCAACCTGATTGATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCA 4481	Db 4422	
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2 A	Db 436	
	Qy 1212	
2 ATTATCAACTACAGCTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTT 4361	Db 430	
2 GTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAATATAGACTCTC	Оу 115	
2 AGAGAGCACGAGCTTCTCTAAGAGGCCGGTTCTCCTCCTCCGCATGGATTCAGGAACGAC 4301	424	
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2 ATTTTCTGGAGAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTC 4181	Db 4122	

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Chlamydophila pneumoniae.
Chlamydophila pneumoniae
                  Knudsen,K., Madsen,Å.S., Mygind,P., Christiansen,G. and Birkelund,S.
                                             Submitted (29-AUG-1997) Knudsen K., Department of Medical Microbiology and Immunology, University of Aahus, The Bartholin building, University of Aahus, C. DENWARK 2 (bases 1 to 6030)
                                                                                                                                     Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
1 (bases 1 to 6030)
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Chlamydia pneumoniae or
AJ001311
AJ001311.1 GI:3255934
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      Identification of two novel genes encoding 97- to 99-kilodalton
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/gene="omp4"
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/dev_stage="elementary body"
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/note="putative"
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/protein_id="CAA04671.1"
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      /db_xref="SPTREMBL:086164"
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Best Local Similarity 50.1%;
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                            681 TGCTGGTAAAGGAGGTGCTATCGCGATTGCCAGACTCTGGCACCCTATCCATTTCTGGAGA 740
                                                                                                                                          621 AAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAGGGGAATACAGCGCCTACGGC 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 TTTTCTTAAATCCCCAGCAAGTACAGTGACTAATGGATTGGGAGCTATCAATGTTAAAGG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456 GAATTTAAGCCTATTGGATAATGATAAGGTATTGATTCAGGACAATTTCTCAACAGGAGA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                  888 CACGTCGATACTATCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTAC 947
AACTCCTAAGGGGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGA 1187
                                                                                                        AAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGC
                                                                                                                                                                                                                 TAAGTCCCTTTCTTTATTGGAAATAGTTCTTCAACACGTGGCGGAGCGATTCATACCAA 620
                                                                                                                                                                                                                                                                                                                            TGGCGGTGCGATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAA 1007
                                                                                                                                                                                                                                                                                                                                                                               TGGCGGAGCAATT------AATTGTGCAGGCTCCTTGAAGATCGCAAACAA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATGTTAGATTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGG 887
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Sequence 1 from Patent WO9858953.
A81827
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1 (bases 1 to 3200)

Madsen,A. and Birkelund,S.

NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
Patent: WO 9858953-A 1 30-DEC-1998;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKTSIPWILVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTF
TPKTSATTYSLTGDVEFYEPGKGTPLSDSCFKQTTDNLTFLGNGISLTFGFIDAGTHA
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FSQEAGSLLGMDSGTTLSTTAGSITITHLGINVDSLGLKQPVSLTAKGASNKVIVSGK
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FARDNDCFTAHNNSRTYGGTLFFKHSHTLQPNYLRLGKKFSSSAINELEKPFREITLAL
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FARDNDCFTAHNNSRTYGGTLFFKHSHTLQPNYLRLGKKFSSSAINELEKPFREITLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVQVSFSHSDNRMETHYTSLPESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQM
KVEMVYVSQNSFFESSSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSD
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/db_xref="GI:6731864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unidentified"
/db_xref="taxon:32644"
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Pred. No. 6.3e-72;
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                                                                                                        1127
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1847	CAAAGACTACTTTATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCA	1788	Qy
2261	TGCTCACACTCTAAAGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGA	2202	Db
1787	GAGGATGCCGGGTGGTGATACCTTGTCTCTGGGTTTTTGCTCAGCTCTTTTGCGCGTG	72	Qy
N		14	ρb
1727	CGGTCGTGAAAATCAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAG	1668	Qγ
2141	TGGTATGGAACAAACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGAC	2082	Db
1667	TGCAGGCAT	1608	Qy
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1607	TCCCTTCCAAAATTTTATAGAGCTAGG	1548	Qy
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1841	TGACCAGCTCTTCTCTCTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGA	1782	망
1370	GGACCATTCCTATGATGGATTCTTGAGTTAGATGCTGG	1332	Qy
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1331	TCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGCTTTTTGAATGA	1272	Оу
1721	AGGICTTAAGCAGCCGTCAGCCTAACAGCAAAAAGGTGCTTCAAATAAAGTGATCGTATC	1662	Db
1271	CAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGATATTCGTATAGA	1212	Qy
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1091	-	1032	Qy
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1031	CTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAACCGCACTTCTAA	972	Qy
1421	CGTATTGAAGATAAACAGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCT	1362	Db
971	TGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACGGGAACCATAGT	912	Qy
1361	AAATCATACAATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCAGA	1308	Db
911	HATATACTTTTATGATCCGATTACTGTAACAGGATCGACATCTGTTGCTG	852	Qy
1307	TAAACGTAATGCGATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAA	1248	망
851	CATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTACGTGCTGCGCA	796	Qy
1247		1188	Db :
795	CAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCTACAGGAACCGTCTCT	741	Qγ

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AUTHORS
TITLE
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Best Local Similarity 99.4%;
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20782 TTTTAG 20787
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                                                                                                                                                                                                                                                                                                                  933 TGATACTGGAGATAACAAAGAGTATACGGGAACCATAGTCTTTTCTGGAGAGAAGCTCAC 992
                                                                                                                                                                                                                                                                                                                                                                                           873 TGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGATGCTCTAATATTAATAGCCC 932
                 TATCGAGTTAACGAATTTGGAAATTAATATAGACTCTCTCAGGAACGGGAAAAAGATAAA 1232
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                                                                                                            TAAAAATGGGACTGTAGTTTTAAAAGGTGATGTCGTTTTAAGTGCGAACGGTTTCTCTCA 1112
                                                                                                                                                                                                                                                                                                 TGATACTGGAGATAACAAAGAGTATACGGGAACCATAGTCTTTTCTGGAGAGAAGCTCAC 512
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A81855
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Madsen, A. and Birkelund, S.
NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
PATENT: WO 9858953-A 29 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
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PPPPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGFFREYTPFVKVQAVYSRQDSFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
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<1. .>1830
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LHRSGRENQRKFRHVSGGAVVGASTRNPGGDTLSLGFAQLFARDKDYFNNTNFAKTYA
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1440	GTGATTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCGTATGGCTATCAGGGA	1381	Q
138 196	TTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACATC	1321 19583	B 68
1320	ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGC	1261	Qy
1958		19523	Db
1260	ATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGAT	1201	Db
1952		19463	Qy
1200 1946	TTAGGGACGTCGTTGGTAGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT	1141 19403	유 양
1140	GATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGAT	1081	₽ Q
1940		19343	
1080 1934	CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGT	1021 19283	Дb
1020	GGAACCATAGTCTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC	961	₽
1928		19223	8
960 1922	TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG	901 19163	D 24
900 1916	CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA	841 19103	당 성
840	ACAGGAACCGTCTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA	781	D <sub>b</sub>
1910		19043	
780	ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT	721	Qy
1904		18983	Db
720	GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC	661	B 8
1898		18923	
660	GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAAĆTCTATTTCAG	601	Db 04
1892		18863	
600 1886	TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTATTGGAAATAGTTCTTCAACACGT	541 18803	₽ Q
540	AAGGTATTGATTCAGGACAATTTCTCAACAGGAGATGGCGGAGCAATTAATT	481	Dp
1880		18743	Q
480	GTGACTAATGGATTGGGAGCTATCAATGTTAAAGGGAATTTAAGCCTATTGGATAATGAT	421	Db Qq
1874		18683	
420 1868	AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTAAATCCCCAGCAAGTACA	361 18623	рb
1862		18563	В

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ОУ	Qy Db	Qy Qy	Qy db	Qу	Qy Db	Qy	Qу Дъ	Qy Db	Оу	Фр	Qу	Qy Db	Qy Db	Qу	Qy VQ	ф
2401	20542 2341 20602	2221 20482 2281	4 4	2101 20362	2041 20302	1981 20243	1921 20183	1861 20123	1801 20063	1741 20003	1681 19943	1621 19883	1561 19823	1501 19763	1441 19703	19643
ATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGCAGCCTTTTCGGGAACTTT	CATGITGTAGGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTTAGGACTACC CATGITGTAGGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTTAGGAAGACAGAC	TRIANCCTTGCGATTCCTCTTGGAATCAAGTTAGAAACGATTTGGAGAGCAATATTATTTTTATAACCTTGGGATTCCTCTTTGGAATCAAGTTAGAAACGGTTTGGAGAGCAATATTATTTTTTATAACCTTGGGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTATTTAT	CGCCAAGATAGCTTTGTTGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTT	AGCGGCAGAGGATTTTTCCGAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACTCG	TCTTGGGGAGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATACC	CATCGCATGAAGACCGAGTCTCTACCCCCCCCCCCCCCGACGGTCTCGACGGATCATACT	TATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGAT	CTATACTCTGTGGTGAGTATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCCT	ATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTCC	GGTGGTGATACCTTGTCTCTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTTT	CAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCCG 	GAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAAT 	TTTATAGATGTTCGTCCCTTCCAAAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTAC	AGTITTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTCT	AAGTGGACAATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCAAAGCAA	GTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGGA
T 20541 C 2340 C 20601 C 20601 T 2400 T 20661	205	228	222 204	G 2160 T 20421	C 2100 C 20361	T 2040   T 20301	T 1980 T 20242	T 1920   T 20182	C 1860     20122	T 1800   T 20062	G 1740	T 1680	C 1620 C 19882	T 1560   T 19822	A 1500 G 19762	A 19702

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AWTGTGNKVGEFFWDKINYKPRPEKEGNLVPNILWGNAVDVRSLMQVQETHASSLQTD
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AYQGDFKETTADGRRFSNGSLTSLSVPLGIRFEKLALSQDVLYDFSFSYLPDLFRKDP
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1 ATGAAGATTCCACTCCGCTTTTTATTGATATCATTAGTACCTACGCTTTCTATGTCGAAT 60
TTTAGCAATATCGATGCAACCACGGCTTCTGGAGCTGCTATTGGAAGTGAAGCAGCTAAT 360
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                                                                                       AAAGATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGT 18502
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AP002545 299650 bp DNA BCT Chlamydophila pneumoniae J138 genomic DNA, cc section 1/4.

AP002545 AB033780 AB033781 AB033792 AB033793 AB033798 AB033799 AB036071 AB036076 AB036076 AB036077 AB036078 AB038047 BA0030008
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Mutsunori Shirai, Yamaguchi University School of Medicine,
Department of Microbiology, 1-1-1 Minamikogushi, Ube, Yamaguchi
755-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-227, Fax:81-836-22-2415)
On Aug 31, 2000 this sequence version replaced gi:6172286
gi:617238 gi:6172310 gi:6172312 gi:6172314 gi:6172316 gi:635162
gi:6172320 gi:6172322 gi:6172324 gi:635158 gi:6635160 gi:6635162
gi:6172320 gi:6172322 gi:6172324 gi:6635158 gi:6635172 gi:8547426
gi:8547426 gi:8547430 gi:8978373.
AB033780-AB033781, AB033792-AB033792, Submitted (14-Feb-2000)
AB036071-AB036078: Submitted (18-Dec-2000).
Iocation/Qualifiers
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Nucleic Acids Res. 28 (12), 2311-2314 (2000)
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Chlamydophila pneumoniae J138
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiaceae
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putative;polymorphic membrane protein G family, authentic
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1680	GAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAAT	1621	Qy
10299	AGATGTTCGTTCCTCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTT	10358	Дb
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1500 10419	AAGTGGACAATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCAAAGCAA	1441 10478	Qy Db
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1440	TGATTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCGTATGGCTATCAGGG	1381	Qy
1380 10539	TTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACATC	1321 10598	Db Qy
10599	ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGC	10658	DЬ
1320	TTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGG	1261	Qγ
10659	ATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGAT	10718	DЬ
1260	agacteteteteaggaacgggaaaaagataaaacteagtgetgeeacageteagaaa	1201	Qγ
1200 10719	TTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT	1141 10778	Qy Db
10779	STTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATG	10838	Db
1140	GATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGAT	1081	Qy
1080 10839	CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGT 	1021 10898	Ωy
1020 10899	GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAC	961 10958	ОУ ОБ
960 10959	TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG	901 11018	Qу Дъ
11019		7	Db -
900	GTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGAC	841	Qy
<u>`</u>	ACAGGAACCGTCTCCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA		Db 2
840	SAACCGTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGT	781	۷0
780 11139	ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT	721 11198	Qy Db
11199	GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGG	11258	DP 43
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660 11259	GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG 	601 11318	Оу
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Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-MAR-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA On Jun 1, 2000 this sequence version replaced gi:7189672.
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Chlamydophila pneumoniae AR39.
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GTGATTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCGTATGGCTATCAGGGA 1440 TTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACATC ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTTATCAAAATGGC ATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGAT TTAGGGACGTCGTTGGTAGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT GATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGAT GATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGAT CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAAGGT CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGT CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTAAATCCCCAGCAAGTACA ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGC TTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 9317 9257 1380 1200 1140 1080 8717 9137 8897 1020 8837 8777 900 840 9197 9077 9017 8957 8597 8537 8477 8417 8357 480 8297 960 8657 780 720 660 600 540 420

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Chlamydia pneumoniae so
AE001586 AE001363
AE001586.1 GI:4376263
                                                                                                                                                                                                                             Submitted (01-DEC-1998) Program in Infectious Diseases, of California, 235 Earl Warren Hall, Berkeley, CA 94720,
                                                                                                                                                                                                                                                                                                                                                                                   Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S. Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
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Best Local Similarity
Matches 2516; Conserv
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-	1591	4 GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC 15973
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-	500T	AGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT 101
	Oy 1200	1 ATAGACTCTCTCAGGAACGGGAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGAT 1260 
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	126	. ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTGTTTTTATCAAAATGGC 13
-	T071	WII CAININANICAICCIAII AIWCIAACWAII NACAWIAWAWAIII II I WICHWWWIAAC 102
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п	_	CAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCC
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н	_	GIGGIGATACCITGICTCIGGGTTTIGCTCAGCICTTIGCGCGIGACAAAGACIACI
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D	b 16754	ATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTC
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EGHILKLQKEATAEVENKILSDAESRLEIVFEDVKEMPCRIEEIEKTLRMAELPLLPT
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DSGLESEVRACREQLRERIQEFETQGLDLVEKELLCVSSRLRNTECDCVSGVKKEAPP
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                                  CGCCAAGATAGCTTTGTTGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTT
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AJ133035

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AJ133035. GI:4455890

HB1 gene; HB2 gene; hb3 gene; hb4 gen
gene; omp15 gene; omp6 gene; omp7 gen
membrane protein 6; outer membrane pr
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Chlamydophila pneumoniae
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Chlamydia
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Submitted (21-JAN-1999) Boesen T., Department of Medical Microbiology and Immunology, University of Aarhus, The Building, DK-8000 Aarhus, DENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Chlamydiales;
1 (bases 1 to 26920)
Daugaard,L., Hjerno,K.,
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Query Match 100.0%; Score 2526; DB 9; Length 2526; Best Local Similarity 100.0%; Pred. No. 0; Matches 2526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 ATGAAGATTCCACTCCGCTTTTATTGATATCATTAGTACCTACGCTTTCTATGTCGAAT 60	H Ce My N M 1 H	RESULT 1 A81833 A81833 LOCUS DEFINITION Sequence 7 from Patent WO9858953. ACCESSION A81833 VERSION A81833.1 G1:6731867 KEYWORDS SOURCE unidentified. ORGANIEM unidentified	74.4 2.9 14482 1 AE002293 62.2 2.5 216 2 CPU59306 57.4 2.3 455 2 CPU59307 52 2.1 1141 10 AX083744 49.8 2.0 1141 10 AX083744 49.2 1.9 5601 1 AE001361 ALIGNMENTS	1 10070 1 AECOUTES 1 AECOUTES 2 1 AECOUTES 2 1 AECOUTES 3 1518 2 AETOUT 3 1518 3 1839 1859 1859 1859 1859 1859 1859 1859 185	9 341 13.5 10757 1 AE001628 AE00162 10 341 13.5 12676 1 AE002192 AE00219 11 341 13.5 10757 1 AE002192 AE00219 12 341 13.5 10780 2 CPN133034 AJ13303 13 340.2 13.5 16448 1 AE002546 AE00254 13 38.6 13.4 2787 9 A81835 14 338.6 13.4 2787 9 A81835 15 313.6 12.4 10757 1 AE001628 AE00158 16 310 12.3 4926 2 CPU72499 U72499 17 309.4 12.2 2815 9 A81829 18 309.4 12.2 2815 9 A81829 19 309.4 12.2 12676 1 AE002192 AE00219 19 309.4 12.2 12676 1 AE002192 AE00219 20 309.4 12.2 12676 1 AE002192 AE00219 21 309.4 12.2 300650 2 AP002546 AE00219 22 287.4 11.4 3000 9 A81851 AB01837 23 287.4 11.4 6030 2 CPONP54 AB1837 26 280 11.1 2793 9 A81851 AB0181 27 280 11.1 2793 9 A81851 AB0181
OY 1021 CGCACTTCTAAATTACTTCAAAATTTCGTTTTTAAAAATTGGGACTGTACTTTAAAAGGT 1080	841 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACAGATCGCCAAGGACGACAGATCGCATACTTTATGATCCGATTACTGTAACAGGATCGACAGATCGACAGATCGACAGATCGACAGGATCGACAGGATCGACAGGATCGACAGGATCGACAGGATCGACAGGATCGCGCAAGGACAGAACAAGAGATATACTTTATGATCCGATTACTGTAACAAGAGATATACGGACATATACGATTACTGGAATAACAAAAGAGTATACGGIIIIIIIIII	Qy 661 GGGAATACAGCGCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 720	541 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTATTGGAAATAGTTCTTCAACACGT 6 [	OY SOL TITAGCAPIAL CARLOCACCOCCENTERS GAVE TRACES AND CARGE TAKE TO THE CARLOCACCE TRACES AND CARGE TAKE TO THE CARLOCACCE TATE OF THE CARLOCACCE TAKE TO THE CARLOCACCE TAKE TO THE TAKE TO THE TAKE THE TAKE TO THE TAKE TO THE TAKE TO THE TAKE THE T	61 TTATTAGGAGCTGCTACTACCGAAGAGCTATCGGCTAGCAATAGCTTCGATGGAACTACA

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: gb_ba1:
2: gb_ba2:
3: gb_ba3:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## SUMMARIE

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A81855 A81827 CPOMP54	A81833 CPN133035 AE001586 AE002235 AP002545	SUMMARIES
A81855 Sequence 29 A81827 Sequence 1 AJ001311 Chlamydia	A81833 Sequence 7 AJ133035 Chlamydia AE001586 Chlamydia AE002235 Chlamydop AP002445 Chlamydop	Description

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RESULT 15
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Matches 296; Conserv
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Q9RB71;
Q1-MAY-2000
Q1-OCT-2000
Q1-MAR-2001
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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37.3%; Pred. No. 2e-73;
tive 135; Mismatches 312; Indels
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psittaci (Chlamydophila psittaci).
Chlamydiales; Chlamydiaceae; Chlamydophila.
                                           (TrEMBLrel. 02, (TrEMBLrel. 02, (TrEMBLrel. 16,
                                                                                                         PRELIMINARY;
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A Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
T "Molecular cloning and characterization of the genes coding for t
T flighty immunogenic cluster of 90-kilodalton envelope proteins fro
T Chiamydia psittaci subtype that causes abortion in sheep.";
Infect. Immun. 66:1317-1324(1998).
R EMBL, U65942; AAC15921.1;
R InterPro; IPR003357;
R InterPro; IPR003357;
R InterPro; IPR003358; -
R InterPro; IPR003358; -
R InterPro; IPR003355; OMP; 1.
R Pfam; PF02385; OMP; 1.
R Pfam; PF02485; DUF145; 1.
R SEQUENCE 847 AA; 90694 MW; 754C958E7F11179E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.; "Identification of a multigene family coding for the 90 kba protein of the ovine abortion subtype of Chlamydia psittaci."; FEMS Microbiol. Lett. 142:277-281(1996).
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NTLWGSFSDIRAIQNLMDISVNGADYHRGFWVSGLGNFLHKSGSDTKRKFRHNSAGYALG
                           NILWGNAVNVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRYRHNSGGYVLS
                                                                                                                                                                                                            QNVNLSAGYLVIKEGAEVTVSKFTQSPGSHLVLDLGTKL---IASKEDIAITGLAIDIDS
                                                                                                                                                                                                                                           GIFFYDPIT--GGGSDELNIN-KQDTVDYTGKIVFSGERLSDEEKKVAANLKSDFK----
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                     The present sequence encodes the Chlamydia pneumoniae 98 kDa outer membrane protein, known as CPMI00640. Chlamydia pneumoniae is a common cause of community acquired pneumonia and upper respiratory tract symptoms and diseases, including bronchitis and sinusitis. It also has an association with atherosclerosis and asthmathe 98 kDa outer membrane protein is a C. pneumoniae-specific antigen which can confer immune protection against chlamydial infection. The nucleotide sequence encoding the protein or the protein itself may be administered as a vaccine to prevent or treat infection and they may also be used to diagnose infection. The gene encoding CPN100640 was amplified from Chlamydia pneumoniae genomic DNA by PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
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Mismatches 1032; Indels 75; Gaps CGATGGTGATATTGATATTGATCAGAATGCTTA 7	T   ttg	TCTCGCC       ttgacac	CTGTTAT	ACATTGO	AGTCTCC           aaagtcc	TGTCTGC     tagcgcg	TAGCAA!	ACGGAGI       cagatgo	ATGATO	TTTTAC	TTACATT	യ — വ	₩ >>	AAAGAA/        caaata	CAGGAA	AAAATGA     gcaatag	GGGCTT	ĹVe
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AATGCTTA 71 all	a :	CAATGCC   gtcattc	AAACACC       agaagct	AGGCCTC       tggctta	GCATTTA     ccgcatc	CTTAGTT      tcttgta	gcaa	₹ ₹	് ∺്	FAAATT        	CCAP         caaccaa	ATTGA         tagc	TCTATTS	CATAATG     attgaca	TCCAGTT       gacagat	GACTACI     ggaagco	CGATGGT        cactgac	Mismato
AATGCTTA 71 all	AGAG     agcc	TATGAAG        tatgaga	GCAAATA         gcagata	GCGATA        gcagtaa	GTTTTAC	ATTAAA(     cttcgtg	TAG      tgc	GTAC †   gtat	AG –	a C	GGAAACO        gtcacco	ACTGGAO      tctgcto	ATCAATI       caaagti	GGTGGC	CCTATTO	GCTATAC        gctcaac	GATATTO	hes 10
AATGCTTA 71 all	CTGG     acgg	SATCTCA        atcata	AAACAGA         aaaaata	BATATAG      Batctct	SATTTAG        atgggg	aAGGGGG          yatggag	ATTTTA       acgtca	ACAGGGA     gggggtg	GGTCTA        Jcagctt	TTACAGG	CGGACGA      aacggaa	3GGGAGA        gggaac	AATATAT         hatatct	3GAGCCA          gagcca	STGACTT        tgactc	GTAAGG          gctcagg	SATATTG      cgatta	
Gaps  Trace 83  CTG 84  TTG 85  TTG 85  TTG 85  TTG 85  TTG 87  TTG 87  TTG 11  ATG 11  ATG 11  ATG 11  ATG 11  ATG 11  ATG 11  TTG 12  TTG 12  TTG 13  TTG 15  TTG 15  TTG 16  TTG 17  TTG 17	ccess       	GAATG   actta	aç TC	ATAGCT	GAACCA         ggacta	CCGAAG         caccg	AATCTA       cctcta	CATA    gatt	CC	CGAGAA      ctgcta	Cac	g A	TATG	TTTATG	TCTCTG       ttactg	GAGGGG         gcgggg	ATCAGA      cagata	
7 Ps	TAGTG     tctgg	GAAATT(      aaagtg	654 	<b>σ</b> Ο	ACTG     actt	TCACAG      taactt	CAATC         ctatc	t ctt	cacat	ATGGATO	CGTTTT gtacaa	~ »	CAAAT   gtagc	TAG	AAT  -	CTGTCTO	GCTT   tttc	5;
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Ωy 밁 Š DЬ В Qy 밁 Qy 밁 Ωy 밁 δÃ 밁 Qy 멍 Qy 밁 δÃ 뭐 Qy В QΥ DЪ Qy 망 QΥ 밁 Qy 밁 Qy 뫄 Qγ B Qy В ρy 2791 2317 1957 2649 2671 2611 2551 2409 2491 2349 2434 2289 2374 2229 2169 2257 2109 2197 2049 1989 1869 1749 1837 2077 1929 2017 1809 1897 tcgtgctgcgaaccatttccaagtgaacccccacatggaaatcttcggtcaattcgcttt 2850 GAGTGGAACGGGTCGGTATCACTTTAACGACTATACTGAGCTCTTATGTCGAGGAAGTAT ACTTTTCCAAGGTGCCATCCCATTTATGAAACTACAATTAGTTTATGCTTATCAGGGAGA CAATTGTTGGGCTATAGAGTGCGGAGGGAGCATGCCTCTATTGGTATTTGAGAACGGAAG CACCAATGATATGAAAACAGACTACGCAAATTTCCCTATGGTGAAAAACAGCTGGAGAAA ACCTAAGCACTATACTTCGATGGCATTTTCCCAACTCTTTAGTAGAGACAAGGACTATGC GAAATTAGCTTGGACA---GGAACTGGAAACAAAGTTGGAGAATTCTTCTGGGATAAAAT 1748 agctagcgatgctaactggatggcctatggtaccaacctcgcacgacaaggtttttctgt GATTAGCGGAGACTCCTGGCTTGTTCCGGCAGCACACGTATCAAGACATGCTTTTGTAGG tactcttatgtatatactcgatgcttaccgacgcaatcctaaatgtcaaacttccctaat TAGTITCTCCTATATTCCTGATATTTTCCGTAAGGATCCCTCATGTGAAGCTGCTCTGGT cttctacgagcgtcatgctgaaggacgcgctttcaataaaagcgagcttatcaacgtaga TTTCAAAGAGACGACTGCAGATGGCCGTAGATTTAGTAATGGGAGTTTAACATCGATTTC tcttctgaaagaagtcgaaccttttgtcaaagtacagtatatctatgcgcatcagcaaga agacaaccacatgaagacatattataccgataactctatcatcaagggttcttggagaaa tgagatctcccagatcattcctttatcg----ttcgatgctaaattcagttatctccatac gctcttcgacatcgccaatttcctctggggaaaagcaacccgagctccctgggtgctctc tacaggtaagaaccacggagatacttacggtgcctctttgtatttccaccatacagaagg GGTTTCCAACAACGAATACAGAATGTATTTAGGATCGTATCTCTATCAATATACAACCTC tgccgaggatcagcttacttttgccttctgccagctctttgctagagatcgcaatcatat ccgccatggtttccgccatatcagcgggggttatgcactagggatcacagcaactactcc CAATATAAGGTACCGTCATAACAGCGGTGGATATGTTCTATCTGTAAATAATGAGATCAC 1988 tgagcgtgagctatggctttcaggaattgcgaatttcttctatagagattctatgcccac AGATCGAGGGCTGTGGATGGAATTGGGAATTTCTTCCATGTATCTGCCTCCGAAGA 1928 ctttatagatatacgctcgatcaatcagcttatagaaaccaagtccagtggggagccttt 2016 TGCTGTAAATGTCAGATCCTTAATGCAGGTTCAAGAGACCCATGCATCGAGCTTACAGAC 1868 aggatacattcctagtcctgagagaaaaagtaatctccctctaaatagcttatggggaaa AAATTATAAGCCTAGACCTGAAAAAGAAGGAAATTTAGTTCCTAATATCTTGTGGGGGAA gcagttgtcttgggcaaatgcaacatcctcaaaaataggaagcatcaactggacccgtac 2708 2648 2670 2610 2408 2490 2256 2048 1808 1896 2730 2588 2528 2468 2550 2348 2433 2288 2373 2228 2316 2168 2108 2196 2076 1956 1836 1691 2790 2136

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RESULT 8
AAC81914/c
ID AAC81914 standard; DNA; 273254 BP
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                                                                    Query Match
Best Local Similarity
Matches 1055; Conserv
                                                                                                                                                                                                       transcriptional termination region; (4) a cell comprising an expression cassette of (3) as part of an extrachromosomal element or integrated into the genome of a host cell as a result of induction of the expression cassette into the host cell, and the cellular progeny of the host cell; (5) a method for producing a Pl comprising growing a cell of (4) where the protein is expressed and isolating the protein free of other proteins; (6) a purified polypeptide composition comprising at least 50 weight % of Pl; and (7) a monoclonal antibody binding specifically to the
                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel nucleic acid (N1) encoding a Chlamydia pneumoniae protein (P1), given in the specification. The isolated nucleic acid is useful for diagnostic and analytical methods, such as, hybridization-based assays or amplification-based assays. The protein may be used for diagnostic purposes, for their enzymatic or structural activity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizing fragment of N1; (2) an isolated nucleic acid (N2) that hybridizes under stringent conditions to N1; (3) an expression cassette comprising N1 under the transcriptional regulation of a transcriptional initiation region functional in an expression host, and a
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| 2911 ga 2912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid for use in diagnostic and analytical methods encodes genomic sequence of Chlamydia pneumoniae -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stephens R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1998;
08-APR-1999;
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                                                                                                                                                           Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other.
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99US-0128606
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                                                                                     8.5%; Score 259.2; DB 21; 48.8%; Pred. No. 1e-62;
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                                                                      Indels
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1748	GAAATTAGCTTGGACAGGAACTGGAAACAAAGTTGGAGAATTCTTCTGGGATAAAAT	1692	dd
109739		109798	Vo
1691	GACTGTAACTGCTGGAGATTTCCTACCGGTAAGTCCCCATTATGGTTTTCAAGGCAATTG	1632	dq
109799		109858	Qy
1631	ACAGACGTTCCCTCTGCTCTCTTTAGAGCCTGGAGCCGGGGTAGTGT	1584	Qy
109859		109918	Qy
1583	CTCTATAGAACTTATCTCGCCTACTGGCAATGCCTATGAAGATCTCAGAATGAGAATTC	1524	Qy
109919		109978	Db
1523 109979	ATCCTCAACAGCAGCTGTTATTAAAGCAAACAGCGCAAATAAACAGATATCCGTGACGGA	1464 110035	ОУ
1463 110036	AGCCTCTAAGGAGACATTGCCATCACAGGCCTCGCGATAGATA	1404	Qy Db
1403	TTCAAAATTCACGCAGTCTCCAGGATCGCATTTAGTTTTAGATTTAGGAACCAAACTGAT	1344	Db
110096		110155	Qy
1343	TCAGAACGTCAACCTGTCTGCAGGATACTTAGTTATTAAAGAGGGGGCCGAAGTCACAGT	1284	Db
110156		110215	Qy
1283	TGGAGAAAAGAGTCTAGCAAACGATCCTAGGGATTTTAAATCTACAATCCC	, 1233	Qy
110216		) 110275	Db
1232 110276	AATTGAATATCAACGGAGATCCTAAAAATAAAGAGTACACAGGGACCATACTCTTTTC	1175 110335	DP GA
117 <b>4</b>	CTCTATAGAATTTTATGATCCTATTACTTCTGAAGCAGATGGGTCTACCC	, 1125	Qy
110336		) 110395	Db
1124 110396	GAATGGCATCCATCTTTACAAAATGCTAAATTCCTGAAATTACAGGCGAGAAATGGATG	1065	QQ Qy
1064	AGAGAAAGGAACAATTACATTCCAAGGAAACCGGACGAGCTTACCGTTTTT	7 1014	Db
110456		5 110515	dd
1013	GCAAAATTTAGGTGGAGCTATTGCCATTGATACTGGAGGGGAGATCAGTTTATCAGC	957	Db
110516		957	Qy
956	ACTTAGCATCTCTTCAGGAGGTCCTACTCTATTATCAATAATATATCATATGCAAATTC	, 897	do
110576		5 110635	Vo
896	ACAGTTAGTCTTTGAAAGAAACCATTCCATAATGGGTGGG	7 837	Qy
110636		5 110695	Qy
836 110696	TIGICITCCCACITCAGGAAGTAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAATAA	777	Db Qy
776	TGTTCTATTTCGAGAAAATGAGGCATTGACTACTGCTATAGGTAAGGGAGGG	717	do
110738		5 110797	Vo

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RESULT
AAA30847
01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
                                                                         This sequence encodes a Chlamydia antigen of the invention, designated CPN100634. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosting Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The infections. Chlamydia is a pathogen implicated in the development of the for example. Comparis a pathogen implicated in the development of the foreventing the accuracy accuracy is a pathogen implicated in the development.
                             (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding preventing, diagnosing pneumonia, bronchitis,
                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 1; 174pp; English.
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P-PSDB; AAY90236.
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/product= Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                          polypeptide antigens from Chlamydia useful for and treating diseases such as community acquires sinusitis and asthmatic bronchitis, adult-onset
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Query Match
Best Local Similarity
Matches 1292; Conserv

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Mismatches 1389;

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11;

8.3%; 46.5%;

Score 252.6; DB Pred. No. 7.8e-62

DB 21;

2950 96;

Sequence 2950 BP; 851 A; 670 C;

596 G;

833 T; 0 other;

1202	TACTTCTGAAGCAGATGGGTCTACCCAATTGAATATCAACGGAGATCCTAAAAA	1149	Qy
1233	cgggaaattcacggaattacgggctgctaaaaatcatacaattttcttctatgatcccat	1174	DЬ
1148	TGCTAAATTCCTGAAATTACAGGCGAGAAATGGATGCTCTATAGAATTTTATGATCCTAT	1089	Qy
1173	ccttacaaccaggaagtaccgatactcctaaacgtaatgcgatcaacataggaagtaa	1114	Đ
1088	CCGGACGAGCTTACCGTTTTTGAATGGCATCCATCTTTTACAAAA	1044	Qy
1043	TACTGGAGGGAGATCAGTTTATCAGCAGAAAGGAACAATTACATTCCAAGGAAA [	1054	Db Qy
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986	TAGGTGGAGCTATTGCCATTGA	927	Q
996	accagoggtggcgccatccatgctaaaaagctagccctttcctctggaggctttacaga	937	ф
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806	TATAGGTAAGGGAGGGCTGTCTGTTGTTCTCCCACTTCAGGAAGTAGTACTCC	747	Qy
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686		627	Qy
626 723	AGCCACTTTTGGAGGTGCTATCCATTCTTCAGGTCCCCTACAGATTGCAGTAAATCAGGC	567 664	Фр
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509	AAACAATTATGTAGTGCGTTTTGAACAAAACCAAAGTAAGACTAAAGGCGGAGCTATTAG	450	Qy
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449	CIT	390	QV
483	THECCAMEATCCTCAMECACGECACGETTTTCTGGTTCTCCAGCTCTCTTTTATTCA	424	ρ 2 <b>γ</b>
423		364	ф
329	TCATGGGTTATATTTAATAATATTTCCTCAGGAACTACAAAGGAAGG	270	γo
363		304	망
269	CATTAAATAAAGCCTGCTTCAATGTGACCTCAGGAAGTGTGACGTTCGCAGGAAATCA	210	Qy
303	tcagccacaacatattctctaacaggagatgtcttcttttacgagcctggaaaaggcac	244	₽.
209	CAAGCTGGGGATGTCTATAGCCTTACTGGTGATGTCTCAATATCTAACGTCGATAACTC	150	Qy
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2249 II	Ωу 2:
251 gagattaggaagagcaaagttttctgaatcagctatagaaaaattccctagggaaatt	Db 2:
2130 TGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAGAAGGTTTCTTCAAAATCC 2189	Оу 21
2070 AATGTATTTAGGATCGTATCTCTATCAATATACAACCTCCCTAGGGAATATTTTCCGTTA 2129	Qy 20 Db 21
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2071 ctctggaggctacgtcatcggtggaagtgctcacactcctaaagacgacctatttacctt 2130	
950 CAGCGGTGGATATGTTCTATCTGTAAATAATGAGATCACACCTAAGCACTATACTTC	Qy 19
1890 YOGAATTICTICCATOTATCTICCTCCAACAATAAAAAAAAAA	Db 20
951 gcaacagcttgtagagatcggcgcaactggtatggaacacaaaacaaaggtttctgggtttc 2	
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770 AAAAGAAGGAAATTTAGTTCCTAATATCTTGTGGGGGAATGCTGTAAATGTCAGATCCTT 1	_
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1662AAGTCCCCATTATGGTTTTCAAGGCAAATTGGAAATTAGCTTGGACAGG 1709	Qy 1
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614 TGGAGCCGGGGTAGTGTGACTGTAACTGCTGGAGATTTCCTACCG	0у 16
651 catttatgaaagtcatatgttcagccatgaccagctcttctctctattaaaaatcacggt	
1554 TGCCTATGAAGATCTCAGAATGAGAAATTCACAGACGTTCCCTCTGCTCTCTTTAGAGCC 1613	0у 15
1494 CACCGCAAATAAACAGATATCCGTGACGGACTCTATAGAACTTATCTCGCCTACTGGCAA 1553 	Qy 14 Db 15
cctaggaatcaatgitgactccttaggtcttaagcagcccgtcagcctaacagcaaaagg 15	Db 15
1434 CCTCGCGATAGATATAGATAGCTTAAGCTCATCCTCAACAGCAGCTGTTATTAAAGCAAA 1493	0y 14
1474 cctcggcatggattcaggaacgacattatcaactacagctgggagtattacaatcaacgaa 1533	
ttagattaggaaccaaactgatagcctctaaggaagacattgccat	Qy 13
1314 AGTTATTAAAGAGGGGGCCGAAGTCACAGTTTCAAAATTCACGCAGTCTCCAGGATCGCA 1373	Qy 13
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Matches 1292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding these proteins
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                                                                                                                                                      GAGCCCCGGAGATATTAAAGAACAGGGATGTCTCTATTCAAAAAATGCACTTATGCTCTT
                                                  aaatattcgtaaacttgtagttgctgggaatttttctactgcagatggtggagctatcaa
                                                                           AAACAATTATGTAGTGCGTTTTGAACAAAACCAAAGTAAGACTAAAGGCGGAGCTATTAG
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CC 16	TGCCTATGAAGAI	S	ογ
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CAAATAAACAGATATCCGTGACGGACTCTATAGAACTTATCTCGCCTACTGGCAA 1553	CACCGCAAATAA	1494	Ωy
cctaggaatcaatgttgactccttaggtcttaagcagcccgtcagcctaacagcaaaagg 1697	cctaggaatcaat	1638	В
GATAGATATAGATAGCTTAAGCTCATCCTCAACAGCAGCTGTTATTAAAGCAAA 1493	CCTCGCGATAGA	1434	Qy
r		1578	В
taggaaccaaactgatagcctctaaggaagacattg	TTTAGTTTTAGAS	1374	Qy
attgctacaaaagggagtcactttagagagcacgagcttctctcaagaggccggttctct 1577	attgctacaaaa	1518	Дb
TAAAGAGGGGGCCGAAGTCACAGTTTCAAAATTCACGCAGTCTCCAGGATCGCA 1373	AGTTATTAAAGAG	1314	Qy
stgacaatttaaaatottcattcacgcagccagtctccctatccggaggaaagtt 1517	ac	1458	DЬ
ATTTTAAATCTACAATCCCTCAGAACGTCAACCTGTCTGCAGGATACT	1	1263	Qy
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nattcacggaattacgggctgctaaaaatcatacaattttcttctatgatcccat 1337	cgggaaattcac	1278	밁
TTACAGGCGAGAAATGGATGCTCTATAGAATTTTATGATCCT	TGCTAAATTCCTC	1089	Qy
caaccg	ccttacaacaac	1218	밁
CCGGACGAGCTTACCGTTTTTGAATGGCATCCATCTTTTACAA	!	1044	Qy
aggagagc	tgcctcaggagag	1158	밁
AGGGAGATCAGTTTATCAGCAGAGAAAAGGAACAATTACATT	- <u>.</u>	987	γQ
ctacgaaataatgtctcatcagcaactcctaaggggggtgctatcagcatcga 1157	gtttctacgaaat	1101	망
CAATAATATATCATATGCAAATTCGCAAAATTTAGGTGGAGCTATTGCCATTGA 986	- 1-3	927	Qy
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TIGGCGGAGCCATTTATGCTAGGAAACTTAGCATCTCTTCAGGAGGTCCTACTCT 926	AATGGGTGGCGG	867	Qy
atctcctgaactgataatctctaacaataagactctgatctttgcttcaaacgtagcaga 1040	atctcctgaactg	981	밁
TATTGTGACTTTCTCTGACAATAAACAGTTAGTCTTTGAAAGAAA	AGTTCCTATTGTC	807	γQ
	tactg	945	밁
TATAGGTAAGGGAGGGGCTGTCTGTTGTCTTCCCACTTCAGGAAGTAGTACTCC 806	TACTGCTATAGG	747	Qy
ggcacgtcgatactatcgaacaacaaatttctatattttgaagggaatgcagcgaaaac 944	aggcacgtcgata	885	р
TC	TGGTGATATTGA	687	Qy
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CTTTAACGACTATACTGAGCTCTTATGTCGAGGAAGTATAGAATGCCGCCCCCATGCTAG 2729	aattcgcggtggcaatctttcaagacaggcatttttactgaggggtagcaacaactacgt 2891	TGTTCCGGCAGCACGTATCAAGACATGCTTTTGTAGGGAGTGGAACGGGTCGGTATCA 2669	tgtctatcgtaacaatccccaatctacagcgactcttgtgatgagcccagactcttggaa 2831	TATTTTCCGTAAGGATCCCTCATGTGAAGCTGCTCTGGTGATTAGCGGAGACTCCTGGCT 2609	cgtgcagggggatatcggagattcctacacctatgatctctcaggattctttgtttccga 2771	TGAGAAGCTGGCACTTTCTCAGGATGTACTCTATGACTTTAGTTTCTCCTATATTTCCTGA 2549	tggccgtggttttagtattggaaggctgcttaacctctcgattcctgtgggtgcgaaatt 2711	TGGCCGTAGATTTAGTAATGGGAGTTTAACATCGATTTCTGTACCTCTAGGCATACGCTT 2489	acagatgaaagtcgaaatggtttatgtatcacaaaatagcttcttcgaaagctctagtga 2651	ATTTATGAAACTACAATTAGTTTATGCTTATCAGGGAGATTTCAAAGAGACGACTGCAGA 2429	cggcctagaccttccttttgttctttccaacccacatcctctttcaagaccttcattcc 2591	CGGAGGGAGCATGCCTCTATTGGTATTTGAGAACGGAAGACTTTTCCAAGGTGCCATCCC 2369	agaatccgaaggttcttggag	CTACGCAAATTTCCCTATGGTGAAAAACAGCTGGAGAAACAATTGTTGGGCTATAGAGTG 2309	tcagacaaccgtatgg	TCTTATGATTTTTCATTTTTTGTGTGCTTATGGTCATGCCACCAATGATATGAAAACAGA 2249	gagattaggaagagcaaagttttctgaatcagctatagaaaaattccctagggaaattcc 2414	TGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAGAAGGTTTCTTCAAAATCC 2189	aacctacggtggaactttattcttcaagcactctcataccctacaaccccaaaactattt 2354	AATGTATTTAGGATCGTATCTATCAATATACAACCTCCCTAGGGAATATTTTCCGTTA 2129	tycyttctyccatctcttttyctagagacaaagattyttttatcyctoacaacaactctag 2294	GGCATTTTCCCAACTCTTTAGTAGAGACAAGGACTATGCGGTTTCCAACAACGAATACAG 2069	ctctggaggctacgtcatcggtggaagtgctcacactcctaaagacgacctatttacctt 2234	TCTATCTG	ctccatgacgaacttcctgcataagactggagatgaaaatcgcaaaggcttccgtcatac 2174	CCATGTATCTGCCTCCGAAGACAATATAAGGTA		STTCAAGAGACCCATGCATCGAGCTTACAGACAGATCGAGGGCTG	aagaaaatctgcgttagtatgcaataccctatggggagtctttactgacattcgctctct 2054	AAAAGAAGGAAATTTAGTTCCTAATATCTTGTGGGGGAATGCTGTAAATGTCAGATCCTT 1829	tacaaatacaaaagaggccacggcaacttggaccaaaacaggatttgttcccagccccga 1994	AACTGGAAACAAAGTTGGAAGAATTCTTCTGGGATAAAATAAAATTATAAGCCTAGACCTGA 1769	tectaatteagaataeggatteeaaggaeaatggaatgttaattggaetaeggataeage 1934	AAGTCCCCATTATGGTTTTCAAGGCAATTGGAAATTAGCTTGGACAGG 1709	tgatgctgatgttgatactaacgttgacatcagcagccttatccctgttcctgctgagga 1874	TGGAGCCGGGGTAGTGTGACTGTAACTGCTGGAGATTTCCTACCGGT 1661

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                    The present sequence encodes the Chlamydia pneumoniae 98 kDa outer membrane protein, known as CPM100640. Chlamydia pneumoniae is a common cause of community acquired pneumonia and upper respiratory tract symptoms and diseases, including bronchitis and sinusitis. It also has an association with atherosclerosis and asthmathe 98 kDa outer membrane protein is a C. pneumoniae-specific antigen which can confer immune protection against chlamydial infection. The nucleotide sequence encoding the protein or the protein itself may be administered as a vaccine to perfection. The gene encoding CPN100640 was amplified from Chlamydia pneumoniae genomic DNA by PCR.
                                                                                                                                                                                                                                                                                                                      01-DEC-1998;
03-MAY-1999;
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                                CACAGACGTTCCCTCTGCT---CTCTTTAGAGCCTGGAGCCGGGGGTAGTGTGACTGTAA 1639
                                                                 gaacgattgcgcttattgacacggaagggtcattctatgagaatcataacttaaaaagtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia
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Nucleic acids encoding preventing, diagnosing pneumonia, bronchitis, polypeptide antigens from Chlamydia useful for and treating diseases such as community acquired sinusitis and asthmatic bronchitis, adult-onset

Claim 2 Page 140-141; 174pp; English

C: This sequence encodes a Chlamydia antigen of the invention, designated CC CPN100634. The nucleic acids (and their complementary sequences) may be CC used as diagnostic agents for detecting the presence of nucleic acids CC encoding Chlamydia antigens in samples according to standard methods. CC and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction CC (PCR) assays. Antisense sequences may be used to down regulate CC expression of the proteins and may be used to treat infections. The CC uncleic acids may also be used to produce the protein antigens they CC encode according to standard recombinant DNA methodologies. The CC (i.e. as vaccines) for preventing infection by Chlamydia. The CC (i.e. as vaccines) for preventing infection by Chlamydia. The CC (infections. Chlamydia is a pathogen implicated in the development of CC (for example) community acquired pneumonia, upper respiratory tract CC disease (especially bronchitis and sinusitis, asthmatic bronchitis,

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcriptional termination region; (4) a cell comprising an expression cassette of (3) as part of an extrachromosomal element or integrated into the genome of a host cell as a result of induction of the expression cassette into the host cell, and the cellular progeny of the host cell; (5) a method for producing a Pl comprising growing a cell of (4) where the protein is expressed and isolating the protein free of other proteins; (6) a purified polypeptide composition comprising at least 50 weight % of Pl; and (7) a monoclonal antibody binding specifically to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used for diagnostic purposes, for their enzymatic or structural activity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizing fragment of NI; (2) an isolated nucleic acid (N2) that hybridizes under stringent conditions to NI; (3) an expression cassette comprising NI under the transcriptional regulation of a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional in an expression host, and a transcriptional initiation region functional initiation region func
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                                                      r membrane protein 5; surface exposed protein; antigen;
diagnosis; vaccine; atherosclerosis; asthma; ss.
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Location/Qualifiers
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the other, and encode polypeptides of about 89.5-100.3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for 0mp4-0mp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) eroding Omp4-Omp15 proteins (see AAX08417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This DNA sequence codes for the novel 97.2 kDa surface exposed protein Omp5 (see AAW88418) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. Phamoniae outer membrane complex, a polyclonal antibody (PAB 150)
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CHRISTIANSEN G.
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Sequence 2815 BP; 790 A; 575 C; 626 G; 824 T; 0 other;

Query Match Best Local Similarity Matches 1021 787 ACTTCAGGAAGTAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAATAAACAGTTAGTC 846 AATTTAGGTGGAGCTATTGCCATTGATACTGGAGGGGGAGATCAGTTTATCAGCAGAGAAA 1020 GGAACAATTACATTCCAAGGAAACCGGACGAGCTTACCGTTTTTG---ggtaatggtggagccatttctatactggcagctggagagtgtagtctttcagcagaagca gcttccggggggggggggggtatctccttttctaacaatatagtccaaggtaccactgca TCTTCAGGAGGTCC-----TACTCTATTTATCAATAATATATCATATGCAAATTCGCAA ttctcaggaaaccaagctgtagctaatggcggagccatttatgctaagaagcttacactg TTTGAAAGAAACCATTCCATAATGGGTGGCGGAGCCATTTATGCTAGGAAACTTAGCATC 906 aatggaggagctctttctggagatgccgatgttaccatatctgggaatcagagtgtaact 834 997; = = = = Conservative 48.78; 0; Score 231.6; DB 20; Pred. No. 7.7e-56; Mismatches 959; Indels Length 90; 2815 Gaps 1014 1065 954 960 894 10;

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                                                  seq length: 0 seq length: 2000000000
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Sequence 21,
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US-08-724-394A-20/c
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ALIGNMENTS	US-09-064-033-16	US-08-454-196-16	US-09-074-912-1	US-08-416-603-1	US-08-723-585-1	US-08-818-070-1	US-08-232-463-14	US-09-266-417-18	US-09-265-315-18	US-09-265-315-18	US-08-714-918-18	US-09-266-417-40	US-09-265-315-40	US-09-265-315-40	US-08-714-918-40	US-08-968-685A-9	US-08-478-370-1
		Patent No. 5495001	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 40, Appl	Sequence 40, Appl	Sequence 40, Appl	Sequence 40, Appl		Sequence 1, Appli

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FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..246240

OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
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                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-CCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-00010
                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SCETTULUS: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                                             MOLECULE TYPE:
                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: not r
                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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Query Match Best Local

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Score 39.8; Pred. No. 1

DB 2;

Length 246240;

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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54152 AGAGTTTTATGATACATTTTGTACTGTATATGTGGATGTTTTCTATTTCATTTAAAAAAT 54093
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITILE OF INVENTION: Megabase Transcript Map: No. 58 ITILE OF INVENTION: Sequences and Antibodies Thereto UMBER OF SEQUENCES: 31
                 NAME/KEY: misc_feature LOCATION: 1..246240 OTHER INFORMATION: /no
                                                                                                                  STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 01-OCT CLASSIFICATION: 536
                                                                                                                                                             TYPE: nucleic acid
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Tsuchihashi, Zenta
Wolff, Roger K.
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Ruddy, David A.
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                                                                                                                                            not relevant
                   /note= "HLA-H.CONTIG"
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; Sequence 22, Application US/08724394A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                   TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1311 CTTAGTTATTAAAGA 1325
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                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 01-OCT-199
CLASSIFICATION: 536
                                                                   FEATURE:
                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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724-394A-22
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              LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                        NAME: Fitts, Renee A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                     TOPOLOGY:
                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
                                               NAME/KEY: misc_feature
                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAATATTGTAGTATTTTTTTATCTCCCTGCCTAAAGGCAATAAACATCTAATCAGCAGA 53973
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                                                                                                                                   nucleic acid
                                                                                                                                                    246240 base pairs
                                                                                                                                                                                                      415-576-0300
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                                                                                             SS: not relevant not relevant
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Ruddy, David A.
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SYSTEM: PC-DOS/MS-DOS
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Sequences and Antibodies Thereto
31
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Pred. No. 1
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                      PILING DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
PILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
APPLICATION DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36,
Patent No. !
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                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
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MEDIUM TYPE: Floppy disk
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           FILING DATE: 6-NOV-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                            USA
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VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: DNA SEQUENCES AND USES THEREOF
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Stinson, Jeffrey R.
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Montoya, Alice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuhaus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harms, Christian
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                                                                                                                                                                                                                                                                                                                                                                        CIBA-GEIGY Corporation
MBER: US 07/678,378
1-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scott J.
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Pred. No. 1
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US-08-181-271A-36
                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                          10168 ACTCCATAACATCACTCCTCCATAGTTGGAATAAGCTTTAATGGTTGGAAGAACTTCAGA 10109
                                                                                                             10228
                                                                                                                                                                                                       1992 TAAGCACTATACTTCGATGGCATTTTCCCCAACTCTTTAGTAGAGACAAGGACTATGCGGT 2051
                2172
                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 07/768,122
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APPLICATION NUMBER: US (
FILING DATE: 6-MAR-1992
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APPLICATION NUMBER:
EILING PARTY
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 12124 base pairs TYPE: nucleic acid
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? AA 2173
||
                                                                            AGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAG 2171
                                                                                                             TCCCTTCAGCTGATATATGCTGTCTTTAATGGCATCGCTGTAGCCATTGTCAAACGCCTT
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                                                                                                                                                                                                                                      Conservative
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6-APR-1993
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Pred. No. 2.
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                                                                                                                                                                                                                                                                    DB 1; Length 12124;
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                                                                                                                                                                                                                                      0;
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                                                                                                             10169
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RESULT 5 US-08-449-315-36/c

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10108 AA 10107

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Sequence 36, Application US/08449315 Patent No. 5650505
                                                                                                                                  APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-193
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
APPLICATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
08/181,271
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APPLICANT
                                                                                PRIOR APPLICATION DATA:
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FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-JUL-
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                                  PRIOR APPLICATION DATA:
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IITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
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                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CLDA CERTON OF THE STREET: 7 Skyline Drive
                                                   APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08 FILING DATE: 13-JAN-94
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/093,301 FILING DATE: 16-JUL-1993
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Stinson, Jeffrey R.
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Meins, Jr., Frederick
Montoya, Alice
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JMBER: US 07/848,506
6-MAR-1992
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                                                                                                                       US 07/632,441
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APPLICANT: APPLICANT

APPLICANT APPLICANT

Moyer, Mary B.

Meins, Jr., Frederick Montoya, Alice

Harms, Christian

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                                                                                                                           Patent No.
                                                                                                                                             Sequence 36,
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Best Local Similarity
Matches 01: Conserv
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                                                                                                             GENERAL INFORMATION:
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               APPLICANT:
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LENGTH: 12124 base pai
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
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                                                                                                                                                                                                                                                                                           ACTCCATAACATCACTCCTCCATAGTTGGAATAAGCTTTAATGGTTGGAAGAACTTCAGA 10109
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                                                                                                                                             Application US/08444803
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Duesing
Friedrich, Lesing
-Aman, Robert M.
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                                             Beck, James J.
Duesing, John H
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                                                                          Alexander, Danny C.
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Pred. No. 2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
OR /181.271
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN'1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
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EILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
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FILING DATE: 1-APR-19
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                               RIOR APPLICATION DATA:
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TTORNEY/AGENT INFORMATION:
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STATE: New York
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                          APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993
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Stinson, Jeffrey R.
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Payne, George
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21-DEC-1990
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1-APR-1991
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Best Local Similarity
Matches 91; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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ORIGINAL SOURCE:
COMPUTER READABLE FORM:
                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                      TITLE OF INVENTION:
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                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                               APPLICANT:
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                        STATE: N
COUNTRY:
                                     CITY: Hawthorne
STATE: New York
                                                   TELEPHONE:
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                         USA
                                                                                                                                              Williams,
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                                                                                                                                                              Ward, Eric
                                                                                                                                                                                     Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                               Beck, James J.
Duesing, John H.
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Moyer, Mary B.
                                                                                                                                                                                                                                                                                                  Friedrich, Leslie B.
Goodman, Robert M.
                                                                                                                                                                                                                                                           Harms, Christian
Meins, Jr., Fred
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                        Alexander, Danny C.
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                                                                             CIBA-GEIGY Corporation
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                                                                                                                                                                           Scott J.
                                                                                                                   s, Shericca C.
CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                Jean-Marc
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Pred. No. 2
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Floppy disk

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US-08-449-043-36
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                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
TYPE: nucleic acid
                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US C
FILING DATE: 6-MAR-1992
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE: 8-MAR-1
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FILING DATE: 16-JUL-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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                                                                                                                                                                                                                                                                                                                                        TTORNEY/AGENT INFORMATION:
                                              INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                      NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 24-MA
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FILING DATE: 20-OCT 1989
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                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 12-AP
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                  pBScucchricht5
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                                                                   Cucumis sativus
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                                                                                                        DNA (genomic)
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20-JUN-1989
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8-MAR-1988
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1-APR-1991
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21-DEC-1990
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24-MAR-1989
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6-APR-1993
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EM: PC-DOS/MS-DOS
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Best Local Similarity 50.0
Matches 91; Conservative
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                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
PRIOR DATE: 6-NOV-1992
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APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CITY: Tarrytown
CTATE: New York
TTCA
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APPLICATION NUMBER: U
FILING DATE: 13-JAN-1
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                                                                                                                          FILING DATE: 6-FEB-1 PRIOR APPLICATION DATA:
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                                                                                        FILING DATE:
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                                                                                                         APPLICATION NUMBER:
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                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stinson, Jeffrey R.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC VENTION: DNA SEQUENCES AND USES THEREOF EQUENCES: 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIBA-GEIGY Corporation
                                                                                        8-MAR-1988
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US 07/632,441
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                                                     US 08/042,847
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Pred. No. 2.
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PRIOR APPLICATION DATA:

21-DEC-1990

US 07/425,504

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Query Match
Best Local Similarity
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                                                                                                                      RESULT
                                                               Sequence 36, Application US/08455416 Patent No. 5777200
                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 27-SEP-1991
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0: FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: |
ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDENNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
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                                                                                                                                                                                                                                       ACTCCATAACATCACTCCTCCATAGTTGGAATAAGCTTTAATGGTTGGAAGAACTTCAGA 10109
                                                                                                                                                                                                                                                                     AGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAG 2171
                                                                                                                                                                                                      2173
Ryals, John A.
Alexander, Danny C.
Beck, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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APPLICATION NUMBER: US
FILING DATE: 6 -APR-139
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DAME: 03
                                                            APPLICATION NUMBER: US FILING DATE: 7-SEP-1990 PRIOR APPLICATION DATA:
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PRIOR APPLICATION UNMBER: US 07/768,122
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APPLICATION NUMBER:
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FILING DATE: 20-OCT 1989
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APPLICATION NUMBER:

20-JUN-1989

US 07/329,018

US 07/368,672

FILING DATE:

27-SEP-1991

US 07/580,431

APPLICATION NUMBER: US FILING DATE: 6-MAR-1992

US 07/848,506

FILING DATE: 21-DEC-1990

US 07/632,441

FILING DATE:

8-MAR-1988

US 07/165,667

UMBER: US 08/042,847 6-APR-1993

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APPLICATION NUMBER: 08/1
FILING DATE: 13-DAN-94
APPLICATION NUMBER: US (
FILING DATE: 16-UU-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
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                                                                 APPLICATION NUMBER: US FILING DATE: 6-NOV-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                     CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams, Shericca C.
WILLIAMS, SHERICALLY REGULATABLE AND ANTI-PATHOGENIC VENTION: DNA SEQUENCES AND USES THEREOF EQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uknes, Scott
Ward, Eric R.
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Stinson, Jeffrey R.
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Friedrich, Les
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Payne, George B.
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Moyer, Mary B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIBA-GEIGY Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert M.
                                                                                                                                                      US 08/093,301
                                                                                                      US 07/937,197
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Best Local Similarity
Watches 91; Conserv.
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Patent No. 5789214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1992 TAAGCACTATACTTCGATGGCATTTTCCCAACTCTTTAGTAGAGACAAGGACTATGCGGT 2051
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
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                                                           APPLICANT:
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UMBER OF SEQUENCES:
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                        PPLICANT
                                                                                                                        PPLICANT:
                                                                                                                                                                    PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Cucumis sativus INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 12124 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAG 2171
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                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           Application US/08455244
                           Williams, Shericca C.
VENTION: CHEMICALLY REGULATABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                         Ward, Eric R.
                                                                        Uknes, Scott J.
                                                                                     Sperison, Christoph
Stinson, Jeffrey R.
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(919)541-8689
                                                                                                                                     Neuhaus,
                                                                                                                                                       moyer,
                                                                                                                                                                    Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                 Goodman,
                                                                                                                   Payne, George B.
                                                                                                                                                                                                                                 Friedrich,
                                                                                                                                                                                                                                                                           Alexander, Danny C.
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                                                                                                                                                    Mary B.
                                                                                                                                                                                               Christian
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                                                                                                                                     Jean-Marc
                                                                                                                                                                                                               Robert M.
106
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Pred. No. 2
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TELEFAX: (919)5
INFORMATION FOR SEQ
                                                                                                                                      REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                     SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 07/678,378
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                                                                                                                                                                                         NAME: Elmer, James Scott REGISTRATION NUMBER: 36,129
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CITY: Hawthorne
STATE: New York
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                                  STRANDEDNESS:
                                               TYPE: nucleic acid
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                     linear
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6-APR-1993
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7-SEP-1990
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21-DEC-1990
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DNA (genomic)
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                                                                                                           ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                  US 08/045,957
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Best Local Similarity
Matches 91; Conserv
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APPLICANT:
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INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
IMMEDIATE SOURCE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: 13-JAN-94
                                                                                                                                                      ZIP: 10532
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                  APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                  CURRENT APPLICATION DATA:
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CITY: H
                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                      APPLICATION NUMBER: US/0 FILING DATE: 31-MAY-1995
                                          CLASSIFICATION:
                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
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Stinson, Jeffrey R.
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Friedrich,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meins, Jr., Frederick
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                                                                                                                                                                                                                                            CIBA-GEIGY Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Christian
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                                                                                                                                                                                                                                                                                                                                                Scott J.
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                                                                   US/08/454,876
            08/181,271
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Pred. No. 2
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                                                                                                Version #1.25
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US-08-454-876-36
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                                                                                                              Query Match
Best Local Similarity
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                                        1992 TAAGCACTATACTTCGATGGCATTTTTCCCAACTCTTTAGTAGAGACAAGGACTATGCGGT 2051
                                                                                                                                                                                                                                               TOPOLOGY: line MOLECULE TYPE: I ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                           NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (912)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 07/425,504
APPLICATION NUMBER: EILING TOTAL
                                                                                                                                                                                                    INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
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PRIOR APPLICATION DATA:

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24-MAR-1989
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21-DEC-1990
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6-APR-1993
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                                                                                                              Score 36.4;
Pred. No. 2.
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RESULT 12
US-08-457-364-36/c
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                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
APPLICATION NUMBER: US 07/937,197
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                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
APPLICATION DATE: 6-FEB-1989
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                               FILING DATE: 8-MAR-1988 PRIOR APPLICATION DATA:
                                                                                                                                                FILING DATE: 6-NOV-1992
PRIOR APPLICATION UMBER: US 07/678,378
FILING DATE: 1-APR-1991
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                                                                               PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 31 CLASSIFICATION:
                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Ward, Eric R.
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Neuhaus, uc...
George B.
                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
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Montoya, Alice
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31-маү-1995
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Christoph
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                                                                US 07/165,667
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                                    US-08-456-262-36/c
                                                   RESULT
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US-08-457-364-36
 Sequence 36, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pair
                                                                                                        10108 AA 10107
                                                                                                                                                                                10168 ACTCCATAACATCACTCCTCCATAGTTGGAATAAGCTTTAATGGTTGGAAGAACTTCAGA 10109
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                                                                                                                                                                                                                                                                                    2052 TTCCAACAACGAATACAGAATGTATTTAGGATCGTATCTCTATCAATATACAACCTCCCT 2111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/768,122
PRITING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                 AGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAG 2171
                                                                                                                                                                                                                                                     TCCCTTCAGCTGATATATGCTGTCTTTAATGGCATCGCTGTAGCCATTGTCAAACGCCTT 10169
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6, Application US/08456262
5851766
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6-MAR-1992
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Pred. No. 2.4;
0; Mismatches 91
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GENERAL INFORMATION:

APPLICANT:

Ryals, John A. Alexander, Danny C.

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/181,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                 PRIOR APPLICATION DATA:
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                                                                                     FILING DATE: 27-SEP-PRIOR APPLICATION DATA:
                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                           APPLICATION NUMBER: 1
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FILING DATE: 16-UU-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
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                                                  APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/165,667 FILING DATE: .8-MAR-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/456,262 FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    APPLICATION NUMBER: US 07/768,122 FILING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 6-FEB-1989
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              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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Friedrich, Les...
Aman, Robert M.
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Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
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Stinson, Jeffrey R.
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Payne, George B.
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                                                                                                                                                                                                                                                                  21-DEC-1990
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MBER: US 07/368,672
20-JUN-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.25
                                                                                                                                                                             US 07/848,506
                                                                                                                                                                                                                                                                                   US 07/632,441
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   10108 AA 10107
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/329,018 FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
                                                   TITLE OF INVENTION:
                                                                                                                                                     APPLICANT
                                                                                                                                                                                                APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ropology: linear
                                                                                                                                                                                                                                                                                                                                             5, Application US/08456240 5856154
Uknes, Scoll ...
Ward, Eric R.
Williams, Shericca C.
Williams, Shericca C.
IVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC INTERVION: DNA SEQUENCES AND USES THEREOF
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                                                                                                                       Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                            Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                      Friedrich, Leslie
                                                                                                                                                                                                                                                                                     Beck, James J.
                                                                                                                                                    Payne, George B.
                                                                                                                                                                                                                                                                       Duesing,
                                                                                                                                                                                                                                                                                               Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                Ryals,
                                                                                                                                                                                                             Meins, Jr.,
                                                                                                                                                                                                                          Harms, Christian
                                                                                                                                                                                                                                          Goodman,
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                                                                                                                                                                   Neuhaus,
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                                                                                                                                                                                                                                                                                                              John A.
                                                                                                                                                                                                                                          Robert M.
                                                                                                                                                                                                 Alice
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Pred. No. 2.
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CORRESPONDENCE ADDRESS:

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TELEFAX: (919)541-868
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                       REFERENCE/DOCKET NUMBER: S-
PELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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PRIOR APPLICATION DATA:
OR APPLICATION UNMBER: US 07/768,122
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
O8/181,271
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APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                        NAME: Elmer, James Scott
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                                                                                                                                                                                                                                                                                   NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 8-MAR
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                                     LENGTH:
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                                 12124 base pairs
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                                                                                                                                             (919)541-8689
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20-OCT 1989
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6-APR-1993
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US-08-456-240-36
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GENERAL I
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Best Local Similarity
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                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ADDITIONATION WINDERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1992 TAAGCACTATACTTCGATGGCATTTTCCCAACTCTTTAGTAGAGACAAGGACTATGCGGT 2051
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ORIGINAL SOURCE:
                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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             RIOR APPLICATION DATA:
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CITY: Hawthorne
STATE: New York
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                             CLASSIFICATION:
                                            FILING DATE:
                                                       APPLICATION NUMBER:
                                                                                                                                                                                                      ADDRESSEE: Clar Carrie Carrett: 7 Skyline Drive
APPLICATION NUMBER:
                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAG 2171
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                                                                                                                                                             10532
                                                                                                                                                                                       New York
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                                                                                                                                                                                                                                                                                                          Williams,
                                                                                                                                                                                                                                                                                                                       Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                   Sperison, Christo
Stinson, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friedrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beck, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alexander, Danny
                                                                                                                                                                                                                                                                                                                                                                                               Neuhaus,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Montoya,
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                                         31-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                 George B.
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CHEMICALLY REGULATED DNA SEQUENCES !
                                                                                                                                                                                                                                                                                                                                        Scott J.
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Teffrey R.
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08/181,271
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Pred. No. 2.4;
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US-08-455-736-36
                                                                                                                             Query Match 1.2%; Score 36.4; D
Best Local Similarity 50.0%; Pred. No. 2.4;
Matches 91; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION UNUMBER: US 08/045,957
EILING DATE: 12-APR-1993
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FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/632,441
FILING DATE: 21-DEC-1990
                                           TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
                                                                                    1992 TAAGCACTATACTTCGATGGCATTTTCCCAACTCTTTAGTAGAGACAAGGACTATGCGGT 2051
ATTORNEY/AGENT INFORMATION:
NAME: Elmer James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (219)541-8614
                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122

APPLICATION DATE: 27-SEP-1991

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-JAN-1994
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
APPLICATION NUMBER: US 07/937,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         ORGANISM: Cucumis sativus INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 6-MAR
                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: li
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6-MAR-1992
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     2112 AGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAG 2171
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10168 ACTCCATAACATCACTCCTCCATAGTTGGAATAAGCTTTAATGGTTGGAAGAACTTCAGA 10109

Qy 2172 AA 2173

10108 AA 10107

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Search completed: October Job time: 51284 sec 2, 2001, 03:44:51

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em\_esthum22:\*

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SOURCE
ORGANISM
                                                                                                                 RESULT
AQ491698
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                               REFERENCE
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                                                                    KEYWORDS
        TITLE
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RPCI-11-271D18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-271D18
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                      Zhao, S., Adams, M.D.,
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae.

1 (bases 1 to 583)
                                                     Homo sapiens
                                                              numan
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                     Nierman, W., Malek, J., de Jong, P. and Venter
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BG291039
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CNS00EPP
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                                      Hominidae;
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AG015509 Homo sapi
AL104267 Drosophil
AI691324 606014C11
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                                                                                                                                                                                                                                                                                                                                          AL078013 Drosophil
AZ529136 ENTCQ50TF
AZ52771 ENTBE37TF
AL069797 Drosophil
AL096927 Drosophil
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AZ551519 ENTEL71TF
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AQ768358 HS_3162_A
AQ793076 HS_5305_A
AL059220 Drosophil
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BG533254
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AL106628
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BF209257 60187293
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AL070493 Drosophil
C40411 C40411 Yuji
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BG291039 602386841
AQ934962 CpG2343A
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AQ113852 CIT-HSP-2
T86457 yd81b10.r1
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AL279351 Tetraodon
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AZ203489 SP_0087_A
BF290068 EST454659
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                                             Euteleostomi;
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JOURNAL COMMENT
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CNS00EPP/c
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Best Local S
Matches 75
                                                                                                                                                                                                           AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGCAATTGGAAATTAGCTTGGACAGGAACTGGAAACAAAGTTGGAGAATTCTTCTGGGA 1742
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDG The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                           fly), genomic survey s
AL069494
AL069494.1 GI:4949637
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNS00EPP 1080 bp DNA GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29N07 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: SP6

Class: BAC ends.
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Tel: 301 838 0200
Fax: 301 838 0208
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Contact: Shaying Zhao, William Nies
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1080)
                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                             Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                      fruit fly.
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/note="Vector: pBACe3.6; Site_
/note="Vector: pBACe3.6; Site_
RPCI11 Human Male BAC Library"
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/clone="RPCI-11-271D18"
/clone_lib="RPCI-11"
/sex="Male"
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/db_xref="GDB:7603769"
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57.7%;
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l (μασες
Elgar,G.,
    Tetraodontidae; Tak
1 (bases 1 to 619)
Elgar, G., Clark, M.,
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                   GSS; genome survey sequence Takifugu rubripes. Takifugu rubripes
                                                                                                                                                                                                  GSS;
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/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone_lib="apcr-98"
/clone="BACR29N07"
/note="end : TET3"
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                                                                                                          Contact: Cameron, RA, Davidson, EH, H
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
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                                                                                                                                                                                                                                                                   additional resources Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                            Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. a
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V_type: phagemid
                                                                                        Plate: 87 row: F
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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AZ203489.1
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Class: BAC ends
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/clone="192G22bG11"
168 c 112 g 149
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/db_xref="taxon:31033"
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                                                                                                                                                                                                                                                                                                                                                           Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockvil
Tel: (301)-838-3529
Fax: (301)-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Other_ESTs: EST352405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pe Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST454659 Rat Gene Index, normalized Rattus norvegicus cDNA clone RGIHN37
                                                                                                                                                                                                                                                                                                              Email: nhlee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF290068.1
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                                                                                 /note="Vector: pT3T7Pac; Site_1: Combination of ROV, RBR, RKI, RLI, RHE, RPC, RPN"

a 85 c 89 g 180 t
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/db_xref="taxon:7668"
/db_xref="hate-87 Col=12 Row=E"
/clone_"plate-87 Col=12 Row=E"
/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                      norvegicus cDNA"
                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIHN37"
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                                                                                                                                                      /tissue_type="mixed tissue"
/lab_host="DH5-alpha"
                                                                             RHE,
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ATGGTAAATAACTGTGAATACCAATCTAAGTCTGTTAATGCATACAAGGTTAGTGTTCAA 317
                                                          ACTTTCCAATGAATCAGTAGAGAACACAGAGCAAAAGCTTTAAGGTATATGAATTTTTGT
                                                                                    CGTTTTGAACAAAACCAAAGTAAGACTAAAGGCGGAGCTATTAGTGGGGGCGAATGTTACT 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI408352 593 bp mRNA
EST236642 Normalized rat ovar:
ROVES15 3' end, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: nhlee@tigr.org
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/note="Organ: ovary; Vector: pT7T3Pac;
Site_2: NotI"
96 c 93 g 191 t
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/db_xref="taxon:10118"
/clone="ROVES15"
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Rodentia;
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                                                                                                                                                                                                                                                                                      556 TATCAGAATGCAGCCACTTTTGGAGGTGCTATCCATTCTTCAGGTCCCCTACAGATTGCA 615
                                                                                                                                                                                                                                                                                                                                                                                 496 GGCGGAGCTATTAGTGGGGCGAATGTTACTATAGTAGGCAACTACGATTCCGTCTCTTTC 555
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                                                                                                                                                                                                                                            WWWWWATWDTWWDKWWWWATAAKTDTAWTWWRTAWRADWAGRDRGAGKRDRDAATDADG
ADDDDGAGDKDDDGKGKDADDDTDGTKDDDDKDKWDDWDKAKGTWGDATWAWAATDWWWW
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                                                                                             TTGTACTCCGATGGTGATATTGATATTGATCAGAATGCTTATGTTCTATTTCGAGAAAAT
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Drosophila melanogaster genome survey sequence TET3 end of BACRO8K10 of RPCI-98 library from Drosophila melanogaster (frigit) genomic survey
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/note="end : TET3"
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/db_xref="taxon:7227"
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14.8%; Pred. No.
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                                                                                                                                                                                                             Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by Partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                          TGGAAAGAAAATGAAATCCATATCCATGAAGCTCAATGGTCTGTTATAGGATAAATTCAA
                                                                                                                    GGCAACTACGATTCCGTCTCTTTCTATCAGAATGCAGCCACTTTTGGAGGTGCTATCCAT 591
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                                                                                                                                                                                  GAAAGAAACAGAAGGGACAGAAAACATTCAGGAAATAATGGCCAGAAAATTTCCTAAGTC 491
                                                                                                                                                                                                                                                                                                             107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 654)
2 (bases 1 to 654)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Thomosome 2nd to be a controlled to the controlled to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masahira Hattori, Kitasato University, Department of Science, Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori6hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
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Homo sapiens genomic DNA,
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Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros B
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
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AI691324.1
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                                                       mRNA sequence.
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Contact: Walbot V
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855 California Ave, Palo Alto,
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human.
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606014 row: C column:
Location/Qualifiers
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/lab_host="XLOLR (Stratagene)
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/cultivar="Ohio43"
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/clone_lib="606 - Ear tissue
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                                                                                                                                                       fruit fly.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brosophila.

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencas
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence T7 end of IBACR22B23 of RPCI-98 library from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey AL056333
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, M
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Tissue Procurement: DCTD/DTP
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//db_xref="taxon:9606"
//clone="IMAGE:4520466"
//clone_lib="NIH_MGC_91"
//tissue_type="adenocarcinoma, cell line"
//tissue_type="ad
                                                                                                                                                                                                                                                                                                                                                                                                        GI:4937102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     753 TTTGMACHCACGCGCKTTTTTTTTGTGATCCCTCYMTDCKCTTTTTTRRSCTTTCMMVSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATATTAAAGAACAGGGATGTCTCTATTCAAAAAATGCACTTATGCTCTTAAACAATTAT 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic Strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ768358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ768358 545 bp DNA GSS 28-JUL-1999
HS_3162_A1_G10_T7C CIT Approved Human Genomic Sperm Library D
Sapiens genomic clone Plate=3162 Col=19 Row=M, DNA sequence.
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                                                                                         University of Washington
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1 (bases 1 to 545)
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                                                                                                                                                   Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
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Queen Anne Avenue North, Sea
: (206) 616-3618
: (206) 616-3887
il: jwallace@u.washington.edu
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                                                                                                                                                                                                 Natl. Acad. Sci. U. S. A.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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/note="end : T7"
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Pred. No. 6.3;
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                                                                                                                                                                       401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ793076 563 bp DNA GSS 03-AUG-1999 HS_5305_A2_A05_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=881 Col=10 Row=A, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76;
                                                           http://www.htsc.washington.edu
Plate: 881 row: A column: 10
                                                                                     library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                             High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                       scanning the human genome Proc. Natl. Acad. Sci. U. S. A.
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High quality sequence stop: 563
                      Class: BAC ends
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: sperm; Vector: pBeloBAC11; BAC
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55.9%;
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column: 19
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ORIGIN
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                                                                                                                                        2761 CGTTTTTAGAAGGTTTCCATTGCCTGTGTGTGTCCGGATCTTAACTATAAAT 2812
                                                                                                                                                                                                    source
                                                                                                              372 AATTTTTGTAAACTCGCCATTGGCTTTTTGTTTTTGGCTCTTCACTTTAAAT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

173 a 104 c 102 g 176 t 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=881 Col=10 Row=A"
/clone_1ib="RPCI-11 Human Male BAC Library"
/sex="male"
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                   2, 2001, 03:06:34
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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1: /SIDSL/gcgdata,
2: /SIDSL/gcgdata,
3: /SIDSL/gcgdata,
4: /SIDSL/gcgdata,
5: /SIDSL/gcgdata,
6: /SIDSL/gcgdata,
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4814
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Gapop 10.0 , Gapext 0.5
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573.050 Million cell updates/sec
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Pred. No. score grea and is der greater t s derived is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score 4814	Query Match Length DB	Length 922	DB 	ID  AAW88419	Description Chlamydia
1	4814	100.0	922	20	AAW88419	
N	4789	99.5	922	21	AAY95548	
ω	4769	99.1	922	20	AAY34597	
4	2099	43.6	400	20	AAW88430	
5	1467.5	30.5	918	21	AAY69369	
o	1444	30.0	928	21	AAY90239	
7	1442.5	30.0	918	20	AAW88422	
8	1442	30.0	928	20	AAW88423	
9	1434	29.8	930	20	AAY35052	
10	1430.5	29.7	928	21	AAY94327	
11	1426	29.6	200	21	2200240	

Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for

44 611 45 609.5	43 686	42 716.5			7		868	æ	931	941	G							11			13	_	ىر	13	13	13	13		1400	1405	14	1423	
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20	20	20	21	20	21	20	20	20	20	20	20	20	21	21	20	21	20	21	20	21	21	21	20	20	20	21	20	21	21	20	20	20	
AAY35162 AAY34609	AAW88431	AAY35064	AAB13638	AAY34617	AAB13632	AAY35048	AAY34614	AAY34611	AAY16738	AAY35050	AAY16737	AAY16735	AAB13633	AAB13639	AAW88420	AAY92818	AAY35056	AAY96274	AAW88428	AAY69368	AAY90238	AAY90236	AAW88417	AAY35060	AAW88429	AAY90237	AAW88418	AAY99842	AAY99843	AAY35054	AAW88424	AAW88421	
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## ALIGNMENTS

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AAW88419
ID AAW8
XX AAW8
XX AAW8
XX Chla
XX Omp6
KW Omp6
KW Infe
XX Omp6
XX Omp6
XX Omp6
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XX Omp6
XX Omp
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N-PSDB; AAX06818.
                                                                                                                                                                                                                                                   Birkelund S, Christiansen G, Mygind P;
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infection; diagnosis; vaccine; atherosclerosis; asthma.
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                                                                                                                                                                                                                                                                                                                                                                               (BIRK/) BIRKELUND S.
(CHRI/) CHRISTIANSEN G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This polypeptide comprises the novel 100.3 kDa surface exposed protein Omp6 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAX06818) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
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                                                                                                                   MRFSLCGFPLVFSLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAGDVYSLTG
                    WGNAVNVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNN
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28 - DEC - 1998
The present sequence is that of Chlamydia pneumoniae antigenic protein CPNIO0877 RY-61, a putative 98 kba outer membrane protein. It is an example of C. pneumoniae antigenic polypeptides of the invention (see AAY95543-55) that are encoded by open reading frame:
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Query Match
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\tt dvsisnvdnsalnkacfxvtsgsvtfagnhhgxyfnnissgttkegavlccqdpqatarf
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97FR-0014673
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Pred. No. 0;
1; Mismatches
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                    Chlamydia pneumoniae
                                        Omp6; outer membrane
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                                                                                AAW88430
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                                                    pneumoniae
                                 diagnosis;
                                                                 (first entry)
                                                                                            Protein;
                                protein 6; surface exposed protein;
; vaccine; atherosclerosis; asthma.
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 398
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Mygind P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encod these proteins
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                      KNSWRNNCWAIECGGSMPLLVFENGRLFQGAIPFMKLQLV 797
                                             HLVLDLGTKLIASKEDIAITGLAIDIDSLSSSSTAAVIKANTANKQISVTDSIELISPTG 517
                                                                                                          VSASEDNIRYRHNSGGYVLSVNNEITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYL
                                                                                                                                                                                                      NAYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKVGE 577
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                                                                                              vsasedniryrhnsggyvlsvnneitpkhytsmafsqlfsrdkdyavsnneyrmylgsyl
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CHRISTIANSEN
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pred. No. 4.2e-157;
2; Mismatches 0;
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20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY69362-69 represent Chlamydia pneumoniae polypeptides. The polypeptides are present in the bacterial membrane structure, in the external vicinity of the membrane structure, in the inclusion membrane structure, in the external vicinity of the inclusion membrane structure, and in the cytoplasm of the infected cell. The polypeptides may be used to prevent, treat and detect the presence of Chlamydia infection and/or the presence of Chlamydia in a sample. The polypeptides may also be used to induce an immune response in a mammal. Antibodies directed against the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia nay also be used therapeutically to treat and/or prevent a Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevent, mammals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 19; Fig 15-E; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antigens and corresponding DNA molecules that can be used to prevent, treat and diagnose disease caused by Chlamydia infection
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27-AUG-1998;
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FSGFSTLSFIQSP-----GDIK-EQGCLYSKNALMLLNNYVVRFEQNQSKTKGGAISGAN
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                                                                                  dvsisqagkqtslttscfsntagnltflgngfslhfdniisstv-agvvvsntaasgitk
                                                                                                                                      DVSISNV-DNSALNKACFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATAR
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This polypeptide comprises the novel 98.4 kDa surface exposed protein omp10 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAX06822) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid sequences encoding them (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encoded to the content of the conte
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Mygind P;
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Pred. No. 9.7e-105;
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Best Local Similarity
Matches 344; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX31990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otilis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae
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21-NOV-1997;
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nlsfiaapgttvasgkstlssagalnltdngtilfsgnvsneannnggaitaktlsisgn
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                                                                                                                                                                                       NV-DNSALNKACFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATARFSGFS 124
                                                                                                                                                                                                                                                   {\tt llisstlvtpillsiatygadaslsptdsfdgaggstftpkstadangtnyvlsgnvyin}
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                                                                                                                                                                                                                                                                                                                                                                                   29.8%; Score 1434; DB 20; 36.6%; Pred. No. 4.2e-104; tive 157; Mismatches 395;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae 98kD putative outer membrane protein.
                                   29-OCT-1999;
                                                                                              11-MAY-2000.
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                                                                                                                                                                                                                                                                              infection; outer membrane protein.
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The present sequence is the 98kDa putative outer membrane protein from Chlamydia pneumoniae. The genomic sequence was amplified using two PCR primers. The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence close to the 5' end of the 98kDa putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BarGl restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame C-terminal fusion with the Histidine tag. The PCR product was cloned into a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with NotI and BamHl and performing a ligation reaction. This expression vector was injected intramuscularly and intranasally into mice, which were subsequently inoculated with Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice were lower than those of the controls. Thus the 98kDa putative outer membrane protein can be used as a vaccine to provide protection against Chlamydia infections, especially Chlamydia pneumoniae infections.
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01-MAR-1999;
27-OCT-1999;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6;
                                          Chlamydia infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Chlamydia 98 kDa putative outer membrane protein antigen, for vaccination and protection against Chlamydia infection
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Query Match 29.7%; Score 1430.5; DB 21; Length 928;
Best Local Similarity 36.7%; Pred. No. 7.8e-104;
Matches 349; Conservative 157; Mismatches 382; Indels 63; Gaps 26;
Matches 349; Conservative 157; Mismatches 382; Indels 63; Gaps 26;

Ş 밁 Q 밁 β 밁 Q 문 γ 밁 δÃ 밁 δÃ В Š 405 181 123 293 GAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFQGN--RT 64 nipgtgtaitkscfnntkgdltftgngnsllfqtvdagtvagaavnssvvdkstt-figf 122 տ 8 FPLVFSLTLLSVFDTSLSATTISLTPEDSFHGDSQN--AERSYNVQAGDVYSLTGDVSIS ttmsalfsentsskkggaiqtsdaltitgnqgevsfsdntssd-sgaaifteasvtisnn TGTILFSGEK---SLANDPRDFKSTIPQNVNLSAGYLVIKEGAEVTVSKFTQSPGSHLVL ttpgtnrssidlgtsakmtalrsaagraiyfydpittgssttvtdvlkvnetpadsalqy SLPFLN--GIHLLQNAKFLKLQARNGCSIEFYDPIT--SEADGSTQLNINGDPKNK--EY akvsfidnkvtgasssttgdmsggaicayktstdtk----vtltgnqmllfsnntsttag AYVLFRENE-----ALITAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIMGG NYDSVSFYQNAAT-FGGAIHSSGPLQIAVNQAEIRFAQNTAKNGSGGALYSDGDIDIDQN gaiyvkklelasggltlfsrnsvnggtapkggaiaiedsgelslsadsgdivflgntvts sslsfiaspgssittgkgavsc--stgslsltknvsllfsknfstdnggaitaktlsltg STLSFIQSPGDIKEQG-----CLYSKNALMLLNNYVVRFEQNQSKTKGGAISGANVTIVG NV--DNSALNKACENVTSGSVTEAGNHHGLYENNISSGTTKBGAVLCCQDPQATARESGE 123 fp-kfvfstfaifpls miatetvlds sasfdgnkngnfsvresqedagttylfkgnvtle461 415 404 355 295 237 180 178 63 65 239

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RESULT 11
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01-DEC-1998;
01-DEC-1998;
Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquiry pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onse
                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia antigen; diagnosis; infection; community acquired pneumonia; therapy; upper respiratory tract disease; bronchitis; sinusitis; asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthm
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                             invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAW88411-28), and nucleic acid sequences encoding them (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                               protein Omp8 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAXO6820) isolated from a C. pneumoniae expression library. T
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N-PSDB; AAX06820.
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                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide comprises the novel 97.6 kDa surface exposed protein Ompl1 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see CC AAX/06823) isolated from a C. pneumoniae expression library. The cinvention provides 12 novel surface exposed proteins, Omp4-Omp15 (2 (see AAW/06823)), and nucleic acid sequences encoding them (see CC AAX/06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for CC pneumoniae. The test comprises detecting antibodies specific for CC pneumoniae. The test comprises detecting antibodies specific for CC membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of CC mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The control of the control
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 63-65; 115pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-1998;
21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                    TAR----FSGFSTLSFIQSPGDIKEQGCLYSKNALMLLNNYVVRFEQNQSKTKGGAISGA 172
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                             GD--PKNKEYTGTILFSGEK---SLANDPRDFKSTIPQNVNLSAGYLVIKEGAEVTVSKF
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                                                                                                                                                  GGAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFQGN---
                                                                                                                                                                                                                                                                        NVTIVGNYDSVSFYQNAAT-FGGAIHSSGPLQIAVNQAEIRFAQNTAKNGSGGALYSDGD
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35.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia pneumoniae
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03-MAY-1999;
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The present sequence is the mature, processed form of CPN100640, t 98 kba outer membrane protein from Chlamydia pneumoniae. Chlamydia

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Claim 16;

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Query Match
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US-08-469-880-2
US-08-728-470-2
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Sequence 21, Appl	Sequence 11, Appl	Sequence 2, Appli	Sequence 5, Appli	Sequence 17, Appl	Sequence 10, Appl	Sequence 3, Appli	Sequence 3, Appli	15,	Sequence 9, Appli	Sequence 15, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 33, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 7, Appli

ALIGNMENTS

## Sequence 9, application US/08728470 Patent No. 5928651 GENERAL INFORMATION: TELECOMMUNICATION. INFORMATION: TELEPHONE: (703) 415-081.0 TELEPAX: (703) 415-081.3 INFORMATION FOR SEQ ID NO: 9: APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9205704.1 ZIP: 2207-0286 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION: NAME: Berkstresser, Jerry V REGISTRATION NUMBER: 22,651 REFERENCE/DOCKET NUMBER: 11 CORRESPONDENCE ADDRESS: TITLE OF INVENTION: High MO. SEQUENCE CHARACTERISTICS: CLASSIFICATION: 424 PRIOR APPLICATION DATA: LENGTH: 1338 amino TYPE: amino acid STRANDEDNESS: sino TOPOLOGY: linear NUMBER OF SEQUENCES: STREET: 2001 Jeff STREET: Bldg. 1 CITY: Arlington STATE: Virginia APPLICATION NUMBER: FILING DATE: COUNTRY: U.S.A 1338 amino acids Shoemaker and Mattare, Ltd. 2001 Jefferson Davis Hwy., 1203 Crystal Plaza Barenkamp, UMBER: GB 9205704.1 16-MAR-1992 single 10 Stephen J igh Wolecular Weight Surface Proteins of No. 5928651-Typeable Haemophilus US/08/728,470 1038-633

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                                                Sequence 9, Application US/08719641
Patent No. 6218141
GENERAL INFORMATION:
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Best Local S
Matches 173
                                                                                                                                                                           1120
                     TITLE OF INVENTION:
                                     APPLICANT:
                                                                                                                                                                                                                                             1060 INGTNSVTTSSQSGDIEGTISGNTVNVTASTGDLTIGNSAKVEAKNGAATLTAESGKLTT 1119
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mes 173; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDIDSLSSSSTAAVIKANTANKQISYTDSIELISPTG---NAYEDLRMRNSQTFPLLSL 536
                                                                                                                                                                         QTGSSITSSNGQTTLTAKDSSIAGN 1144
                                                                                                                                                                                                           KHYTSMAFS--QLFSRDKDYAVSNN 687
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Barenkamp, Stephen J
VENTION: High Molecular Weight Surface Proteins
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; STRANDEDNESS: si:
; TOPOLOGY: linear
US-08-719-641-9
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/302,832

FILING DATE: 16-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US PCT/US93/0

PRIOR APPLICATION NUMBER: US PCT/US93/0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CORRESPONDENCE ADDRESS:
                                                   648
                 287
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STREET: 2001 Je
STREET: Bldg. 1
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1338 amino acids
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SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/719,641
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                                                                                                                                                     240 V-----LFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNK-QLVFERN 286
                                                                                                                                                                                                                                                                                                              185 FYQNA-ATFGGAIHSSGPLQIAVNQAEIRFAQNTAKNG----SGGALYSDGDIDIDQNAY 239
                                                                                                                                                                                                                                                                                                                                                                                                 535 SIENDLNLNATGGNITIRQVEGTDSRVNKGVAAKKNITFKGGNITFGSQKATTEIKGNVT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 STGPSIRNAELNGITFNKATFNIAQGSTANFSIKASIMPFKSNANYALFNEDISVSGG-- 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 KEGAVLCCQDPQATARESGESTLSFIQSPG-------DIKEQGCLYSKNAL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 TLNISGTVDISMKAPKVSW-----FYRDK---GRTYWNVTTLNVTSGSKFNLSIDSTGSG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 SLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSY------NVQAGDVYSLTGD-----
HSIMGGGAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFQ 346
                                                                                                                                                                                                                                        INKNTNATLRGA-----NFAENKSPLNIAGNVINNGNLTTAGSIINIAGNLTVSKGAN
                                                                          LQAITNYTENVAGSEDNNGASNISIARGGAK--FKDINNTSSLNITTNSDTTYRTIIKGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GSVNFKLNASSSNIQTPGVIIKSQNFNVSGGSTLNLKAEGS--TETAF 534
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.0%; Score 192.5; DB 4;
20.0%; Pred. No. 1.8e-07;
ative 125; Mismatches 278;
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42;

APPLICATION NUMBER: US/08/617,697 FILING DATE: 01-APR-1996 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/302,832 FILING DATE: 05-OCT-1994 PRIOR APPLICATION NUMBER: US PCT/US93/02166 APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 ATTORNEY/AGENT INFORMATION: NAME: Berkstresser, Jerry W REGISTRATION NUMBER: 22,651 REFERENCE/DOCKET NUMBER: 1038-557 TELECOMMUNICATION INFORMATION:	POM S: Of	Qy 480 AIDIDSLSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDLRMRNSQTFPLLSL 536  : ::       :: ::     :     ::     :	Db 706 IS
Oy 537 EPGAGGSVTVTA-GDFLPVSPHYGFQGNWKLAWTGTGNKVGEF 578		Qy 13 SITLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAGDVYSLTGD	TELEPHONE: (703) 415-0810 TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 1599 amino acids TYPE: amino acids TRANDEDNESS: single TOPOLOGY: linear US-08-617-697-9  Query Match Best Local Similarity 20.0%; Pred. No. 2.4e-07; Matches 173; Conservative 125; Mismatches 278; Indels 289; Gaps

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FAGNHHGLYFN---NISSGTT 103
                           TTLNVTSGSKFNLSIDSTGSG 690
                                                                      DB 2; Length 1599;
-07;
278; Indels 289; Gaps
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42;

В

1380 QTGSSITSSNGQTTLTAKDSSIAGN 1404

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Best Local Similarity
Matches 174; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,682
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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271 PIVTFSDNKQLVFERNHSIMGGGAIY-----ARKLSI----SGGPTLFINNISYANSQ- 320
                                                                  896 A-----GNLTVESNA-----NFKAITNFTFNVGG------
                                                                                                         212 RFAQNTAKNGSGGALYSDGDIDIDQNAYVLFRENEALTT-AIGKGGAVCCLPTSGSSTPV 270
                                                                                                                                                                                             156 RFEQNQSKTKGGAI--SGANVTIVG-NYDSVSFYQNAATF-GGAIHSSGPLQIAVNQAEI 211
                                                                                                                                                                                                                                       784 --TSGSTKTGFSI---EKDLTLNATGGNITLLQVEGTDGMIGKGIVAKKNITFEGGNITF 838
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                                                                                                                                                                                                                                                                             97 NISSGTTKEGAVLCCQDPQATARFSGFS-TLSFIQSPGDIKEQGCLYSKNALMLLNNYVV 155
                                                                                                                                                                                                                                                                                                                                                          54 -DVYSLTGDVSIS---NVDNSAL-------NKACFNVTSGSVTFAGNHHGLYFN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                   GSRKAVTEIEGNVTINNNANVTLIGSDFDN----HQKPLTIKKDVIINSGNLTAGGNIVNI
                                                                                                                                                                                                                                                                                                                         LNYASFNGNISVSGGGSVDFTLLASSSNVQTPGVVINSKYFNVSTGS-----SLRFK 783
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0%; score 192; DB 1; Length 1536; 20.7%; Pred. No. 2.5e-07; Live 119; Mismatches 276; Indels 27
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H D O O	Db 1326  RESULT US-08-302- Sequence Fatent of Patent of FITLL TITLL INUMBE CORRES ADD STITE STITE ADD STITE STITE ADD STITE ST	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
CITY: AILIN STATE: Virg COUNTRY: U ZIP: 22202- COMPUTER READA MEDIUM TYPE: COMPUTER: I OPERATING SY SOFTWARE: P CURRENT APPLICATION FILING DATE: CLASSIFICATICATI PRIOR APPLICATION FILING DATE: TELECOMMUNICAT TELECOMMUNICAT TELECOMMUNICAT	2	16 24 71 71 64 22 22 82	20 21 73 63 63 63 77 20
CITY: ATINGTON STATE: Virginia COUNTRY: U.S.A. ZIP: 22202-0286 COMPUTER READABLE FORM MEDIUM TYPE: Floppy COMPUTER: IBM PC CO. DERATING SYSTEM: PATENTIAN DATA APPLICATION NUMBER: FILLING DATE: 16-SEP CLASSIFICATION UNMBER: FILLING DATE: 16-MAR APPLICATION NUMBER: FILLING DATE: 11-MARE: FILLING DATE: 11-MARE: FILLING DATE: 11-MARE: FILLING DATE: 11-MARE: REPLICATION NUMBER: REPLICATION NUMBER: REPLICATION NUMBER: REGISTRATION NUM	KHITSMAFSULISA SAKGQVNLSA  32-2 32-2 32-2 33-2 INFORMATION: ANT: BATENKA ANT: BATENKA OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION: OF SOUTHOESE ESSEE: Shoem ESSEE: Shoem ESSEE: Shoem ESSEE: Shoem ESSEE: Shoem ESSEE: Shoem	NAGLTIDAKNVT RMRNSQTFPLLSILGILG WKLAWTGTGNKV : : ESVTTSSQSGDI AVNVRSLMQVQE I   :	LEDNKGNSNISINLGGAIAIDTGGEIS-
LINGTON LITGINA LITGIN LITGINA LITGINA LITGINA LITGINA LITGINA LITGINA LITGINA LITGINA	AFSULFSKUN GQVNLSAQDG GQVNLSAQDG Ilication U 938 BATION: BATION: H ENTION: H ENTION: O QUENCES: Shoemake OO1 Jeffer 1dg 1	AKNYTVNNNITS FPLLSLEPGAGG :   ILGGIESSSG TGNKVG QSGDIGGTISGG MQVQETHASSIO :      NAGDLT	-LEDNKGNSNIS
disk disk C-DOS/ C-DOS/ C-DOS/ C-DOS/ C-DOS/ C-DOS/ C-DOS/ C-DOS/ C-DOS/ TA: US/08 -1994 -1994 -1992 : US/08 -1993	ISMARSQUESKURLY ANNUT IN I I I I I I I I I I I I I I I I I I	VNNNITSHKAVSIS LEPGAGGSVTVTA- GIESSSGSVTLTAT G GGTISGGTVEVKAT GGTISGGTVEVKAT THASSLQTDRGLWI -NAGDLT	SIAKGGA SOKEGNL SOKEGNL SOKEGNL SOKEGNL SOKEGNL SOKEGNL SOKEGNL
#1.0 02,8 1038-4	A 6 8 1 1 - 1	NAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTINATTGNVEITAQTGS- RMRNSQTFPLLSLEPGAGGSVTVTA	LEDNKGNSNISIAKGGARFKDIDNSKNLSITTNSSSTNLGGAIAIDTGGEISLSAEKGTITFQ NITNEGSDTEMQIGGDVSQKEGNLTISSDKINITKQITIKAGVD NAKFLKLQARNGCSIEFYDPITSEADGSTQLNINGDPKNKEYT
, Version 32 1 1 /02166	Weight Typeabl Ltd.	ATSGEITTKTGTTINAGELPV  : :   : :   : :   : :   : :     : :   - :    VGNGAEINATEGAA	DIDNSKNLSITT  SERINITKQITI STQLNINGDPKN
<b>*1.</b> 30	I I I I I I I I I I I I I I I I I I I	GTTINATTGNV GDFLPYSPHYG [:: : :  GNTVTVTANSG PRPEK-EGNL- :  :  IKATTGEANVT ASEDNIRYRHN  ::   :  ATEGAATLTTS	TNSSSTY  IKAGVDG  IKAGVDG  NKEYT         -AEITAK  GSHLVLD
	TTGTLTTVKGSNI TTGTLTTVKGSNI	NVEITAO YG SGALTTL L E VTSATGT VTSATGT I-  I-  I-  I-  I-  I-  I-  I-  I-  I-	RTIISGN NRTSLPF ENSDSDA -GTILFS   :   DGSDLTI LGTKLIAN SIELISP
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	1372	·	972 362 103 419 107 107 477 477

TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1536 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-302-832-2
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                                                                                                                                                                                                                              WKLAWTGTGNKVG------EFFWDKINYKPRPEK-EGNL-----VPNILWGN 603
                                                                                                                                                                                                                                                                                                                                                                                                             GLAIDID------SLSSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRDFKSTIPQ--NVNLSAGYLVIKEGAEVTVSKFTQSPGSHLVLDLGTKLIASKEDIAIT 477
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----SAKGQVNLSAQDGSVAGSINAANVTL-----NTTGTLTTVKGSNINATSGTL 1372
                                           PKHYTSMAFSQLESRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGIL 722
                                                                                                                                   AVNVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNNEIT 663
                                                                                                                                                                                 ESVTTSSQSGDIGGTISGGTVEVKATESLTTQSNSKIKATTGEANVTSATGTIGGTISGN 1281
                                                                                                                                                                                                                                                                            -----ILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGSTIKGT 1221
                                                                                                                                                                                                                                                                                                                       RMRNSQTFPLLSLEPGAGGSVTVTA-----GDFLPVSPHYG-----FQGN 563
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                                                                                        -----VGNGAEINATEGAATLTTSSGKLTTEASSHIT 1325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.0%; Score 192; DB 2; I Best Local Similarity 20.7%; Pred. No. 2.5e-07; Matches 174; Conservative 119; Mismatches 276;
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APPLICANT: BARENKAMP, STEPHEN J

APPLICANT: ST. GEME III, JOSEPH W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: JWB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/530,198
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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                         321
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                                                                                                                                                                                                     212 RFAQNTAKNGSGGALYSDGDIDIDQNAYVLFRENEALTT-AIGKGGAVCCLPTSGSSTPV
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TYPE: amino acid
STRANDEDNESS: si
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---NLGGAIAIDTGGEIS------LSAEKGTITFQ------GNRTSLPFLNGIHLLQ 362
                                                                    ----LFDNKG----NSNISIAKGGARFKDIDNSKNLSITTNSSSTYRTIISGNITNKNGDL 972
                                                                                                                PIVTFSDNKQLVFERNHSIMGGGAIY-----ARKLSI----SSGGPTLFINNISYANSQ- 320
                                                                                                                                                           A------GNLTVESNA-----NFKAITNFTFNVGG------
                                                                                                                                                                                                                                                    GSRKAVTEIEGNVTINNNANVTLIGSDFDN---HQKPLTIKKDVIINSGNLTAGGNIVNI 895
                                                                                                                                                                                                                                                                                               RFEQNQSKTKGGAI--SGANVTIVG-NYDSVSFYQNAATF-GGAIHSSGPLQIAVNQAEI
                                                                                                                                                                                                                                                                                                                                           --TSGSTKTGFSI---EKDLTLNATGGNITLLQVEGTDGMIGKGIVAKKNITFEGGNITF 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1536 amino acids
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01 Jefferson Davis Hwy., 1203 Crystal Plaza
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39;

INFORMATION FOR SEQ ID NO:

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US-08-469-880-2

; Sequence 2, Application US/08469880

; Patent No. 5876733
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/469,880
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/469,880
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/469,800
FILING DATE: 16-MAR-1992
PRIOR APPLICATION NUMBER: US/08/469,800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1116 NAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTINATTGNVEITAQTGS----- 1170
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NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE,DOCKET NUMBER: 1038-516 MIS:vg
PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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STREET: Bldg. 1
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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RESULT 8
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LENGTH: 1536 amino acids
                                                                                          1326 ----SAKGQVNLSAQDGSVAGSINAANVTL-----NTTGTLTTVKGSNINATSGTL 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1072 TNAKKYTFNQYKDSKISA-----DGHKYTLHSKYETSGSN------NNTEDSSDN 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       784 --TSGSTKTGFSI---EKDLTLNATGGNITLLQVEGTDGMIGKGIVAKKNITFEGGNITF 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 RFEQNQSKTKGGAI--SGANVTIVG-NYDSVSFYQNAATF-GGAIHSSGPLQIAVNQAEI
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STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 -DVYSLTGDVSIS---NVDNSAL------NKACFNVTSGSVTFAGNHHGLYFN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 NISSGTTKEGAVLCCQDPQATARFSGFS-TLSFIQSPGDIKEQGCLYSKNALMLLNNYVV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 FSLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAG------
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                                                                                                                                                                                                                   AVNVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRVRHNSGGYVLSVNNEIT 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTINATTGNVEITAQTGS----- 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLAIDID-----SLSSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAKFLKLQARNGCSIEFYDPITSEADGSTQLNINGDPKNKEYT---GTILFSGEKSLAND 419
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                                                                                                                                  PKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGIL 722
                                                                                                                                                                                 TVNVTA-----NAGDLT---
                                                                                                                                                                                                                                                                       ESVTTSSQSGDIGGTISGGTVEVKATESLTTQSNSKIKATTGEANVTSATGTIGGTISGN 1281
                                                                                                                                                                                                                                                                                                                                                               -----ILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGSTIKGT 1221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFAQNTAKNGSGGALYSDGDIDIDQNAYVLFRENEALTT-AIGKGGAVCCLPTSGSSTPV 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TQDLNISGFNK-AEITAKDGSDLTIGNTNSADG
                                                                                                                                                                                 -----VGNGAEINATEGAATLTTSSGKLTTEASSHIT 1325
                                                                                                                                                                                                                                                                                                                    EFFWDKINYKPRPEK-EGNL-----VPNILWGN 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 4.0%; Score 192; DB 2; Length 1536; Best Local Similarity 20.7%; Pred. No. 2.5e-07; Matches 174; Conservative 119; Mismatches 276; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
COUNTRY: Virginia
COUNTRY: V.S.A.
ZIP: 2202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08728470 Patent No. 5928651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JETRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
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APPLICANT: Barenk
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
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                                                                                                                                                                                                                                                                                   732 LNYASFNGNISVSGGGSVDFTLLASSSNVQTPGVVINSKYENVSTGS------SLRFK 783
                                                                                                                                                                                                                                                                                                                                                                              676 FNLTI----DSRGSDSAGTLTQPYNLNGISFNKDTTFNVERNARVNFDIKAPIGINKYSS 731
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896 A-----GNLTVESNA-----NFKAITNFTFNVGG------
                                            212 RFAQNTAKNGSGGALYSDGDIDIDQNAYVLFRENEALTT-AIGKGGAVCCLPTSGSSTPV 270
                                                                                                                                    156 RFEQNQSKTKGGAI--SGANVTIVG-NYDSVSFYQNAATF-GGAIHSSGPLQIAVNQAEI 211
                                                                                                                                                                                                                                                                                                              54 -DVYSLTGDVSIS---NVDNSAL--------NKACFNVTSGSVTFAGNHHGLYFN 96
                                                                                                                                                                                                                                                                                                                                                                                                                     12 FSLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAG-------
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                                                                                                                                                                                                                                    97 NISSGTTKEGAVLCCQDPQATARFSGFS-TLSFIQSPGDIKEQGCLYSKNALMLLNNYVV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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                                                                                             GSRKAVTEIEGNVTINNNANVTLIGSDFDN---HQKPLTIKKDVIINSGNLTAGGNIVNI 895
                                                                                                                                                                                          --TSGSTKTGFSI---EKDLTLNATGGNITLLQVEGTDGMIGKGIVAKKNITFEGGNITF 838
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16-MAR-1992
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APPLICA FILING FILING CLASSII CLASSII CLASSII PRIOR APP APPLICA FILING FILING FILING FILING APTORNEY NAME: REGISTI	COMPUTE COMPUTE MEDIU COMPUTE COMPUTE COMPU COMPU COPERA SOFTW	CORR AD ST	Sequence Patent N GENERAL APPLI TITLE TITLE	RESULT	1326	1282	1222	524 1171 564	478 1116	420 1072	363 1033	321 973	271 920
APPLICATION NUMBER: US/08/617,697 FILING DATE: 01-APR-1996 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION UMBER: US 08/302,832 FILING DATE: 05-OCT-1994 PRIOR APPLICATION DATA: BAPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 ATTORNEY/AGENT INFORMATION: NAME: Berkstresser, Jerry W NAME: Berkstresser, Jerry W REGISTRATION NUMBER: 22,651	RY: UISIAL RY: U.S.A. 2202-0286 R READABLE FORM: M TYPE: Floppy TER: IBM PC con TING SYSTEM: PC ARE: PATENTIN DAT	SECUENCES: 11 SINCE ADDRESS: E: Shoemaker and Mattare 2001 Jefferson Davis Hwy Bldg. 1	2, Application U 2, Application U 5, 5977336 INFORMATION: DANT: Barenkamp, OF INVENTION: H OF INVENTION: C	9	PKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGIL 722SAKGQVNLSAQDGSVAGSINAANVTLNTTGTLTTVKGSNINATSGTL 1372	TVNVTANAGDLTVGNGAEINATEGAATLTTSSGKLTTEASSHIT 13	AVANVEST MOVOPTERA SET OTTOROT WITHOUT STANDARD WITHOUT SET OTTOROT WITHOUT SET OF THE SET OTTOROT WITHOUT SET OTTOR	RMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQGN 563 RMRNSQTFPLLSLEPGAGGSVTLTA	GLAIDIDSLSSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDL 523	PRDEKSTIPQNVNLSAGYLVIKEGAEVTVSKETQSPGSHLVLDLGTKLIASKEDIAIT 477	NAKFLKLQARNGCSIEFYDPITSEADGSTQLNINGDPKNKEYTGTILFSGEKSLAND 419	NLGGAIAIDTGGEISLSAEKGTITFQGNRTSLPFLNGIHLLQ 362	PIVTFSDNKQLVFERNHSIMGGGAIYARKLSISSGGPTLFINNISYANSQ- 320

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    1171
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                                         664 PKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGIL 722
                                                                                                                               604 AVNVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNNEIT 663
                                                                                                                                                                                                                      564 WKLAWTGTGNKVG------EFFWDKINYKPRPEK-EGNL-----VPNILWGN 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                    TVNVTA-----NAGDLT------VGNGAEINATEGAATLTTSSGKLTTEASSHIT 1325
                                                                                                                                                                                                                                                                                                                                                                               GLAIDID------SLSSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDL 523
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                                                                                                                                                                           ESVTTSSQSGDIGGTISGGTVEVKATESLTTQSNSKIKATTGEANVTSATGTIGGTISGN 1281
                                                                                                                                                                                                                                                                  -----ILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGSTIKGT 1221
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SAKGQVNLSAQDGSVAGSINAANVTL-----NTTGTLTTVKGSNINATSGTL 1372
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20.7%; Pred. No.
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US-08-719-641-2
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                                                                                                                                                                                                                                                                                                                                              Matches 174;
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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STREET: Bldg 1
CITY: Arlington
STATE: Virginia
839 GSRKAVTEIEGNVTINNNANVTLIGSDFDN---HQKPLTIKKDVIINSGNLTAGGNIVNI 895
                                                                                                                                                                                                                                                          676 FNLTI----DSRGSDSAGTLTQPYNLNGISFNKDTTFNVERNARVNFDIKAPIGINKYSS 731
                                                                                    784 --TSGSTKTGFSI---EKDLTLNATGGNITLLQVEGTDGMIGKGIVAKKNITFEGGNITF
                                                                                                                                                                      732 LNYASFNGNISVSGGGSVDFTLLASSSNVQTPGVVINSKYFNVSTGS------SLRFK 783
                                                                                                                                                                                                                54 -DVYSLTGDVSIS---NVDNSAL------NKACFNVTSGSVTFAGNHHGLYFN 96
                                                                                                                                                                                                                                                                                                  12 FSLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                      RFEQNQSKTKGGAI--SGANVTIVG-NYDSVSFYQNAATF-GGAIHSSGPLQIAVNQAEI 211
                                                                                                                            NISSGTTKEGAVLCCQDPQATARFSGFS-TLSFIQSPGDIKEQGCLYSKNALMLLNNYVV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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01 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 192; DB 4; 20.7%; Pred. No. 2.5e-07;
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US-08-728-470-10
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FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1326
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                            CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 RFAQNTAKNGSGGALYSDGDIDIDQNAYVLFRENEALTT-AIGKGGAVCCLPTSGSSTPV 270
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGIL 722
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           US PCT/US93/02166
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        1129
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PRIOR APPLICATION DATA:
APPLICATION UNBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                               1307 KLTTQTGSSITSSNGQTTLTAKDSSIAGNINAANVTLNTTGTLTTTGD---SKIN---- 1358
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590 EKEGNLVPNI----LWGNAVNVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNI 645
                                                                                                                                                                                                                                                                                                                                                                409 LFSGEKSLANDPRDFKSTIPQ---NVNLSAGYLVIK----EGAEVTVS----KFTQSPGS 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           894 NGNITNEKGDLNIKNIKADAEIQIGGNISQKEGNLTISSDKVNITNQITIKAGVEGGRSD 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
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REGISTRATION NUMBER: 22,651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTSLPFLNGIHLLQNAKFLKLQARNGCSIEFYDPITSEADGSTQLNINGDPKNKEYTGTI 408
                                                                                         ----AGGSVTVTAGDFLPVSPHYGFQGNWKLA----WTGTGNKVGEFFWDKINYKPRP
                                                                                                                                     VGSTINGTNSVTTSSQSGDIEGTISGNTVNVTASTGDLTIGNSAKVEAKNGAATLTAESG
                                                                                                                                                                                TISATTGNANITTKTGDINGKVESSSGSVTLVATGATLAVGNISGNTVTITADSGKLTST
                                                                                                                                                                                                                                                                         HLVLDLGTKLIASKE------DIAITGLAIDIDSLSSSSTAAVIKA----NT
                                                                                                                                                                                                                                                                                                                                                                                                             ITS------NAVINAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGLTISAKDVTVNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNGTI--KGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GGAIYARKLSISSGGPTLFINNISYA--NSQNLGGAIAIDTGGEISLSAEKGTITFQGN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS-----GALYSDGDIDID 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG-----DSVSFYQ----NAATFGGAIH 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCQDPQATARFSGFSTLSFIQSPGDIKEQGCLYSKNALMLLNNYVVRFEQNQSKTKGGAI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKANVTLQADTSNSNTGLKKRTLTLGNISVEGNLSLTGANANIVGNLSIAEDSTFKGE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1529 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.7%; Score 178.5; DB 2; 21.2%; Pred. No. 3.7e-06;
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-719-641-10
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US-08-719-641-10
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                                                                                                                                                                                                                                       Query Match 3.7%; Score 178.5; DB 4; Best Local Similarity 21.2%; Pred. No. 3.7e-06; Matches 170; Conservative 109; Mismatches 266;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08719641 Patent No. 6218141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAYFETCHOOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,641
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1406 TGDLNTINGLNIISENGRNT 1425
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LENGTH: 1529 amino aci
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CITY: Arlington
STATE: Virginia
                                                                                                                                                     724 DLTINATGSNFSLKQTKDSFYNEYSKHAINSSHNLTILGGNVTLGGENSSSSITGNINIT 783
784 NKANVTLQADTSNSNTGLKKRTLTLGNISVEGNLSLTGANANIVGNLSIAEDSTFKGE-- 841
                                                                                                        66 NVDNSALNKACFN-----VTSGSVTFAGN-----HHGLYFN-NISSGTTKEGAVL 109
                                                                                                                                                                                                 21 DTSLSATTISLT---PEDSFHGD----SQNAERSYNVQAGDV-----YSLTGDVSIS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1529 amino acids
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                                                                                                                       Indels 255; Gaps
                                                                                                                                                                                                                                                                                  Length 1529;
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170 SS
QAEIRFAQNTAKNGSGGALYSDGDIDID 235

CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.5
Best Local Similarity 22.4
Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
1390 VASVEEVIEAK-----RVLEKVKDLSDEERETLAKLG 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1147 EKVTTTAGSTINATNGKASITTKTGDISGTISGNTVSVSA-----TVDLTTKS- 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1014 KKGIDG---EDSSSDATSNANLTIKTKELKLTE-----DLSISGFNKAE--ITAKDG 1060
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LENGTH: 1477 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 TKGGAI----SGANVTIVGNYDSVSFYQNAATFGGAI-HSSGPLQIAVNQAEIRFAQNTA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              914 -- RDTLNITGNFTNNGTAEINITQGVVKLGNVTNDGDL-----NITTHAKRNQRS
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STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                 -NWKLAWTGT----GNKVGEFFWDKINYKPRPEKEGNLVPNT----LWG------N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVDNSALN-----KACFNVTSGSVTFAGNHHGLYFN-NISSGTTKEGAVL 109
                                           VLSVNNEITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLG
                                                                                          AVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDG-RNTVRLRGKEIEVKYIQPG---
                                                                                                                                                                                  ANVTLNTTGTLTTVAGSDI -------KATSGTLVINAKDAKLNGDASGDSTEVN
                                                                                                                                                                                                                                                                                                                          TDSIELISPTGNAYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQG---- 562
                                                                                                                                                                                                                                                                                                                                                                                                                       GSHLVLDLGTKLIASKEDIAITGLAIDIDSLSSSSTAAVIKANTAN------KQISV 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIGGDIINKKGSLNITDSNNDAEIQ-----IGGNISQKEGNLTISSDKINIT-KQITI 1013
                                                                                                                                      AVNVRSLMQVQETHASS-----LQTDRGLWI---DGIGNFFHVSASEDNIRYRHNSGGY 654
                                                                                                                                                                                                                                                                                 TEGAATLTATGN------TLTTEAGSSITSTKGQVDLLAQNGSIAGSINA 1286
                                                                                                                                                                                                                                                                                                                                                                           -----GSKIEAKSGEANVTSATGTIGGTISGNTVNV----TANAGDLTVGNGAEINA 1242
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US-08-302-832-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
1014 KKGIDG---EDSSSDATSNANLTIKTKELKLTE------DLSISGFNKAE--ITAKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810 TELEFAX: (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                         219 KNGSGGALYSDGDIDIDQNAYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDN 278
                                                                                             962 IIGGDIINKKGSLNITDSNNDAEIQ------IGGNISQKEGNLTISSDKINIT-KQITI 1013
                                                                                                                                     164 TKGGAI----SGANVTIVGNYDSVSFYQNAATFGGAI-HSSGPLQIAVNQAEIRFAQNTA 218
                                                                                                                                                                                      914 -- RDTLNITGNETNNGTAEINITQGVVKLGNVTNDGDL------NITTHAKRNQRS
                                                                                                                                                                                                                                   110 CCQDP-QATARESGESTLSE-----IQSPGDIKEQGCLYSKNALMLLNNYVVRFEQNQSK 163
                                                                                                                                                                                                                                                                                    855 KAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISESATFKGKT- 913
                                                                                                                                                                                                                                                                                                                                                                             795 DLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSSITGNITIE 854
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STRANDEDNESS: si
TOPOLOGY: linear
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
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REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US pct/us93/02166 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 Match 3.5%; Score 170.5; DB 1; Local Similarity 22.4%; Pred. No. 1.7e-05; les 170; Conservative 88; Mismatches 283;
                                                                                                                                                                                                                                                                                                                                                                                                                         21 DTSLSAT----TISLTPEDSFHGDSQNAERS-YNVQ--AGDV------YSLTGDVSIS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/302,832 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                NVDNSALN------KACFNVTSGSVTFAGNHHGLYFN-NISSGTTKEGAVL 109
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                                                                                                                                                                        COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,198
FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
PROPROFICE YOUTEN WINDED: TUR-1186
              TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1477 amino acids
                                                                                                          REFERENCE/DOCKET NUMBER: JWB-1186
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2001 Jef
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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amino acid
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101 Jefferson Davis Hwy., 1203 Crystal Plaza
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Best Local Similarity
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VASVEEVIEAK-----RVLEKVKDLSDEERETLAKLG
                                          VLSVNNEITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLG
                                                                                    AVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDG-RNTVRLRGKEIEVKYIQPG---
                                                                                                                            AVNVRSLMQVQETHASS-----LQTDRGLWI---DGIGNFFHVSASEDNIRYRHNSGGY 654
                                                                                                                                                                        ANVTLNTTGTLTTVAGSDI-----
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    1421
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Search completed: October 2, 2001, 03:27:36 Job time: 7218 sec

Title: Perfect score: OM protein - protein search, using sw model Scoring table: Sequence: Run on: US-09-446-677B-6 4814 1 MRFSLCGFPLVFSLTI BLOSUM62 Gapop 10.0 , Gapext 0.5 October 2, 2001, 03:28:49; Search time 76.79 Seconds (without alignments) 914.610 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. MRFSLCGFPLVFSLTLLSVF.....IECRPHARNYNINCGSKFRF 922

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

219241

219241 seqs, 76174552 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

25 27 28 29	13 14 16 17 18 19 20 20 22 23 24	1 2 3 3 5 4 4 7 7 1 1 1 1 1 1 1 1 1	Result
951.5 901 796.5 774.5	1393 1344 1344 1344 1344 1249 1137.5 1137.5 1137.5 1163.5 1063.5 1060 1060	4794 4794 4790 1441 1441 1434 1434 1434 1430 1400.5 1400.5 1400.5	Score
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## ALIGNMENTS

Qy 1 MRFSLCGFPLVFSLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAGDVYSLTG 6	Query Match 99.6%; Score 4794; DB 2; Length 922; Best Local Similarity 99.7%; Pred. No. 2e-281; Matches 919; Conservative 1; Mismatches 2; Indels 0; Gaps	RESULT 1 B72131 B72131 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C;Accession: B72131 R;Ralman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606 A;Accession: B72131 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-922 <arn> A;Cross-references: GB:AE001585; GB:AE001363; NID:g4376255; PIDN:AAD18163.1; PID:g437 A;Experimental source: strain CWL029 C;Genetics: A;Gene: pmp_1</arn>
G 60 G 60 F 120 F 120 F 120	Gaps 0;	e (strain CWL029 y-2000 , L.; Grimwood, s.

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polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae (str. C;Species: Chlamydophila pneumoniae, Chlamyddia pneumoniae (c;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: E86491
R;Shirai, M; Hirakawa, H; Kimoto, M; Tabuchi, M; Kishi, F; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MOID:20330349
A;Accession: E86491
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-922 <STO>
A;Cross-references: GB:BA000008; NID:g8978378; PIDN:BAA98215.1; GSPDB:GN00142
A;Experimental source: strain J138
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A; Cross-references: GB:AE002237; GB:AE002161; NID:g71896
A; Strains Source: Strain AR39, HL cells
A; Genetics: CP0770 RESULT 3
F81.539
c; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_c
C; Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_c
C; Accession: F81539
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelt
C; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolona 37; GB:AE002161; NID:g7189684; AR39, HL cells Heidelberg, J.F.; White
; Kolonay, J.; McClarty, #text\_change MoPn and Chlamydophila pneumoniae PIDN: AAF38570.1; Chlamydia 11-May-2000 White, pneumon1ae ှင် ( o :: PID: 9718 ; Hicke Salzbe

Query Match Best Local S

99.5%;

Score 4790; Pred. No. 3

DB 2; 3.5e-281;

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                                                                               YDFSFSYIPDIFRKDPSCEAALVISGDSWLVPAAHVSRHAFVGSGTGRYHFNDYTELLCR
                                                                                                                 NGRLFQGAIPFMKLQLVYAYQGDFKETTADGRRFSNGSLTSISVPLGIRFEKLALXQDVL
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 outer membrane
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protein G/I family [imported] -
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pneumoniae
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-1
C;Accession: E85346
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Oucl
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumonia
A;Reference number: A86491; MUID:20330349
A;Accession: E86346
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <STO>
A;Cross-references: GB:BA000008; NID:g8978819; PIDN:BAA98655.1; GSPI
A;Cross-references: GB:BA000008; NID:g8978819; PIDN:BAA98655.1; GSPI
A;Cenetics:
A;Gene: pmp_9
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                                                                                GLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNNEITPKHYTSMAFSQLFSRDKDYAVS
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KNRASAYAASLHLQHLATLSSPSLLRYLPGSES
                                                              GIWCEGISNFFHKDSTKINKGFRHISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFIN
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                                                                                                                                           -TGTGNKVGEFFWDKINYKPRPEKEGNLVPNILWGNAVNVRSLMQVQETHASSLQTDR
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EQP-VLFDAQISYIYS
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polymorphic membrane protein G family CP0306 [imported] - Chlamydophila pneumoniae (stra C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: B72077; B81592
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Accession: B72077
A;Molecule type: DNA
A;Residues: 1-928 <ARN>
A;Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:AAD18591.1; PID:g437673
A;Experimental source: strain CWLO29
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Accession: B81590; MUID:20150255
A;Molecule type: DNA
A;Reference number: A81500; MUID:20150255
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A; Gene:
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A;Residues: 1-928 <REA>
A;Cross-references: GB:AE002192; GB:AE002161;
A;Experimental source: strain AR39, HL cells
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                                                                              GGAIYTDNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLSALGGDITFEGNTVV
                                                                                                                   GGAIYARKLSISSGGPTLFINNISYANSONLGGAIAIDTGGEISLSAEKGTITFQGN---
                                                                                                                                                            SFISSNKAISF-INNSVTATSATGGAIYC---SSTSAPKPVLTLSDNGELNFIGNTAITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348;
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                          ----RTSLPFLNGIHLLQNAKFLKLQARNGCSIEFYDPITSE--ADGSTQLNIN
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-TNAKIVQLRASQGNTIYFYDPITTSITAALSDALNLN
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4.5e-79;
ches 373;
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                   LVDPSGNVYEDVSWNNPQVFSCLTLTADDPANIHITDLAADPLEKNPIHWGYQGNWALSW
LINNTSWKTTGTNLSRQAGIGRAGIFYAFSPNLEVTSNLSMEIRGSSRSYNADLGGKFQF
                                                                  FKE-TTADGRRFSNGSLTSISVPLGIRFEKLALSQDVLYDFSFSYIPDIFRKDPSCEAAL
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polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae (st C)Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Species: Chlamydophila pneumoniae C;Species: O2-Mar-2001 #sequence\_revision O2-Mar-2001 #text\_change O2-Mar-2001 C;Accession: D86546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349 A;Accession: D86546 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-930 <STO> A;Cross-references: GB:BA000008; NID:g8978818; PIDN:BAA98654.1; GSPDB:GN00142 A;Experimental source: strain J138 C;Genetics: A;Gene: pmp\_8

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õ 밁 Qγ В Дb QΥ Query Match Best Local Similarity Matches 344; 125 126 66 10 LVFSLTLLSVFDTSLS--ATTISLTPEDSFH--GDSQNAERSYNVQAGDVYSLTGDVSIS æ NLSFIAAPGTTVASGKSTLSSAGALNLTDNGTILFSQNVSNEANNNGGAITAKTLSISGN TLSFIQSPGDIKEQG--CLYSKNALMLLNNYVVRFEQ---NQSKTKGGAISGANVTIVGN 179 DAGKGTALTGCCFTETTGDLTFTGKGYSFSFNTVDAGSNAGAAASTTADKALT--FTGFS NV-DNSALNKACENVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATARFSGFS LLISSTLVTPILLSIATYGADASLSPTDSFDGAGGSTFTPKSTADANGTNYVLSGNVYIN Conservative 29.8%; Score 1434; DB 2; 36.6%; Pred. No. 1.2e-78; 157; Mismatches Length 930; Indels 44; Gaps 125 124 67 65

Query Match Best Local ( Matches 344;

Similarity

Conservative 157; 29.8%; 36.6%;

Score 1434; DB 2; Pred. No. 1.2e-78; 7; Mismatches 395;

Length 930;

44;

Gaps

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polymorphic membrane protein G family CP0307 [imported] - Chlamydophila pneumoniae (strees, chlamydophila pneumoniae, Chlamydia pneumoniae (strees, chlamydophila pneumoniae) (species: Chlamydophila pneumoniae) (species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C; Accession: A81591 R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000 A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A; Reference number: A81500; MUID:20150255 A; Accession: A81591 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-930 <REA> A; Cross-references: GB:AE002193; GB:AE002161; NID:g7189234; PIDN:AAF38164.1; PID:g71892: A; Genetics: GB:AE002193; GB:AE002161; NID:g7189234; PIDN:AAF38164.1; PID:g71892: A; Genetics: CP0307
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                                                                                                                                         NNSGALELGGSLALYLPKEAPFFQGYFPFLKFQAVYSRQQNFKESGAEARAFDDGDLVNC
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                                                                                                                                                                                                                 FLGGL------PMPSFGSITDMLKDIPL-ILNAQLSYSYTKNDMDTRYTSYPEAQGSWT
                                                                                                                                                                                                                                    SLGNIFRYASRNPNVNVGILSRRFLQNPLMIFHFLCAYGHATNDMKTDYANFPMVKNSWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGEKSLANDPR---DFKSTIPQNVNLSAGYLVIKEGAEVTVSKFTQSPGSHLVLDLGTKL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRNAIYLGSSAKITNLRAAQGQSIYFYDPIASNTTGASDVLTINQPDSNSPLDYSGTIVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLFFSGNTA-TDAAGKGGAIYCEKTG----ETPTLTISGNKSLTFAENSSVTQGGAICAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIMGGGAIYAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAGKGTALTGCCFTETTGDLTFTGKGYSFSFNTVDAGSNAGAAASTTADKALT--FTGFS
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                           SLGNIFRYASRNPNVNVGILSRRFLQNPLMIFHFLCAYGHATNDMKTDYANFPMVKNSWR
                                                         TNQAFRHKSYGYIVGGSAEDFSENIFSVAFCQLFGKDKDLFIVENTSHNYLASLYLQHRA
                                                                                   DNIRYRHNSGGYVLSVNNEITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTT
                                                                                                                                               INYKPRPEKEGNLVPNILWGNAVNVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASE
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                                                                                                                  TGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGLWASGTANFFHKDKSG
                                                                                                                                                                            AFTQPLVVFTAATAASDIYIDALLTSPVQTPEPHYGYQGHWEATWADTSTAKSGTMTWVT
                                                                                                                                                                                                     SQTFPLLSLEPG-AGGSVTVTAGDFLPV---SPHYGFQGNWKLAWTGTGN-KVGEFFWDK
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PMPSFGSITDMLKDIPL-ILNAQLSYSYTKNDMDTRYTSYPEAQGSWT
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polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae (st C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: C86546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-936 <STO> A;Residues: 1-936 <STO> A;Experimental source: Strain J138 C;Genetics: A;Genee: pmp_7
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 KEANLSLNGLAVNLSSLDGTNKAA-LKTEAADKNISLSGTIALIDTEGSFYENHNLKSAS
                                   SKEDIAITGLAIDIDSLSSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDLRMRNSQ 529
                                                                           EKLSPTEKAIAANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQSPGSRILMDGGTTLSA
                                                                                                 EKSLAND---PRDFKSTIPQNVNLSAGYLVIKEGAEVTVSKFTQSPGSHLVLDLGTKLIA
                                                                                                                                                       AINIIDTAKVTSIRAATGQSIYFYDPITNPGTAASTDTLNLNLADANSEIEYGGAIVFSG
                                                                                                                                                                                           GIHLLQNAKFLKLQARNGCSIEFYDPITS--EADGSTQLNINGDPKNK--EYTGTILFSG
                                                                                                                                                                                                                                 SISAGGPTLFQSNISGSSAGQGGGGAINIASAGELALSATSGDITFNNNQVTNGSTSTRN
                                                                                                                                                                                                                                                                                                           IFDGNSAWEAAQAQGGAICCTTTDKT-----VTLTGNKNLSFTNNTALTYGGAISGLKV
                                                                                                                                                                                                                                                                                                                                 LFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIMGGGAIYARKL
                                                                                                                                                                                                                                                                                                                                                                                     SFYQNAA---TFGGAIHSSGPLQIAVNQAEIRFAQNTAKNGSGGALYSDGDIDIDQNAYV
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C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Species: Chlamydophila pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: B81591
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C:Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
A;Accession: B81591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-936 <REA>
A;Cross references: GB:AE002193; GB:AE002161; NID:g7189234; PIDN:AAF38165.1; PID:g718923
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0308
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GNIFRY----ASRNPNVNVGILSRRFLQNPLMIFHFLCAYGHATNDMKTDYANFPMVKNS
                                                                                             SFYQNAA---TFGGAIHSSGPLQIAVNQAEIRFAQNTAKNGSGGALYSDGDIDIDQNAYV
                                                                                                                                  SIISCPSLLLSPTGQCALKSVGNLSLTGNSQIIFTQNFSSDNGGVINTKNFLLSGTSQFA
                                                                                                                                                                                                        ALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSS-AGTVASTSAADKNLLFNDFSRL
                                                                                                                                                                                                                                                                                  PLFSSLSIVAA-EVTLDSSNNSY---DGSNGTTFTVFSTTDAAAGTTYSLLSDVSFQNAG
                                                                                                                                                                                                                                                                                                                     PLVFSLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAGDVYSLTGDVSISNVD 68
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                                                          SFSRNQAFTGKQGGVVYATGTITIENSPGIVSFSQNLAK-GSGGALYSTDNCSITDNFQV
                                                                                                                                                                     SFIQSPGDIKE---QGCLYSKNALMLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYDSV
                                                                                                                                                                                                                                             -- NSALNKACFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATARFSGFSTL 126
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                                                                                                                                                                                                                                                                                                                                                                             29.1%; Score 1400.5; DB 2; 35.9%; Pred. No. 1.3e-76;
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PLVFSLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAGDVYSLTGDVSISNVD 68

Matches

Conservative

Query Match Best Local Similarity

29.1%; 35.9%; 166;

Score 1400.5; DB Pred. No. 1.3e-76; Mismatches

391; DB 2;

Indels Length

47;

Gaps

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A; Experimental : C; Genetics: A; Gene: pmp_7
                                      A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Recession: C72078
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-936 <ARN>
A;Residues: 1-936 <ARN>
A;Coss-references: GB:AE001627; GB:AE001363; NID:94376721; PIDN:AAD18589.1; PID:9437
A;Experimental source: strain CWL029
                                                                                                                                                                                                                    polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C;Accession: C72078 C;Accession: C72078 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grim Nature Genet. 21, 385-389, 1999
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polymorphic outer membrane protein G family [imported] - Chlamydophila C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C:Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 02-Mar-C; Accession: G86546 R; Shirai, M; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, Nucleic Acids Res. 28, 2311-2314, 200.
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A;Accession: G86546
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <STO>
A;Cross-references: GB:BA000008; NID:g8978821; PIDN:BAA98657.1;
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_10
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TEGRSFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPDLIRNDPKCTTALVISGAS
                                                                  ADGRRFSNGSLTSISVPLGIRFEKLALSQDVLYDFSFSYIPDIFRKDPSCEAALVISGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SISFEGNKSSATGKKGGAICATGTVDITNNTAPTLFSNNIAE-AAGGAINSTGNCTITGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGAISTKNLSLKNSTG
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pred. No. 3.5e-76;
62; Mismatches 374;
                                                                                                                                                                                                                                                                                  IGCLLDKLPGSWSHKPLVLEGQL-AYSHVSNDLKTKY
                                                                                                                                            -EYLHCFDTYAPYIKLNLTYIRQDSFSEKG
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255
A;Accession: G81591
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-928 <REA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
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Matches 344; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 TSLVFSENSVTATA-GNGGAL----SGDAD----VTISGNQSVTFSGNQAVANGGAIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
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GEFFWDKINYKPRPEKEGNLVPNILWGNAVNVRSLMQVQETHASSLQTDRGLWIDGIGNF
                                                                                                                                                                                                                                                            GTKLIASKEDIAITGLAIDIDSLSSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FL---NGIHLLQNAKFLKLQARNGCSIEFYDPITSE--ADGSTQLNIN-GDPKNK-EYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKLSISS--GGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFQGNR--TSLP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIMGGGAIYA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSFYQNAATF----GGAIHSSGPLQIAVNQAEIRFAQNTAKNGSGGALYSDGDIDIDQN 237
                                                                                       DLGKTQDFSFVQL--SALGTATTTDVPAVPTVATPTHYGYQGTWGMTWVDDTASTPKTKT 590
                                                                                                                                                                                                                                                                                                                                                                                         TILFSGEKSLANDPR----DFKSTIPQNVNLSAGYLVIKEGAEVTVSKFTQSPGSHLVLDL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITFNGNAIVATTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGAISTKNLSLKNSTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKS--SAEGAALSVTTDK-NLSLTGFSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V-DNSALNKACENVTSGSVTFAGNHHGLYENNISSGTTKEGAVLCCQDPQATARESGEST 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNTTTGIDYTLTGDITLQN 67
                                                                                                                                                  RMRNSQTFPLLSLEPGAGGSVTVTAGDFLP---VSPHYGFQGNWKLAW-----TGTGNKV 575
                                                                                                                                                                                                             GTTLKASTEEVTLTGLSIPVDSLGEGK-KVVIAASAASKNVALSGPILLLDNQGNAYENH 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.9%; Score 1393; DB 2; 36.1%; Pred. No. 3.5e-76;
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	408	351 SLPFLNGIHLLQNAKFLKLQARNGCSIEFYDPITSEADGSTQLNINGDPKNKEYTG	_
	345	:  ::       :   :    :	
	350	Oy 298 RKLSISSGGPTLFI-NNISYANSONLGGAIAIDTGGEISLSAEKGTITFOGNRT	_
	297 287	Qy 238 AYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIMGGGAIYA ::	п о
	237 235	Qy 179 NYDSVSFYQN-AATFGGAIHSSGPLQIAVNQAEIRFAQNTAKNGSGGALYSDGDIDIDQN     ::        ::	п о
	178 176	Qy 121 SGFSTLSFIQSPGDIKEQGCLYSKNALMLLNNYVVRFEQNQSKTKGGAISGANVTIVG	п о
	120 116	Qy 62 VSISNV-DNSALNKACENVTSGSVTFAGNHHGLYFNNISSGTTKBGAVLCCQDPQATARF	
	61 58	Qy 10 LVFSLTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQAGDVYSLTGD	
22;	aps	Query Match 27.9%; Score 1344; DB 2; Length 928; Best Local Similarity 35.3%; Pred. No. 3.2e-73; Matches 337; Conservative 152; Mismatches 385; Indels 80; G	
pneumoniae (st 2001 K.; Shiba, T.; 138.	1 pnew K.; 13138.	H86546 polymorphic outer membrane protein G family [imported] - Chlamydophila pneu C; Specles: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: H86546 R;Shiral, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349 A;Reference number: A86491; MUID:20330349 A;Rocession: H86546 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-928 <stoo- a;cross-references:="" a;experimental="" c;genetics:="" gb:ba000008;="" gspdb:gn001="" j138="" nid:g8978822;="" pidn:baa98658.1;="" pmp_11<="" source:="" strain="" td=""><td></td></stoo->	
		ESULT 14	
		Qy 869 WLVPAAHVSRHAFVGSGTGRYHFNDYTELLCRGSIECRPHARNYNINCGSKFRF 922       ::	
	868 874	Qy 809 ADGRRFSNGSLTSISVPLGIFFEKLALSODVLYDFSFSYIPDIFRKDPSCEAALVISGDS         :   :   :   :	
	808 814	Qy 752 ANFPMYKNSWRNNCWAIECGGSMPLLVFENGRLFQGAIPFMKLQLVYAYQGDFKETT	
	751 758	Qy 696 YLYQYTTSLGNIFRYASRNPNVNVGILSRRFLQNPLMIFHFLCAYGHATNDMKTDY :  :   :   :       :	
	695 710	Qy 636 FHVSASEDNIRYRHNSGGYVLSVNNEITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGS :	
	650	Db 591 ATLAWTNTGYLPNPERQGPLVPNSLWGSFSDIQAIQGVIERSALTLCSDRGFWAAGVANF	_

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A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
A;Accession: D72077
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <ARN>
                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:AAD18593.1; PID:g43767:A;Experimental source: strain CWL029 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymorphic outer membrane protein g family - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-C;Accession: D72077
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                                 WLVPAAHVSRHAFVGSGTGRYHFNDYTELLCRGSIECRPHARNYNINCGSKFRF
                                                                       SDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDS
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Search completed: October 2, 2001, 03:29:00 Job time: 1317 sec

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Result
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### Query Match Best Local Similarity Matches 236; the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL; AE001360; AAC68467.1; Outer membrane; Signal. SIGNAL 19 964 SEQUENCE 964 AA; 104703 M STRAIN-D/UW-3/CX; MEDLINE-99000809; PubMed=9784136; Stephens R.S., Kalman S., Lammel C. Mitchell W.P., Olinger L., Tatusov PMPE OR CT869. Chlamydia trachomatis. Chlamydiales; Chlamydiaceae; Chlamydia. "Genome sequence of an obligate intracellular pathogen Chlamydia trachomatis."; Science 282:754-759(1998). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -Davis R.W.; SEQUENCE FROM N.A. NCBI\_TaxID-813; 90-MAY-2000 (Rei. 39, Last annotation update) 90-MAY-2000 (Rei. 39, Last annotation update) PUTATIVE OUTER MEMBRANE PROTEIN E PRECURSOR. -! - SUBCELLULAR LOCATION: CELL WALL 149 133 GDIKEQGCLYSKNALMILNNYVYRFEQNQSKTKGGAISGANVTIVGN-----YDSVSF 185 45 57 (POTENTIAL). --IREGGAIHAQNLYINHNHDVVGFMKNFSYVQGGAISTANTFVVSENQSCFLFMDNICI PESGGAIGYASPNSPTVEIRDTIGPVIFENNTCCRLFTWRNPYAADK--KE--GAV-----SLTGDTHNLTNCYLDNLRYILAILQKTPNEGAAVTITDYLSFFDTQKEGIYF---AKNLT 101 SLTGDV-SISN--VDN-----SALNK-----ACFNVTSGSVTFAGNHHGLYFNNISSGTT 103 Conservative 147; Mismatches 358; 18 POTENTIAL. 964 PUTATIVE OUTER MEMBRANE PROTEIN 104703 MW; 1B998A7D2E571CE2 CRC64; 11.8%; 24.6%; Score 567; DB 1; Pred. No. 7.7e-27; .J., Fa SURFACE (ELEMENTARY BODIES) Fan J., Mar .., Zhao Q., Marathe R. Length 964; Indels Koonin of humans: R., Aravind ... 220; Ħ Gaps 148 ۲. 43;

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                                                                                                                                             Chlamydia trachomatis. Bacteria; Chlamydiales;
SEQUENCE FROM N.A. STRAIN=D/UW-3/CX; MEDLINE=99000809;
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"Genome sequence of an obligate Chlamydia trachomatis.";
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Comanducci M., Christianen G., Birkelund S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
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les 231; Conserv
                                   --TTLKFGTLAIEDDAELEIFNIPFTQNPTSLLALGSGATLTVGKHGKLNITNLGVILPI 541
                                                                QNVNLSAGYLVIKEGAEVTVSK--FTQSPGSHLVLDLGTKLIASKE-DIAITGLAIDI--
                                                                                                     QWERVKENTSNNPPSPTSRNTITVNPETEFSGAVVFSYNQMSSDIRTLMGKEHNYIKEAP
                                                                                                                                                                        ----TGDIVFNNN----VVFTLDGNLLGKRKLFHINNNEITPYTLSLGAKKDTRIYFYDLF
                                                                                                                                                                                                    LSAEKGTITFQGNRTSLPFLNGIHLLQNAKF------LKLQARNGCSIEFYDPI 383
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42; Mismatches
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MW; 445FF4C35D463AE7 CRC64;
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Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H. Kashinoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K. Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  Mau B., Shao Y.; "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
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between
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Hussain K., Elliott E.J., Salmond G.P.C.;
"The parD-mutant of Escherichia coli also
The complete sequence of gyra.;
Mol. Microbiol. 1:259-273(1987).
                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
used by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
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Carlson J., Fuchs J.A., Messing J.;
Primary structure of the Escherichia coli ribonucleoside
reductase operon.";
 SEQUENCE
                                                                                                                            DOMAIN
                                                                                                                                                  Hypothetical protein; SIGNAL 1 2
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SIMILARITY: TO E.COLI YDEK.
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LRVIGG -> LLTSRC (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                          "AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli strain 2787 (0126:H27), is synthesized via a precursor molecule."; Mol. Microbiol. 6:1539-1546(1992).

-i- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR TH
                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSYNVQAGDVYSLTGDVSISN------VDNSA------LNKACFNVTSG
                           SRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNV------GILSRRFLQN 729
                                                          LGIMGGYANAKGKTINYTSNKAARNTLDGYSVGVYGTWYQNGENATGLFAETWMQYNWFN 1110
                                                                                      -----HVSASEDNIRYRHNSG-----
                                                                                                                   FRAMSDNTQPESASVWMKITGGISSGKLNDGQNKTTTNQFINQLGGDIYKFHAEQLGDFT
                                                                                                                                                THASSLQT---DRGLWI-----DG-----
                                                                                                                                                                             N----ESGTONK----GWYLTSHLPTSDTRQYRPE-NGSYATNMALANSLFLMDLNERKQ
                                                                                                                                                                                                          NWKLAWTGTGNKVGEFFWDKINYKP------RPEKEGNLVPNILWGNAVNVRSLMQVQE
                                                                                                                                                                                                                                        --TRDGINIISVEGNSDAEFSLKN----
                                                                                                                                                                                                                                                                   ISVTDSIELISPTGNAYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQ-G
                                                                                                                                                                                                                                                                                                   NTLTVSNYTGTPGS--VISLGGVL---EGDNSLTDRLVVKGNTSGQSDIVYVNEDGSGGQ
                                                                                                                                                                                                                                                                                                                              AEVTVSKFTQSPGSHLVLDLGTKLIASKEDIAITGLAIDIDSLSSSSTAAVIKANTANKQ
                                                                                                                                                                                                                                                                                                                                                         SVNN---NGSIVINNSIINGNITNDADLSFGTAKLLSATVNGSLVNNKNIILNPTKESAG
                                                                                                                                                                                                                                                                                                                                                                                        DPKNKEYTGTILFSG---EKSLAND------PRDFKSTIPQNVNLSAGYLVIKEG
                                                                                                                                                                                                                                                                                                                                                                                                                     SGYLYKDNTGIMTYAGTLTQAQGYNYKNGGIIFDSAYYNADMAYNQNAYINISDQATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GCSIEFYDPITSEADG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGRLRIDDGGTIN-----GTTTINAD-----GIVAGTNIQNDGNFILNLAENYDFETELSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAIAIDTGGEISLSAEKGTITFQGNRTSLPFLNGIHLLQNAKFLKLQARN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATLPELTIMA----ALSVSQNHASNIVLENGGL----LRVTSGG-----TATDTTVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSTPVPIVTFSDNKQLVFERNHS---IMGGGAIYARKLSISSGGPTLFINNISYANSQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAQFVYDGGQVTGTNIKNG-----GTIRVDSGA-----SALNIALSSGGN----LFTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIRF----AQNTAKNGSGGALYSDGDIDIDQNAYVLFRENEALTTAIGKGGAVCCLPTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGRQY - - VYSGATATSTYGNNEGREYYLSGGITDGTYLNSGGLQAVSSGGKASATYINEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSKTKGGAISGANVT-IVGNYDSVSFYQNAATFGGAIHSSGPLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAEVYSGGKQTVYLWRGIWYSNFLTAVWSMFPGTASGANVNLSGRLNAFAGNVVGTILNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVTF - - - - AGNHHGLY - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt RNGGIASGTIVNQSGYVNISSGGYAESTIINSGGTLRVLSDGYARGTILNNSGRENVSNG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198;
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7
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19.3%;
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 -LNGLTASAGGGY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 198.5; DB 1
Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------FNNISSGTTK--EGAVLCCQDPQATAR-- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                      -GYVLSV-----NNEITPKHY--TSMAFSQLF
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                                                                                                                                                                                                                                         ----RVVAGAY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----STQLNING
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 NLNVHTWTSPEGITGEFWLQP 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                         -DYTLQKG
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RESULT 5

190K_RICRI STANDARD; PRT; 2249 AA.

ID 190K_RICRI STANDARD; PRT; 2249 AA.

AC P15921;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-CTT-1994 (Rel. 30, Last annotation update)

DE 190 KDA ANTIGEN PRECURSOR (CELL SURFACE ANTIGEN).
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            Query Match 4.1%; Score 196; DB 1; Length 2249; Best Local Similarity 19.6%; Pred. No. 0.00075; Matches 217; Conservative 111; Mismatches 369; Indels 41
                                                                                                                                                                                                                                                                                                                  PIR; A41477;
Antigen; Repe
SIGNAL
                                                                                             CHAIN
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;

"A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";

Infect. Immun. 58:2760-2769(1990).

-I- FUNCTION: ELLCITS PROTECTIVE IMMUNITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettslaceae; Rickettsieae; Rickettsia. NCBI_TaxID=783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1207 TGRRFR----PYIEANWIHNTH-EFGVKMSDDSQLLSGSRNQGEIKTGIEGVITQNLSVNG 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1158
                                                                                                                                                                                                                                                                                                                                                        EMBL; M31227; AAA26380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia rickettsii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90354033; PubMed=2117568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        730 PLMIFHELCAYGHATNDMKTDYANFPMVKNSWRNN------CWAIECGGSMPLLVFE 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: GLYCOSYLATED (POSSIBLE).
DISEASE: PROBABLY PLAYS AN IMPORTANT ROLE IN THE PATHOGENESIS OF AND IMMUNITY TO ROCKY MOUNTAIN SPOTTED FEVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGRLFQGAIPFMKLQLVYAYQGDFKETTADGRRFSNGSLTSISVPLGIR---FEKLALSQ 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----HLQAVWMGVTPDTHQE-DNGTVVQGAGKNNIQTKAGIRASWKVK-----STLDKD 1206
                                                                                                                                                                                                                                                                                                                            Repeat; Signal; S-layer; Glycoprotein.
                                                                                  AA;
                                                                                                           430
505
577
652
724
799
874
949
1021
1093
                                                                                               1180
                                                                                  224333
                                                                                  MW.
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                                                                                               TYPE
                                                                                                                                                                                                                                                                                      190 KDA ANTIGEN.
13 X APPROXIMATE TANDEM REPEATS.
                                                                                                          (TYPE II).
(TYPE II).
(TYPE II).
                                                                                                                                                                                        D (TYPE I).
E (TYPE II).
F (TYPE I).
S (TYPE II).
                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                  (TYPE I). (TYPE I). (TYPE I).
                                                                                                                                                                                                                                              (TYPE
                                                                                                                                                                                                                                                                         (TYPE I).
                                                                                  A9D6646C089DF087 CRC64;
                                                                                                (INCOMPLETE)
              Indels 410;
              Gaps
               51;
δõ
 847 -----YIPDIFRKDPSCEAALVISGD 867
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	VIDDIFRKNDSCEAALVISCD 867	847	Q
1838	GVSTLALVYTATNEDMNNISPDTKYTVISAETAGGLKPTSKENVKITINNDNREVDETED	1779	рь
846	TSISVPLGIRFEKLALSQDVLYDFSFS	820	Qy
1778	TTLGANQVTYTGTGSFTDTLTLNTTFDGAAKSGGNILIKSGSTLDLS	1732	ДЬ
819	LLVFENGRLFQGAIPFMKLQLVYAYQGDFKETTADGRRFSNGSL	776	Qy
1731	VTLAKGSITSFAKNVTATSFVANSATINFSNSLAFNSNITGGGTT	1687	뫄
775	RRELQNPLMIFHFLCAYGHATNDMKTDY	722	Qy
1686	ITTAGATSFASSTNTGA	1651	Ф
721	ITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGI	662	Qy
1650	TLT	1606	Дb
661	LQTDRGLWI	620	Оу
1605	GASNLNRVNGIAMLKVGAGNVTIAKGKVKIGEIQGTGTN	1566	Db
619	GTGNKVGEFFWDKINYKPRPEKEGNLVPNILWGNAVNVRSLMQVQETHAS	570	Qу
1565	QLTQTGNIGGFLDFNAKNGMVTLNNNVNVAGAVQNTGGTNNGTLIVL	1519	DЪ
569	-ISPTGNAYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDELPVSPHYGFQGNWKLAWT	513	Qy
1518	AGGKTFGGAHKLQTILFKGAGDCSTAGT-TFNTTNIVLDITGQLELGATTANVVLFNDAV	1460	В
512	AIDIDSLSSSSTAAVIKANTANKQISVTDSI	480	Qy
1459	INIPAGNIQFAHADAQLVLQNSSGNDRTITLGANIDPDNDDEGIVILNSVTAGKKLTI	1402	οь
479	VNLSAGYLVIKEGAEVTVSKFTQSPGSHLVLDLGTKLIASKEDIAITGL	431	Qy
1401	NTLLIYNAVTITDDVNLEGIQNVLINKNADFTSSTAFNAGAIQINDATYTIDANNGN	1345	Ф
430	YDPITSEADGSTQLNINGDF	380	Qy
1344	TGYGVNNILLAADLVAPGADEGTVVFNGGVNGLNVGSNVAGTARNIGDGGGNKF	1291	Db
379	KGTITFQGNRTSLP	337	Qy
1290	LNVNTKLLTASHLTIGTVAEINIGAGNLFTIDASVGDVTILNAQNINFRARDSVLVLSNL	1231	Дb
336	FINNISYANSQULGGAIAIDTG-G	310	ОУ
1230	ATVNVGAGITLQ	1173	рь
309	CCLPTSGSSTPVPIVTFSDNKQLVFER	259	Qy
1172	QGGVVKANTINLTDNASAVTFTNDVVVTGAIDNTGNANNGIVTFTGNSTVTGDIGNTNAL	1113	Db
258	-GGALYSDGDIDIDQNAYYLFRENEALTTAIGKGGA	223	Qy
1112	AVTF-TNPVVVTGAIDNTGNANNGIVTFTGNSTVTGNVGNTNALATVNVGAGLLQV	1058	Db
222	SVSFYQNAATFGGAIHSSGPLQ	182	Qy
1057	NA NNGIVTETGNSTVTGNVGNTNALATVNVGAGLLQVQGGVVKANTINLTDNAS	1004	Дb
181	SKNALMLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYD	143	Qy
1003	IGNTNSLATISVGAGTATLGGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTG	950	Db
142	VTFAGNHHGLYFNNISSGT-TKBGAVLCCQDPQATARFSGFSTLSFIQSPGDIKEQGCLY	. 84	Qy
949		898	Дb
83	LSATTISLTPEDSFHGDSQNAERSYNVQAGDVYSLTGDVSISNVDNSALNKACFNVTSGS	24	Qy

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1839

ASTLTLFAEDI ---

-AADVIDGD

1857

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IDENTIFICATION OF CLEAVAGE SITE.

IDENTIFICATION OF CLEAVAGE SITE.

MEDIINE-92104668; PubMed=1729180;

Hackstadt T., Messer R., Cieplak W. Jr., Peacock M.G.;

Hackstadt T., Messer R., Cieplak W. Jr., Peacock M.G.;

"Evidence for proteolytic cleavage of the 120-kilodalton outer

"Evidence for proteolytic cleavage of the 120-kilodalton of an avirulent mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence Submitted
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053020; 092CM0;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
00TER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCAS) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).
                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sit
the S-layer protein antigens of Rickettsia
prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99039499; PubMed-9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin
                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92114896;
Ching W.M., Carl N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
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EUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR. SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
                        SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation on it with the confidence of the contraction on it with the confidence of the contraction of the contracti
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nalysis of ompB of Rickettsia prowazekii.";
JUN-1999) to the EMBL/GenBank/DDBJ databases
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                       ----TDSIELISPTGNAYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQG
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32 KDA BETA PEPTIDE
V -> A (IN STRAIN BREINL).
Y -> D (IN STRAIN BREINL).
A -> S (IN STRAIN BREINL).
AA -> VC (IN REF. 1).
TTQEAPLTLGA -> INSRSSSYHLVS (1)
T -> I (IN REF. 1).
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01-OCT-2000 (Rel. 40, Last annotation update)
0UTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE 120 KDA SUFFACE-EXPOSED PROTEIN IS A MAJOR-
-I- STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A FICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
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      Conservative
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  Score 175; DB 1;
Pred. No. 0.0091;
4; Mismatches 318;
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                                                                                                                   GNIYSQVIDFGTYNLGIVNSNVI--
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(Rel. 14, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DISEASE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNGEN DURING INFO SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERN S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                     DISEASE: RICKETTSIA RICKETTSII IS THE CAUSATIVE AGENT OF MOUNTAIN SPOTTED FEVER (RMSF).
MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EF CONFERRING ANTIGENICITY TO THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ng, expression and sequence analysis of surface-exposed protein of Rickettsia icrobiol. 3:1579-1586(1989).
                                                                                                                                                                                                                                                                                        Glycoprotein;
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                              ----EDNIRYRHNSGGYVLSVNNEITPKHYTSMAFSQLFSRDKDY
                                                                 ANDNLMIGAAIGITKTDIKHQDYKKGDKTD----VNGFSFSLYGAQQLVKNFFAQGSAIF
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30-MAY-2000 (Rel. 39, Last sequence update)
0UTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(COUTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                Bacteria; Proteobacteria; alpha
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                  na subdivision; Rickettsiales; Rickettsia.
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Best Loca Matches Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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---RTSLPFLNG----IHLLQNAKFLKLQARNGCSIEFYDPITSEADGSTQLNINGDPKN |:| || || :| : | |
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56; Conservative
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15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
00UTER MEMBRANE PROTEIN B PRECURSOR (158 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SURFACE PROTEIN ANTIGEN)
(SURFACE PROTEIN OMPB); 32 KDA BETA PEPTIDE).
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           1464
                                                                                                                                                                                                          Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments
the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRALN=WILMINGTON;
STRALN=WILMINGTON;
MEDLINE=94040787; PubMed=8224886;
MEDLINE=94040787; PubMed=8224886;
"Cloning and Sequence analysis of the gene ensurface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria; alpha subdivision; aceae; Rickettsieae; Rickettsia.
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1283 -- NNMLLAKDSSDVATFIGAIATDTGAAVATVNLNDTQKTQDLLGNRLGALRYLSNSETA 1340
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                                                                                                1235 ANQDYVLTRTNDVLNVVTTAVGNSAIANAPGVHQNIAI-----CLESTDTAAY----
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12 KDA BETA PEPTIDE.
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G -> A (IN REF. 2).
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Aa; 169698 MW; 0CB5641C7EB185EE CRC64;
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1353 120 KDA SURFACE-EXPOSED PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                           NISYANSQNLGGAIAIDTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNLGSSSEGNNTGMLEVNNNSAFNNRGEFILDNDKNAVHINQSGTLYNTGHMNIS----
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                                             SALKQVSGSQATTVFREARVLSNRFSMLAD-----
                                                                                                                                                                     MNGVEINTG-FT-----AGTADTTVSFDNVVEGSNLTDADAITSTSVVWTAKGST
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                                                                                                       DASGNVDVTMS-----KNAYTDVATDASVNDTAKALDAGYTNNELFTSLNVGTTAELN
                                                                                                                                      -ANKQISVTDSIELISPTGNAYEDLR---
                                                                                                                                                                                                  -EGAEVTVSKFTQSPGSHLVLDLGTKLIASKEDIAITGLAI-DIDSLSSSSTAAVIKANT
                                                                                                                                                                                                                                 SDEAGGSMNNLNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NSSHNGAVNMWGGNGRFINDGTIDVSAKSLVVSANNAGDQNAFFWNQDNGVINFDHDSA 1405
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                                                                            -SLEPGAGGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKVGEFFWDKINYK--PRPEK
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95 I -> V (IN REF. 2).
205949 MW; B83A12C8B53220EE CRC64;
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Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QSKTKGGAISGANV--TIVGNYDSV 183
                                                                                                                                                                                                                                                                                                                                                                                           -----GEISLSAEK-----
                                                                                                                                                                                                                                   ----YVVGTNVNGSAGKLKVNNAS
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                                             - AAPKVGNGLAFNVVAKGDPRAEL
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                                                                                                                                      ---MRNSQTFPLL-----
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P52143; P76610; P77U1/; ...

01-OCT-1996 (Rel. 34, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

01-OCT-2000 (Rel. 40, PROTEIN IN ALPA-GABD INTERGENIC
                                                                                             between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as used by non-profit institutions as Important modified and this statement is not removed. Use entitles requires a license agreement (See http: or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itono S., Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori I Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
                                                                                                                                                                                                                                  Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. -:- SUBCELLULAR LOCATION: OUTER MEMBRANE (POTENTIAL). -:- SIMILARITY: STRONG, TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bur Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
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                                               EMBL; U36840; AAA79815.1; ALT_SEQ. EMBL; AE000350; AAC75695.1; -.
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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Escherichia
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                                                                                                                (See http://www.isb-sib.ch/announce/
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                                                                                                                                  Usage by and
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MBL outstation -
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EMBL; D90889; BAA16514.1; ALT\_INIT EMBL; D90890; BAA16518.1; ALT\_INIT

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HLYA_PE
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P16466;
Ol-AUG-1990 (Rel. 15, Created)
Ol-AUG-1990 (Rel. 15, Last seq
Ol-NOV-1990 (Rel. 16, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Outer membrane. SEQUENCE 1569 AA; 162774 MW; 0D006A9A32154596 CRC64;
   Bacteria;
Proteus.
                                   Proteus mirabilis
                                                                     HEMOLYSIN PRECURSOR.
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                                                                                                                                                                                                                                            TVSANGEAIKTKINEGG-TLTVND
                                                                                                                                                                                                                                                                               HVSASEDNIRYRHNSGGYVLSVNN 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLNNGGVLEVQDGGEAKHVEQQSGGALIASTTSGTLIEGTNSYGDAFYIRNSEAKNVVLE 623
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                                                                                                                                                                                                                                                                                                                 -----TQVNMGGREIVKTKATATGTTLTGGEQIVEGVANETTINDGGIQ
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                   Proteobacteria;
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                                                                                       Last sequence update)
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                   subdivision; Enterobacteriaceae;
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Best Local
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"Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";

J. Bacteriol. 172:1206-1216(1990).

-I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
MAY BE RESPONSIBLE FOR PORE FORMATION.
-!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN-ISOLATE 477-12; SECOLORE 170827; PubMed=2407716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 AERSYNV-----QAGDVYSLTGDVSISNVDNSALNK-----ACFNVTSGSVTFAGN 89
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NKLHD--QGTHYQSTQEGISLTANTHTSEATLDKHQTTFHETKGGGQIGVSTKTGSDITV
                                          RTSLPFLNGIHLLQNAKFLKLQARN----
                                                                                  LTKKVTARDAIANLANLSNLETPNVGVEVGIKGGGSQQSQTDSQAVSTSINAGKIDIDSN
                                                                                                                                                                 QESGENIQHLAVNDSETSKTDSLNVGIDVGVNLDYSGVTKPVKKAIEDGVNTTKPGNNTD
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                                                                                                                                                                                                                                                                                   QNAYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVP-IVTFSDNKQLVFE-RNHSIMG--
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1577 AA;
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                                                                                                                         -LFINNISYANSONLGGAIAIDTGGE-----ISLSAEKGTITFQGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLYA_SERMA STANDARD; PRT; 1608 AA P15320; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1462
                                                                                                                                                                     Marcescens.,
J. Bacteriol. 170:3177-3188(1988).
-i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1191
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                                                                                                                                                                                                                                                           Poole K., Schiebel E., Braun V.; "Molecular characterization of the hemolysin determinant
                                                                                                                                                                                                                                                                                                                                                                                                                                           Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEMOLYSIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                         STRAIN-SN8
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                      Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                     MEDLINE=88257037; PubMed=3290200;
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                                                     SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                              FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SH REQUIRES SHLB FUNCTION.
                                                                                  SUBCELLULAR LOCATION:
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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MS NOT CLEARL
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             1314
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1466 QGPLWDR
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                                                                                                                                                                            468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAATFGGAIHSSGPLQIAVNQAEIRFAQNTAKNGSGG--ALYSDGDIDIDQNAYVLFREN 245
                                 GEFFWDK 582
                                                                    TTDKYNSVARR
                                                                                                     TGNAYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKV 575
                                                                                                                                         VESRKDVE-NGVKVDVDAGLSHSNDPGSSITSKLSKVGTPRYAGKVKEKLEAGVNKVADA 1423
                                                                                                                                                                          IASKEDIAITGLAIDIDS-LS-----SSSTAAVIKANTANKQISVTDSIE-----LISP
                                                                                                                                                                                                           K-VGVEQQD--KTTHANTGITAGDVTLNSG-----KDTRLAGARVDADSVQGKVGGDLH 1364
                                                                                                                                                                                                                                KSLANDPRDFKSTIPQNVNLSAGYLVIKEGAEVTVSKFTQSPGSHLVLDL-----GTKL
                                                                                                                                                                                                                                                                                  GILLESAK---NEQHKDNWSL-----GIKANAKGGQTFNKDAGGKVDPNTGKDTHT-LGAGL
                                                                                                                                                                                                                                                                                                                 IHLLQNAKFLKLQARNGCSIEFYDPITSEADGSTQLNING----DPKNKEYTGTILFSGE
                                                                                                                                                                                                                                                                                                                                                       GGAFDIAKVNESATERQGATIASD--GKYTLSANGKGDDALHLQGAKVSGGSAALEAKNG
                                                                                                                                                                                                                                                                                                                                                                               GPTLFINNISYANSQNLGGAIAIDTGGEISLSAE-KG--TITFQGNRTS-----LPFLNG
                                                                                                                                                                                                                                                                                                                                                                                                                               TLQGTDVKSQGDVSLSAGNKVALQAAESTQTRKESKLSGNIDLGAGSSDSKEKTGGNLSA 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMGGGATYARKLSISSG--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESRSGFNVKASAKGGFTADSKNFGAGFGGGTHNGESSSSTAQVGNISGQQGVELKAGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EALT-----TA-----IGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAVT - - GSIDAANGINVNVKKDAI - - YQGTALNGGRGKTAVNAGGDIRLDQAS - - - DKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAVNLTADSHRSEAAANRQDEQSRDTRGSAGVRVYTTTGSDLTVDAKGEGGTQRSNSSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NALMLL-----NNYVVRFEQNQSK-TKGGA-----ISGANVTI-----VGNYDSVSFYQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G---GIGAPNYGLDIGAQGGSSEKRSSSSQAYVSSVQAGSIDINAKGEVRDQGTQYQASK 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNHHGLYENNISSGTTKEGAVLCCQDPQATARFSGFSTLSF-IQSPGDIKEQGCLY--SK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENAAGVDHLAAADTASTTTTKTDVGVNIGANVDYSAVTRPVERAVGKAAKLDATGVINDI 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNAERSYNVQAGDVYSLT---GDVSI---SNVDNS-----ALNKACFNVTSGSVTFA
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1608 AA;
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22.2%;
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Pred. No. 0.
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W; D669B476FE7DAD51 CRC64;
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.038;
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RESULT 15
YIQ9\_YEAST
ID YIQ9\_Y
AC P40442
DT 01-FEB
DT 01-FEB

STANDARD;

PRT;

995

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YIQ9\_YEAST P40442; 01-FEB-1995 01-FEB-1995

(Rel. 31, Rel. 31,

Created) Last sequ

sequence update)

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Query Match 3.4
Best Local Similarity 22.1
Matches 119; Conservative
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CARBOHYD
SEQUENCE
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Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Last annotation update)
HYPOPHETICAL 99.7 KDA PROTEIN IN SDL1 5'REGION PRECURSOR.
YIL169C OR YI9402.07C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z46921; CAA87023.1; -. SGD; S0001431; YIL169C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; SIGNAL 1 23
                                                                                                                                                                                                                                                                                    308
                              394 NINGD-----PKNKEYTG-TILFSGEKSLANDPRDFKST-IPQNVNLSAGYLVIKEGAEV
                                                                                                               431
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-ISGNLYLHYPDT--FTGQTVVFKGEGVLAVDPTETNATPIP----VVGY------
                                                                                                            SGAFSFSNAI - - LNGGSVSGLQRRDDTEGSVNNGEINLDNGSTYVIVEPVSGK - - GTVNI
                                                                                                                                                                                                                                                                              TLFIN-----NISYANSQNLGGAI-----AIDTGGEISLS---AEKGTITFQ--GN
                                                                                                                                                                     RTSLPFLNGIHLLQNAKFLKLQAR-----
                                                                                                                                                                                                                              EFDISGENFDVTGNFNAEESAATSASIYSFTPSSFDNSGDISLSLSKSKKGEVTFSPYSN
                                                                                                                                                                                                                                                                                                                                              VVVAAGAK - - -
                                                                                                                                                                                                                                                                                                                                                                                                 LTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIMGGGAIYARKLSISSGGP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSATSNSLSSITSSASSASATASNSLSSSDGTIYLPTTTISGDLTLTGKVIA----TEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGATHSSGPLQIAVNQAEIRFAQNTAKNGSGGALY----SDGDIDIDQNAYVLFRENEA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDVSSSVSQSA-SSTSDVSSSVSQSASSTSGVSSSGSQSVSSASGSSSSFPQSTSSASTA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATARFSGFSTLSFIQSPGDI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVSDVSSSVSQSSSSASDVSSSVSQSASSTSDVSSSVSQSSSSASDVSSSVSQSSSSASD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVFDTSLSATTISLTPEDSFHGDSQNAERSYNVQA--GDVYSLTGDVSISNVDNSALNKA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEQGCLYSKNALMLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYDSVSFYQ---NAATF 192
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28
35
468
664
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22.1%; Pred. No. 0.029;
ative 73; Mismatches 220;
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                                                                                                                                                                                                                                                                                                                                           -----LTLLDGDKYSFSADLKVYGD--LLVKKSKETYPGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.

HYPOTHETICAL PROTEIN YIL169C.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                               -----NGCSIEFYDPITSEADGSTQL 393
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447 TVSKFTQSPGSHLVLDLGTKLIASKEDIAITGLAIDIDSLSSSTAAVIKANTANKQIS 505	Ъ		Qy
AITGLAIDIDSLSSSSTAAVIKANTANKOI	530TGKNQI		н
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Search completed: October 2, 2001, 03:32:18 Job time: 253 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                          SPTREMBL_16:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_bhage:*
10: sp_plant:*
11: sp_rodent:*
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13: sp_virus:*
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4814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425026 segs, 132305027 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                            sp_human:*
sp_invertebrate:*
sp_manmal:*
sp_mhc:*
                                                                                                                                                                        sp_organelle:*
sp_phage:*
                                                                        sp_unclassified:*
sp_vertebrate:*
sp_virus:*
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# SUMMARIES

ţ	10	18	17	16	15	14	13	12	11	10	9	8	7	0	U	4	w	2		Result
	1117 5	1137.5	1202	1242	1249	1258	1344	1344	1353	1393	1400.5	1400.5	1432	1434	1441	1516	4790	4794	4814	Score
	2				25.9	26.1	27.9	27.9	28.1	28.9	29.1	29.1	29.7	29.8	29.9	31.5	99.5	99.6	100.0	Query Match
999	005	973	846	839	772	847	949	928	914	928	936	936	930	930	928	926	922	922	922	Length
	J	N	N	N	2	N	2	N	N	N	N	N	2	N	2	N	N	N	N	BIG
007601	700001	092896	P71133	P77792	Q9RB71	P71132	Q9K299	086164	086163	Q9RB65	Q9JS42	Q9Z898	Q9Z393	Q9RB66	Q9Z398	P71135	Q9K1Y9	Q9Z9G5	Q9Z4H9	ID
Ø77.291	00533	09z896	P71133	P77792	Q9rb71	P71132	Q9k299	086164	086163	Q9rb65	Q9js42	868z6Ö	Q9z393	Q9rb66	Q9z398	P71135	Q9k1y9	Q9z9g5	Q9z4h9	Description
Cirrailly dra p	ablamidia a	chlamydia p	chlamydia	chlamydia	chlamydia	ption														

45	44	<b>4</b> 3	42	41	40	39	38	3 <b>7</b>	36	35	34	33	32	31	30	. 29	28	27	26	25	24	23	22	21	20
558.5	559	561	569.5	569.5	569.5	574	576.5	577	577	581	581	610	610	610	629.5	678	720	727	774.5	796.5	901	951.5	1007	1060	1063.5
11.6							•	•	12.0	•		•		•		٠			•			9.		22.0	2
1672	983	1016	952	934	934	938	427	1609	1609	946	946	1732	1723	1723	359	649	445	878	867	712	987	1013	841	1276	1407
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Q9PJY2	Q9PL44	084880	Q9K2A5	Q9JSE7	Q9Z882	Q9Z883	Q9RB70	Q9Z6U5	Q9RB58	Q9RB60	Q9Z880	Q9K2C1	Q9RB59	Q9Z812	Q9JSK6	P71134	Q9RB67	084882	Q9PL41	Q9RB73	Q9PL45	084879	Q9Z3A1	Q9JRW2	Q9Z899
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## ALIGNMENTS

1 92449 92419; 1-MAY-1999 (TIEMBLIEL 10, Created) 1-MAY-1999 (TIEMBLIEL 10, Last sequence update) 1-MAY-1999 (TIEMBLIEL 10, La	ОУ	Db Db	Que Bes Mat		RESULT Q9Z4H9 ID Q
ပ	DVSISNVDNSALNKACFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATARF	MRESLCGFPLVESLTLLSVEDTSLSATTISLTPEDSFHGDSQNAERSYNVQAGDVYSLTG 	.0%; Score 4814; DB 2; Length 922; .0%; Pred. No. 0; O; Mismatches 0; Indels 0;	1999 (TrEMBLrel. 10, Created) 1999 (TrEMBLrel. 10, Last sequence update) 2001 (TrEMBLrel. 16, Last annotation update) MEMBRANE PROTEIN 6 PRECURSOR.  His pneumoniae (Chlamydophila pneumoniae).  Las: Chlamydiales; Chlamydiaceae; Chlamydophila.  EE FROM N.A.  PK1310;  LVR1310;  LVR1310;  S. Boesen T. Daugaard L., Knudsen K., Madsen A.,  axid—83558;  Long J. Daugaard L., Knudsen K., Madsen A.,  axid proteins containing the GGAI-repeat belong to a  transporting pathogenicity factors.";  ted (JAN-1999) to the EMBL/GenBank/DDBJ databases.  ALI33035; CAB37075.1;  TO; IPR003357;  PF023415; DUF145; 1.  POTENTIAL.  POTENTIAL.  POTENTIAL.	1 9z4h9 Preliminary; Prt;

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Chlamydia
Bacteria;
                    SEQUENCE FROM STRAIN=CWL029
                                                                            NCBI_TaxID=83558;
  MEDLINE-99206606;
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  PubMed=10192388;
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X Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouc Shirai M., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
X Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
X Comparison of whole genome sequences of Chlamydia pneumonia from Japan and CWL029 from USA.";
X Nucleic Acids Res. 28:2311-2314(2000).
X REMBL; AE001585; AAD18163.1; -.
X REMBL; AE001585; BAA98215.1; -.
X RINTERPO; IPR003357; -.
X RINTERPO; IPR003357; -.
X RINTERPO; IPR003358; -.
X RINTERPO; IPR003358; -.
X Pfam; PF02385; OMP; 1.
X Pfam; PF02415; DUF145; 1.
X SEQUENCE 922 AA; 100457 MW; DFF2AB6333AB031C CRC64;
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Olinger L., Grimwood J., Davis R.W.,
"Comparative genomes of Chlamydia pne
Nat. Genet. 21:385-389(1999).
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                                             WGNAVDVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNN
                                                         WGNAVNVRSLMQVQETHASSLQTDRGLWIDGIGNEFHVSASEDNIRYRHNSGGYVLSVNN
                                                                                            GGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKVGEFFWDKINYKPRPEKEGNLVPNIL
                                                                                                         GGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKVGEFFWDKINYKPRPEKEGNLVPNIL
                                                                                                                                                         IDIDSLSSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDLRMRNSQTFPLLSLEPGA
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Q9K1Y9;
01-OCT-2000
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01-MAR-2001
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J. McClarty G., Salberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
SEQUENCE 922 AA; 100480
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TIGR;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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Longbottom D., Russell M., Dun
Submitted (SEP-1996) to the EM
EMBL; U72499; AABIB188.1; -.
InterPro; IPR003357; -.
InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02315; OMP; 1.
Pfam; PF02415; DUF145; 1.
SEQUENCE 926 AA; 98439 MW;
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01-FEB-1997 (TREMBLrel. 02, Created)
01-FEB-1997 (TREMBLrel. 02, Last sequence up
01-FEB-1997 (TREMBLrel. 16, Last annotation
20TATIVE 98 KDA OUTER MEMBRANE PROTEIN.
Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlam
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98439 MW;
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                                                                                                                                       ATNLARQAFIVRAGNHIALTSGVEMFSQFGFELRSSSRNYNVDLGAKVAF
                                                                                                                                                                                                                                                                                                                                          VYYQHVSKFDDLTRLFN-GPNTCCSGFSKEI---PI----FLDAQITYCHTANNMTTSYT
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Last sequence update)
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Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AE001628; AAD18591.1;
EMBL; AJ133034; CAB37069.1;
EMBL; AP002546; BAA98655.1;
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Nat. Genet. 21:385-389(1999).
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
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OUTER MEMBRANE PROTEIN PRECURSOR (POLYMORPHIC MEMBRANE PROTEIN
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InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
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LTGDVSITNAGSPTALTASCFKETTGNLSFQGHGYQFLLQNIDAGAN-----CTFTNT
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                                                                        LTGDVSISNVDN-SALNKACFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQA
                                                                                                                       MKSSLHWFLISSSLALPLSLNFSAFAAVVEINLGPTNSFSGPGTYTPPAQTTNADGTIYN
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59; Mismatches
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OUTER MEMBRANE PROTEIN
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Nakazawa T.;
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Kishi F.,

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Craven B.,

Fan J.,

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CRC64;

Length

Indels

70;

Gaps

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Q9RB66 PRELIMINARY;
Q9RB66;
Q9RB66;
Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 13, L
Q1-MAR-2001 (TrEMBLrel. 16, L
POLYMORPHIC OUTER MEMBRANE PR
                                                                                       PROTEIN G FAMILY).

PMP_B OR CP0307.
Chlamydia pneumoniae (Chlamydophila pnobacteria; Chlamydiales; Chlamydiaceae;
MEDLINE=20330349; PubMed=10871362; Shirai M., Hirakawa H., Kimoto M.,
                             STRAIN-J138
                                             SEQUENCE FROM N.A.
                                                                         NCBI_TaxID=83558
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InterPro; IPR003368; -.
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Pfam; PF02415; DUF145; 1.
SEQUENCE 930 AA; 97639 M
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White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B
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EMBL; AP002246; BAA98654.1; -.
EMBL; AP002745; BAA98854.1; -.
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Nucleic Acids Res. 28:2311-2314(2000).
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Q1-MAY-1999 (TrEMBLrel. 10, Last sequence upda-
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation up-
Q1-MAR-2001 (TrEMBLrel. 11 PRECURSOR.

QMP11 OR PMP_8.

Chlamydia pneumoniae (Chlamydophila pneumoniae Chlamydiaceae; Chla
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SIGNAL
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"Chlamydia proteins containing the GGAI-repeat belong of autotransporting pathogenicity factors.";
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Pred. No. 2.9e-85;
7; Mismatches 395
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OUTER MEMBRANE PROTEIN 11.
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POLYMORPHIC
                                    Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
NCBI_TaxID-83558;
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EMBL; AE001627; AAD18589.1; -.
InterPro; IPR003357; -.
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               WRNNCWAIECGGSMPLLVFENGRLFQGAIPFMKLQLVYAYQGDFKETTADGRRFSNGSLT
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WRNDAFCADLGASLP-FVISVPYLLKEVEPFVKVQYIYAHQQDFYERHAEGRAFNKSELI
                                                                                                                                 HGFRHISGGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGDTYGASLYFHHTEGL
                                                                                                                                                              IRYRHNSGGYVLSVNNEITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSL
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InterPro; IPRO03357; -.
InterPro; IPRO03358; -.
Pfam; PF02385; OMP; 1.
Pfam; PF024815; DUF145; 1.
ProDom; PD004952; -; 1.
SEQUENCE 936 AA; 100105 M
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O9JS42;
01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-MAR-2001 (TremBLrel. 16, Last annotation update)
POLYMORPHIC OUTER MEMBRANE PROTEIN G FAMILY (POLYMORPHIC PROTEIN G FAMILY)
PMP_7 OR CP0308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B. Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay W., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AP002546; BAA98653.1; -.
EMBL; AP002546; BAA98653.1; -.
EMBL; AP00261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20330349; PubMed=10871362; Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa "Comparison of whole genome sequences of Chlamydia pfrom Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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SFYQNAA---TEGGAIHSSGPLQIAVNQAEIRFAQNTAKNGSGGALYSDGDIDIDQNAYV
                                                                                                                                                                                                                                                                                                                 PLFSSLSIVAA-EVTLDSSNNSY---DGSNGTTFTVFSTTDAAAGTTYSLLSDVSFQNAG
                                                                                   SIISCPSLLLSPTGQCALKSVGNLSLTGNSQIIFTQNFSSDNGGVINTKNFLLSGTSQFA
                                                                                                                                           SFIQSPGDIKE---QGCLYSKNALMLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYDSV
                                                                                                                                                                                                   ALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSS-AGTVASTSAADKNLLFNDFSRL
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35.9%; Pred. No. 3.4e-83;
"1-6. Mismatches 391;
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                        MEDLINE=20330349; PubMed=10871362; Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneum from Japan and CWL029 from USA.";
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Q9RB65; Q9RB64; Q9S6P2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
POLYMORPHIC OUTER MEMBRANE PROTEIN G FAMILY (OUTER MEMBRANE PRECURSOR) (POLYMORPHIC MEMBRANE PROTEIN G FAMILY).
PMP_10 OR OMP5 OR CP0303.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydop
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heid White O., Hickey E.K., Peterson J., Umayam L.A., Berry K., Bass S., Linher K., Weldman J., Khouri Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy McClarty G., Salzberg S.L., Eisen J., Fraser C.M. "Genome sequences of Chlamydia trachomatis MoPn a pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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DLGKTQDFSFVQL--SALGTATTTDVPAVPTVATPTHYGYQGTWGMTWVDDTASTPKTKT
                                               RMRNSQTFPLLSLEPGAGGSVTVTAGDFLP---VSPHYGFQGNWKLAW-----TGTGNKV
                                                                                                       GTTLKASTEEVTLTGLSIPVDSLGEGK-KVVIAASAASKNVALSGPILLLDNQGNAYENH
                                                                                                                                   GTKLIASKEDIAITGLAIDIDSLSSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDL
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L.A., Utterback T.,
houri H., Craven B.,
DeBoy R., Kolonay J.,
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Best Local :
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SEQUENCE
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SIGNAL
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STRAIN-CDC/CWL-029/VR-1310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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                                                                                                                                    V-DNSALNKACFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATARFSGFST 125
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LTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGAISTKNLSLKNSTG
                                         LSFIQSPGDI-----KEQGCLYSKNALMLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYD 181
                                                                                        LGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKS--SAEGAALSVTTDK-NLSLTGFSS
                                                                                                                                                                                     LVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNTTTGIDYTLTGDITLQN
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Chlamydia pneumoniae (C. Bacteria; Chlamydiales;
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01-NOV-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
OUTER MEMBRANE PROTEIN 4
                           SEQUENCE FROM N.A.

STRAIN-CDC/CWI-029/VR-1310;

STRAIN-CDC/CWI-029/VR-1310;

Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelu "Identification of two novel genes encoding outer membrane c "Identification of two novel genes encoding outer membrane c associated surface layer proteins in Chlamydia pneumoniae.";
                   Submitted
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EMBL; AJ001311; CAA04672.1; -. EMBL; AJ013034; CAB37072.1; -. EMBL; AJ03034; CAB37072.1; -. EMBL; AD00128; AAD18593.1; -. EMBL; AP002546; BAA98658.1; -. Interpro; IPR003357; -.
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InterPro; IPR003368; -.
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Claim 7; Page 63-65; 115pp; English.

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This polypeptide comprises the novel 97.6 kDa surface exposed compromentation ompil of the human respiratory pathogen Chlamydia CC protein Ompil of the human respiratory pathogen Chlamydia CC preumoniae. Its amino acid sequence was deduced from DNA (see CC AAX06823) isolated from a C. pneumoniae expression library. The CC invention provides 12 novel surface exposed proteins, Omp4-Ompi5 CC (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia CC pneumoniae. The test comprises detecting antibodies specific for CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer CC membrane proteins, especially by PCX. The proteins are also used CC in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of CC waccines for effecting in vivo expression of antipgens. The vaccines for effecting in vivo expression of antipgens. The which are possibly associated with C. pneumoniae.

XX Sequence 930 AA;
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Query Match 42.2%; Score 2024; DB 20; Length 930; Best Local Similarity 44.5%; Pred. No. 8.3e-125; Matches 423; Conservative 158; Mismatches 326; Indels 44; Gaps 17; 1 MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNT--TTGIDYT 58

Дb δÃ 망 QΥ В Ωy 밁 δÃ 120 118 178 ktlsisgntssitftsnsak---klggaiyssaaasisgntgqlvfmnnkgetgggalgf 60  $\vdash$ KNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPTLFSNNIAEAAGGAINS tftgfsnlsfiaapgt--tvasgkstlssagalnltdngtilfsqnvsneannnggaitt SLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEE---NGGAIST MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNT--TTGIDYT 117 234 177 119 234 59

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643 WAAGVANFLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENLISFAFCQLFGSDKDFLVAKN 70

586 --tstaksgtmtwvttgynpnperrasvvpdslwasftdirtlqqimtsqansiyqqrgl

643

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RESULT 1
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20-AUG-1998;
20-AUG-1998;
20-AUG-1998;
27-AUG-1998;
                                                                                                                                                                                                              mammals,
                     external vicinity of the membrane structure, in the inclusion membrane structure, in the external vicinity of the inclusion membrane structure, and in the cytoplasm of the infected cell. The polypeptides may be
                                                                                          AAY69362-69 represent Chlamydia pneumoniae polypeptides. The polypeptides are present in the bacterial membrane structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia
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used to prevent,
                                                                                                                                                                                                                                 Novel antigens and corresponding DNA molecules that can prevent, treat and diagnose disease caused by Chlamydia
                                                                                                                                                                                                                                                                                                                                                                             Murdin
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RQDSFSEKGTEGRSFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPDLIRNDPKCT
                                                         {\tt syshrnndmktkyttypeaqgswandvfglefgattyyypnstflfdyyspflrlqctya}
                                                                                        AYSHVSNDLKTKYTAYPEVKGSWGNNAFNMMLGASSHSYPEYLHCFDTYAPYIKLNLTYI
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                                                                                                                                                                                                                       This polypeptide comprises the novel 98.4 kba surface exposed protein Omp10 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAX06822) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAX06817-28), and nucleic acid sequences encoding them (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of waccines may also prevent atheroscierosis and bronchial asthma, which are notes that a speciated with C. pneumoniae and bronchial asthma,
Query Match 40.3%;
Best Local Similarity 44.7%;
Matches 423; Conservative 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encocedute.
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                                                                                                                                               Sequence
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Pred. No. 1.1e-118;
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AAY90239 standard;

Protein;

AAY90239; 29-AUG-2000

(first entry)

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                                                     gdlinvsvpigitferfsrnerasyeatviyvadvyrknpdcttallinntswkttgtnl
                                                                      esswyndgcalelasslphtalsheglfhayfpfikveasyihqdsfkernttlvrsfds
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Chlamydia antigen

CPN100638.

Chlamydia

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Query Match
Best Local S
Matches 421
                                                                                                                                                                                                                                                                                                                                                        (PCR) assays. Antisense sequences may be used to treat infections. The expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
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01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is a Chlamydia antigen of the invention, designated CPN100638. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquired pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
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N-PSDB; AAA30851, AAA30852.
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NLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPTLFSNNIAEAAGGAINST
                                 llsfsgfsylsliqttnat----tgtgaikstgacsiqsnyscyfgqnfsndnggalqgs
                                                                                                    NLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGAISTK 175
                                                                                                                                          -YTLTGDITLQNLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKSSAEGAALSVTTDK 115
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upper respiratory tract disease; bronchitis; sinusitis;
c bronchitis; adult-onset asthma; acute exacerbations of asthma
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44.5%; Pred. No. 5.7e-118;
tive 151; Mismatches 338;
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Sequence 10, Application US/08617697
Patent No. 5977336
GENERAL INFORMATION:
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APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
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    Shoemaker and Mattare, Ltd.
    2001 Jefferson Davis Hwy., 1203 Crystal Plaza

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REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-APR-CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  1187 LVTTENAVINATSGTVNISTKTGDIKGGIESTSGNVNITASGNTLKVSNITGODVTVTAD 1246
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                                                                                                                                                                                                                                         1307 TADSGKLTSTYGSTINGTNSYTTSSQSGDIEGT-----ISGNTV----NYTASTGDL
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                                                                               1400 SSIAGN-INAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAASGDRTVVNATN 1458
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                                        495 SIGEGKKVVIAASAASKNV----ALSGPILLLDNQGNAYENHDLGKTQDFSFVQLSALG
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                                                                                                                  TLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDAGTTLKASTEEVTLTGLSI-----PVD 494
                                                                                                                                                             TIGNSAKVEAKNGAATLT---AESGKLTTQTGSSITS------SNGQTTLTAKD 1399
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01-APR-1996
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22.5%; Pred. No. 6.
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Sequence 10, App...
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Best Local Similarity
Matches 150; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 415-081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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  951 RSDSSEAENANLTIQTKELKLAGDLNISGFNKAEITAKNGSDLTIGNASGGNADAKKVTF 1010
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                                                                                891 TIINGNITNEKGDLNIKNIKADAEIQIGGNISQKEGNLTISSDKVNITNQITIKAGVEGG 950
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CLASSIFICATION: 424
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REGISTRATION NUMBER: 22,651
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                                                                                                                                                                                                             30 NIGPSDSFDGSTN----TGTYTPKNTTT----
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
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STREET: Bldg.
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                                       ----SSAEGAALSVTTDK-----NLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTF 152
                                                                                                                                                                 SIAEDSTFKGEASDNLNITGTFTNNGTANINIKQGVVKLQGDINNKGGLNITTNASGTQK 890
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Y: U.S.A.
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01 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                                                                                                                                                       6.0%; Score 285.5; DB 2; 22.4%; Pred. No. 7.5e-15;
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                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                       PRIOR APPLICATION DATA:
                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 16-SEP-1994
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1175 ADAGALTTTAGSTISATTGNANITTKTGDINGKVESSSGSVTLVATGATLAVGNISGNTV 1234
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                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1283 DLTIGNSAKVEAKNGAATLT---AESGKLTTQTGSSITS------SNGQTTLTA 1327
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2001 Jef:
STREET: Bldg. 1
CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 PVTLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDAGTTLKASTEEVTLTGLSI-----P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 FEGNKSSATGKKGGAICA-TGTVDITNNTAPTLFSNNIAEAAGGAIN---STGNCTITGN 243
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APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992
                                                                              APPLICATION NUMBER:
                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Virginia
                                                               FILING DATE:
                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                              22202-0286
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
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                                                             16-MAR-1993
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                                                                                                                                             US 08/302,832
                                                                                US PCT/US93/02166
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RESULT 5
US-08-728-470-9
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Sequence 9, Application US/08728470 Patent No. 5928651
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Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                        1440 PGVASVEEV 1448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berkstresser, Jerry W
REGISTION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1069
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TITADSGKLTSTVGSTINGTNSVTTSSQSGDIEGT-----ISGNTV----NVTASTG 1282
                                                                                                                                                                                                     TNASGSGN--VTAKTSSSVNITGDLNTINGLNIISENGRNTVRLR--GKEIDVKYIQ---
                                                                                                                                                                                                                                           VDSLGEGKKVVIAASAASKNV-----ALSGPILLLDNQGNAYENHDLGKTQDFSFVQLSA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLSAEAGDITFN-GNAIVATTPQTTKRNSIDIGSTAKITNLRAISGHSIFFYDPITANT- 390
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                                                                                                                                                             LGTATTTDV
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                                                                                                                                                                                                                                                                                                                                                                                                       -----AADSTDTLNLNKADAGNSTDYSGSIVFSGEKLSEDEAKVADNLTSTLKQ 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150;
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22.4%; Pred. No. 7.
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REGISTRATION NUMBER: 22,651
REFERENCE,DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                           875 TINISAAAGNVTTKEGTTINATTGSVEVT------AQNGTIKGNITSQNVTV
                                                                                                                                                                                                                                                                                                                                                                                 646 ANLQAITNYTFNVAGSFDNNGASNISIARGGAKFKDINNTSSL---NITTNSDTTYRTII 702
241 TGNTSLVFSENSV-TATAG------NGG--ALSGDADVTISGN----QSVTFSGN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB 9 FILING DATE: 16-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                   -ISFEGNKSSATGKKGGAICA-TGTVDITNNTAPTLFSNNIAEAAGGAIN---STGNCTI
                                                                                                                              VTFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGND--NSTGLTISAKDVTVNNNVTSHK 874
                                                                                                                                                                                                           EGGRSDSSEAENANLTIQTKELKLAGDLNISGFNKAEITAKNGSDLTIGNASGGNADAKK 816
                                                                                                                                                                                                                                                                                              KGNISNKSGDLNIIDKKSDAEIQIGGNISQKEGNLTISSDKVNITNQ-----ITIKAGV 756
                                                                                                                                                                                                                                                                                                                                        ----TGDITLQN-----LGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIK--- 101
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                                                                                                                                                                                                                                                       ----SSAEGAALSVTTDK-----NLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1338 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barenkamp, Stephen J
VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 5928651-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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)1 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%; Score 284.5; DB 2; 22.5%; pred. No. 7.3e-15; 22.5%; mismatches 223;
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                                                                                                                                                                    --- NNGTILFKQDYCEENGGAISTKNLSLKNSTGS-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                           920
                                                                                     240
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single

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US-08-719-641-9
; Sequence 9, Application US/08719641
; Patent No. 6218141
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                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1249
                                                                                                                    NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1089
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1193 VNATNASGSGN--VTAKTSSSVNITGDLNTINGLNIISENGRNTVRLR--GKEIDVKYIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1134 LTAKDSSIAGN-INAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAASGDRTV 1192
                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1041 NTVTITADSGKLTSTVGSTINGTNSVTTSSQSGDIEGT-----ISGNTV----NVTA 1088
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2001 Je
STREET: Bldg. 1
                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                        FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
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                 LENGTH:
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amino acid
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                   1338 amino acids
                                                                             (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                     (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556
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                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                    Sequence 9, Application US/08617697
Patent No. 5977336
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 151; Conserv
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                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           1249 --- PGVASVEEV 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                            1193 VNATNASGSGN--VTAKTSSSVNITGDLNTINGLNIISENGRNTVRLR--GKEIDVKYIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1041 NTVTITADSGKLTSTVGSTINGTNSVTTSSQSGDIEGT-----ISGNTV----NVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1089 STGDLTIGNSAKVEAKNGAATLT---AESGKLTTQTGSSITS------SNGQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 LKQPVTLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDAGTTLKASTEEVTLTGLSI-----
                                                                                                                                                                                                                                                                                                                                                                                                  545 LSALGTATTTDV 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     981 TVTADAGALTTTAGSTISATTGNANITTKTGDINGKVESSSGSVTLVATGATLAVGNISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 -ISFEGNKSSATGKKGGAICA-TGTVDITNNTAPTLFSNNIAEAAGGAIN---STGNCTI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646 ANLQAITNYTFNVAGSFDNNGASNISIARGGAKFKDINNTSSL---NITTNSDTTYRTII 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703 KGNISNKSGDLNIIDKKSDAEIQIGGNISQKEGNLTISSDKVNITNQ-----ITIKAGV
                                         STREET: 2001 Je
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 STLACFTSCSTVFAATAENIGPSD-----SFDGSTNTGTYTPKNTTTGIDYTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PVDSLGEGKKVVIAASAASKNV-----ALSGPILLLDNQGNAYENHDLGKTQDFSFVQ 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTAKDSSIAGN-INAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAASGDRTV 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NT-----AADSTDTLNLNKADAGNSTDYSGSIVFSGEKLSEDEAKVADNLTST 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAVANGGAI - - YAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAG - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGNTSLVFSENSV-TATAG-----NGG--ALSGDADVTISGN----QSVTFSGN | :| :| :| :| ::| ::| ::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TGDITLQN------LGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIK--- 101
Arlington : Virginia
                                                             2001 Jefferson
                                                                                                                                                                                         Barenkamp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 111; Mismatches 223;
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                                                      Shoemaker and Mattare, Ltd.
01 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.9%;
                                                                                                                                           High Molecular Weight Surface Proteins of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                       Stephen
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Pred. No. 7.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1338,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1040
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

COUNTRY:

22202-0286

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     1135
                                                                                                                                                                                                                                                              1181
1349 STGDLTIGNSAKVEAKNGAATLT---AESGKLTTQTGSSITS----
                                                                                  1301 NTVTITADSGKLTSTVGSTINGTNSVTTSSQSGDIEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                            1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/302,832 FILING DATE: 05-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697
FILLING DATE: 01-APR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                         389
                                                                                                                                                                                                                                                                                                                                                                                                 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
                                                                                                                                                                                                                283 QAVANGGAI--YAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAG-----
                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 LTFD------NNGTILFKQDYCEENGGAISTKNLSLKNSTGS-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      963 KGNISNKSGDLNIIDKKSDAEIQIGGNISQKEGNLTISSDKVNITNQ-----ITIKAGV 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           906 ANLQAITNYTENVAGSEDNNGASNISIARGGAKFKDINNTSSL---NITTNSDTTYRTII 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 STLACFTSCSTVFAATAENIGPSD------SFDGSTNTGTYTPKNTTTGIDYTL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                              -ECSLSAEAGDITFN-GNAIVATTPQTTKRNSIDIGSTAKITNLRAISGHSIFFYDPITA 388
                                                                                                                                                                       TVTADAGALTTTAGSTISATTGNANITTKTGDINGKVESSSGSVTLVATGATLAVGNISG 1300
                                                                                                                                                                                                                                                       TATENLYTTENAVINATSGTVNISTKTGDIKGGIESTSGNVNITASGNTLKVSNITGQDV 1240
                                      NT-----AADSTDTLNLNKADAGNSTDYSGSIVFSGEKLSEDEAKVADNLTST 436
                                                                                                                                                                                                                                                                                                     TGNTSLVFSENSV-TATAG-----NGG--ALSGDADVTISGN----QSVTFSGN 282
                                                                                                                                                                                                                                                                                                                                                 TINISAAAGNVTTKEGTTINATTGSVEVT------AQNGTIKGNITSQNVTV 1180
                                                                                                                                                                                                                                                                                                                                                                                            -ISFEGNKSSATGKKGGAICA-TGTVDITNNTAPTLFSNNIAEAAGGAIN---STGNCTI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGGRSDSSEAENANLTIQTKELKLAGDLNISGFNKAEITAKNGSDLTIGNASGGNADAKK 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TGDITLQN------LGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIK--- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                          VTFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGND--NSTGLTISAKDVTVNNNVTSHK 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SSAEGAALSVTTDK-----NLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151;
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                                                                                ISGNTV----NVTA 1348
---SNGQTT 1393
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33 PSDSFDGST---NTGTYT---PKNTTTGIDYTLTGDITLQNLGDSAALTKGCFSDTTESL 86

PSSGVSGSTLSLTTGTDTLTGTANNDTFVAGEVAGAATL-TVGDT--LSGGAGTDVLNWV 299

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Query Match 5.9%; Score 284; DB 2; Best Local Similarity 23.9%; Pred. No. 5.3e-15; Matches 187; Conservative 98; Mismatches 300
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APPLICANT: NO. 5976864ellini, J
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: HETEROLOGOU
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1509 --- PGVASVEEV 1517
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: Fish & Richardson PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
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CLASSIFICATION: 435
APPLICATION NUMBER: US 07
FILING DATE: 09-JUNE-1992
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CITY: Boston
                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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15976864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTAKDSSIAGN-INAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAASGDRTV 1452
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POLYPEPTIDES FROM CAULOBACTER
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        Mismatches 300;
                                                                         Length 1026;
        Indels 198;
    Gaps
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RESULT 9
US-09-142-648B-7
  SOFTWARE: Fas
SEQ ID NO 7
LENGTH: 1026
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                                                      APPLICANT: Bingle, Wade H.

APPLICANT: NO. 6210948ellini, John F.

APPLICANT: NO. 6210948ellini, John F.

TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULA

FILLE REFERENCE: 08106/002002

CURRENT EPLICATION NUMBER: US/09/142,648B

CURRENT EPLING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: PCT/CA97/00167

PRIOR APPLICATION NUMBER: US 07/614,377

PRIOR APPLICATION NUMBER: US 07/614,377

PRIOR FILING DATE: 1996-03-12

NUMBER OF SEQ ID NOS: 12
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFV 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKLSEDEAKVADNLTSTLKQPVTLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDAGTTLKA 479
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                                             FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                            Smit, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GAGADTLYYTGGTDTFTGGTGADIFDINAIGTST
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                                                                                                        RESULT 10
US-08-038-682-2
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                                      Sequence 2, Application US/08038682 Patent No. 5549897 GENERAL INFORMATION:
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Best Local Similarity
Matches 187; Conserv
APPLICANT:
                                                                                                                                                                                                 917 AFV 919
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                                                                                                                                                                                                                                             GFI 723
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                                                                                                                                                                                                                                                                                      AGADSLTGSA-TANDTIIG------GAGADTLVYTGGTDTFTGGTGADIFDINAIGTST
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                                                                                                                                                                                                                                                                                                                                                                                                                   ROGPLVPNSLWGSFSDIQAIQGVIERSALTLCSDRGFWAAGVANFLDKDKKGEKRKYRHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GGSV---NGGDGTDVLVANVNGSSFSADPAFGGFETLRVAGAAAQGSHN---
BARENKAMP, STEPHEN J
ST. GEME III, JOSEPH
                                                                                                                                                                                                                                                                                                                                                                          NTAVTSF-DASAVTGT--APAVTFVS
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Pred. No. 5.3e-15;
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Best Local Similarity 25.5%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
                                                                                         1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
1341 AGSINAANVTL-----NTTGTLTTVKGSNINATSGTLV----INAKDA----
                                                                                                                                                                                1222 ESVTTSSQSGDIGGTISGGTVEVKATESLTTQSNSKIKATTGEANVTSATGTIGG-TISG 1280
                                                                                                                                                                                                                                                                              1172 L-----GGIESSSGSVTLTATEGALAVSNISGNTVTVTA-NSGALTTLAGSTIKGT 1221
                                                                                                                                                                                                                                                                                                                                                                         1112 SSDNNAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTINATTGNVEITAQTGSI 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1056 KDGSDLTIGNTNSADGTNAKKYTFNQVKDSKISADGHKYTLHSKVETSGSNNNT----ED 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2001 Jet:
STREET: Bldg. 1
CITY: Arlington
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                                                                                                                                                                                                                                                                                                                            219 LFSNNIAEAAGGAINSTGNCTITGNTSLV----FSENSVTATAGNGGALSGDADVTISGN 274
                                                                                                                                                                                                                                                                                                                                                                                                                       164 YCEENGG-AISTKNLSLKNSTGS---ISFEGNKSSATGKKGGAICA-TGTVDITNNTAPT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        936 ARFKDIDNSKNLSITTNSSSTYRTIISGNITNKNGDLNITNEGSDTEMQIGGDVSQKEGN 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AEGAALSVTTDKNLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            996 LTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITA 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 ATAENIGPSDSFDGSTN-----TGTYTPKN----TTTTGID--YTLTGDITLQ--N 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                      TFNGNAIVATTPQTTKRNSIDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLN 401
                                                                                      NTVNVTANAGDLTVGNGAEINATEGAATLTTSSGKLTTEASSHITSAKGQVNLSAQDGSV 1340
                                                                                                                                  NIVQGT-----TAGNGGAISIL----
                                                                                                                                                                                                                                QSVTFSGNQ----AVANGGAIYAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139;
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                                                                                                             -----KLTLASGGGGGISFSN 310
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                                                                                                                                                                                                                                            Matches 139;
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US POSITION OF THE PROPERTY AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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1056 KDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTLHSKVETSGSNNNT----ED 1111
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                                       104 AEGAALSVTTDKNLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQD 163
                                                                            996 LTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITA 1055
                                                                                                                                                         936 ARFKDIDNSKNLSITTNSSSTYRTIISGNITNKNGDLNITNEGSDTEMQIGGDVSQKEGN 995
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                 26 ATAENIGPSDSFDGSTN-----TGTYTPKN-----TTTGID--YTLTGDITLQ--N 67
                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 16-SE
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 22,651
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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VENTION: High Molecular Weight Surface Prote
VENTION: of No. 5603938-Typeable Haemophilus
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                     linear
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Pred. No. 1.3e-12;
                                                                                                                                                                                                                                            Mismatches 184;
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                                                                                                                                                 TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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              MOLECULE TYPE:
                                    LENGTH: 1536 amino
TYPE: amino acid
STRANDEDNESS: sin
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STREET: Bldg. 1
CITY: Arlington
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                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 22202-0286
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                                 TOPOLOGY:
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01 Jefferson Davis Hwy., 1203 Crystal Plaza
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Best Local Similarity
Matches 139; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,880
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
NUMBER OF SEQUENCES: 8
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1341 AGSINAANVTL-----NTTGTLTTVKGSNINATSGTLV-----INAKDA-----ELN 1382
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                                                                                                                                                                                                                                                             ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bidg. 1
CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 22202-0286
                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 L---GDSAALTK------SCFSDTTESLSFAGKGYSLSF---LNIK-----SS 103
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Pred. No. 1.3e-12;
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                                                                                                             Version
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US-08-728-470-2; Sequence 2, A
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
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APPLICATION NUMBER:
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REGISTRATION NUMBER: 22,651
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                                                                                              VLLKG 1438
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                                                                                                                                                                                                               KADAG-----NSTDYSGSIVFSGEKLSEDEAKVADNLTSTLKQPVTLTAGNLVLKRGV-T 455
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                                                                                                                                                                                                                                                                                            TENGNAIVATTPQTTKRNSIDIGSTAKITNLRAISGHSIEFYDPITANTAADSTDTLNLN 401
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Application US/08728470
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16-SEP-1994
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                                                                                                                                                                             -SGSVIATTSSRV--NITGDL---ITINGLNIISKNGINT 1433
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Pred. No. 1.3e-12;
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Best Local Similarity
Matches 139; Conserv
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GENERAL INFORMATION:
APPLICANT: Barenk
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FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9:
FILING DATE: 16-MAR-1992
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MEDLUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 01 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA:
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                             164 YCEENGG-AISTKNLSLKNSTGS---ISFEGNKSSATGKKGGAICA-TGTVDITNNTAPT 218
                                                                                                                                                                                                                                                                                                                                                     936 ARFKDIDNSKNLSITTNSSSTYRTIISGNITNKNGDLNITNEGSDTEMQIGGDVSQKEGN 995
                                        219 LFSNNIAEAAGGAINSTGNCTITGNTSLV----FSENSVTATAGNGGALSGDADVTISGN 274
                                                                                                                                                                                                                                                                 996 LTISSDKINITKQITIKAGYDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITA 1055
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                              26 ATAENIGPSDSTDGSTN-----TGTYTPKN----TTTGID--YTLTGDITLQ--N 67
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TOPOLOGY: lir
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                                                                                 SSDNNAGLTIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTINATTGNVEITAQTGSI 1171
                                                                                                                                                                        KDGSDLTIGNTNSADGTNAKKVTFNQVKDSKISADGHKVTLHSKVETSGSNNNT----ED
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GGIESSSGSVTLTATEGALAVSNISGNTVTVTA-NSGALTTLAGSTIKGT 1221
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Pred. No. 1
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US-08-617-697-2
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    Query Match
Best Local Similarity
Matches 139; Conserv
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                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US PCT/US:
APPLICATION NUMBER: US PCT/US:
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BerKstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                          TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/617,697 FILING DATE: 01-APR-1996 CLASSIFICATION: 424
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STREET: Bldg.
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16-MAR-1993
                                                                                                                                DNA (genomic)
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5.4%; Score 259; DB 2; Length 1536; 25.5%; Pred. No. 1.3e-12; tive 70; Mismatches 184; Indels 152;
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Compugen Ltd

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## ALIGNMENTS

polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae (st C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001 C;Accession: 686546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000 N;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349 A;Reterences: A86491; MUID:20330349 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-928 <STO> A;Cross-references: GB:BA000008; NID:g8978821; PIDN:BAA98657.1; GSPDB:GN00142 A;Experimental source: strain J138 C;Genetics: A;Gene: pmp\_10 Ş 밁 ğ В õ 밁 B Q δÃ 밁 γQ В δã RESULT Matches 928; Query Match Best Local Similarity 361 241 301 301 241 181 121 121 61 61 TGNTSLVFSENSYTATAGNGGALSGDADYTISGNQSVTFSGNQAVANGGAIYAKKLTLAS IDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLNKADAGNSTDYSGSIVFSGE Conservative 100.0%; Score 4795; DB 2; 100.0%; Pred. No. 1.2e-256; 0; Mismatches 0 Length Indels 928; 0; Gaps 420 60 360 360 300 240 60 300 240 0; (st

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IDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLNKADAGNSTDYSGSIVFSGE

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polymorphic membrane protein G family CP0303 [imported C;Species: Chlamydophila pneumoniae, Chlamydia pneumon C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #te C;Accession: G81591

R;Read, T.D.; Brunham, R.C.; Shen, C; Gill, S.R.; Hel C; Dodson, R; Gwinn, M; Nelson, W; DeBoy, R.; Kc Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoF A;Reference number: A81500; MUID:20150255

A;Accession: G81591

A;Residues: 1-928 <REA>
A;Cross-references: GB;AE002192; GB;AE002161; NID:9718

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polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain c;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 05-May-2000 C;Accession: D72078 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grim Nature Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Beference number: A72000; MUID:99206606 A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-930 <ARN>
A;Cross-references: GB:AE001627; GB:AE001363; NID:g4376721;
A;Experimental source: Strain CWL029
C;Genetics:
A;Gene: pmp\_8 PIDN: AAD18590.1;

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Local Similarity 44.6%; Pred. No. 1.9e-104;
hes 424; Conservative 158; Mismatches 325;
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C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: D86546
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.;
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Accession: D86546
A;Status; preliminary
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A; Cross-references: GB:BA000008; NID:g8978818; A; Experimental source: Strain J138 C; Genetics: A; Gene: pmp_8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 --TSTAKSGTMTWVTTGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGL
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mes 423; Conserv
                                               HTDTYAGAFYIQHITECSGF----IGCLLDKLPGSWSHKPLVLEGQLAYSHVSNDLKTKY 758
                                                                                                                           WAAGVANFLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENLISFAFCQLFGSDKDFLVAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSHNYLASLYLQHRAFLGGLPMPSFGSITDML----KDIPLILNAQLSYSYTKNDMDTRY
                                                                                                                                                                                                                                                                                                                                                                                                LMQPGTKLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTITLTSPLVFQDSSGNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIYAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITFNGNAIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTLSISGNTSSITFTSNSAK---KLGGAIYSSAAASISGNTGQLVFMNNKGETGGGALGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASTPKTKTATLAWTUTGYLPNPERQGPLVPNSLWGSFSDIQAIQGVIERSALTLCSDRGF
                                                                                                                                                                                                                                                                                                                                                ENHDLGKTQDFSFVQLSALGTATTT-----DVPAVPTVATP-THYGYQGTWGMTWVDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMDAGTTLKASTEEVTLTGLSIPVDSLGEGKKVVIAASAASKNVALSGPILLLDNQGNAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AICAHGLDLSA--AGPTLFSNNRCGNTAAGKGGAIAIADSGSLSLSANQGDITFLGNTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EASSSITQNSSLFFSGNTATDAAGKGGAIYCEKTGETPTLTISGNKSLTFAENSSYTQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFTGFSNLSFIAAPGT--TVASGKSTLSSAGALNLTDNGTILFSQNVSNEANNNGGAITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNT--TTGIDYT 58
                                                                                                 WASGTANFFHKDKSGTNQAFRHKSYGYIVGGSAEDFSENIFSVAFCQLFGKDKDLFIVEN
                                                                                                                                                                                                                                                                                                    ESHTINQ----AFTQPLVVFTAATAASDIYIDALLTSPVQTPEPHYGYQGHWEATWAD--
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A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A; Reference number: A81500; MUID:20150255
A; Accession: A81591
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-930 < REA>
A; Cross-references: GB:AE002193; GB:AE002161; NID:g7189234; PIDN:AAF38164.1; PID:g718923
A; Experimental source: strain AR39, HL cells
C; Genetics:
C; Genetics:
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A;Title: Genome sequences of Chlamydia trachomatis A;Reference number: A81500; MUID:20150255
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                                                                                                                                                                                                                                                                                        LCKNLARQAFLASAGSHLTLSPHVELSGEAAYELRGSAHIYNVDCGLRYSF 930
                                                            IMDAGTTLKASTEEVTLTGLSIPVDSLGEGKKVVIAASAASKNVALSGPILLLDNQGNAY
                                                                                                                         DYSGTIVFSGEKLSADEAKAADNFTSILKQPLALASGTLALKGNVELDVNGFTQTEGSTL
                                                                                                                                                                                                                                                             STSAPTSTRNAIYLGSSAKITNLRAAQGQSIYFYDPIASNTTG-ASDVLTINQPDSNSPL
                                                                                                                                                                                                                                                                                                                                                                                          AICAHGLDLSA--AGPTLFSNNRCGNTAAGKGGAIAIADSGSLSLSANQGDITFLGNTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIYAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITFNGNAIV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTGDITLQNLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKS-SAEGAALSVTTDKNL 117
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Boy, R.;
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Kolonay, J.; McClarty, G.;
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polymorphic outer membrane protein G/I family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: E86546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T. Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349 A;Accession: E86546
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A;Residues: 1-928 <570>
A;Cross-references: GB:BA000008; NID:g8978819;
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_9
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                                                                                               MKSQFSWLVLSSTLACFTSCS-TVFAATAE-NIGPSDSFDGSTNTGTYTPKNTTTGID--
ASSFISSNKAISFINNSVTATSATGGAIYCSSTSAPKPVLTLSDNGELNFIGNTAITSGG
                   GNCTITGNTSLYFSENSYTATAGNGGAL---SGDAD---YTISGNQSYTFSGNQAYANGG
                                                                           SISL-SLNPNLTFAKNKAT----QKGGALYSTGGITINNTLNSASFSENTAANNGGAIYTE
                                                                                                                                                       LLSFSGFSYLSLIQTTNAT----TGTGAIKSTGACSIQSNYSCYFGQNFSNDNGGALQGS
                                                                                                                                                                                        NLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGAISTK 175
                                                                                                                                                                                                                                IYNLTGDVSITNAGSPTALTASCFKETTGNLSFQGHGYQFLLQNIDAGANCTFTNTAANK
                                                                                                                                                                                                                                                                    -YTLTGDITLQNLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKSSAEGAALSVTTDK 115
                                                                                                                                                                                                                                                                                                          MKSSLHWFLISSSLALPLSLNFSAFAAVVEINLGPTNSFSG---PGTYTPPAQTTNADGT
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44.5%; Pred. No. 1.9e-98;
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A; Residues: 1-928 <REA>
A; Cross-references: GB: AEO02192; GB: AE002161;
A: Cross-references: strain AR39, HL cells
                                                                                                             A;Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:AAD18591.1; PID:g437673 A:Experimental source: strain CWL029 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
A;Accession: B81592
                                                                                                                                                                                                                                                                                                                              polymorphic membrane protein G family CP0306 [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change l1-May-2000 C;Accession: B72077; B81592 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood Nature Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
A; Experimental source: C; Genetics: A; Gene: pmp_9; CP0306
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A; Residues: 1-928 <ARN>
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                                                    NID: 97189226;
                                                        PIDN:AAF38163.1;
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                                                                                                                                                          SROAGIGRAGIFYAFSPNLEVTSNLSMEIRGSSRSYNADLGGKFOF
                                                     GDLINVSVPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTSWKTTGTNL
                                                                       SNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPDLIRNDPKCTTALVISGASWETYANNL
                                                                                                        ESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIKVEASYIHQDSFKERNTTLVRSFDS
                                                                                                                                KGSWGNNAFNMMLGAS-SHSYPEYLHCFDTYAPYIKLNLTYIRQDSFSEKGTE-GRSFDD
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44.5%; Pred. No. 1.9e-98;
tive 151; Mismatches 338;
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RESULT C72078

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polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain CWL029) c; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: C72078
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Recession: C72078
A;Recession: C72078
A;Status: preliminary
A;Molecula type: DNA
A;Residues: 1-936 <ARN>
A;Residues: 1-936 <ARN>
A;Cross-references: GB:AE001627; GB:AE001363; NID:94376721; PIDN:AAD18589.1; PID:9437672
A;Genetics:
A;Genetics: pmp_7
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Best Local Similarity 42.0%;
Matches 399; Conservative 17
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                                                                   GVANFLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENLISFAFCQLFGSDKDFLVAKNHTD
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                                                                                                                                                                                    YENHDLGKTQDFSFVQLSALGTATTTDVPAVPTVA---TPTHYGYQGTWGMTWVDDTAST 585
                                                                                                                                                                                                                                                                                  IEYGGAIVESGEKLSPTEKAIAANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQSPGSR
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TYGASLYFHHTEGLFDIANFLWGKATRAPWVLSEISQIIPLSFDAKFSYLHTDNHMKTYY
                          TYAGAFYIQH---ITECSGFIGCLLDKLPGSWSH----KPLVLEGQLAYSHVSNDLKTKY
                                                     GIANFFYRDSMPTRHGFRHISGGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGD
                                                                                                             --- KIGSINWTRTGYIPSPERKSNLPLNSLWGNFIDIRSINQLIETKSSGEPFERELWLS
                                                                                                                                                                    YENHNIKSASTYPILEITTAGANGTITIGALSTITIQEPETHYGYQGNWQISWANATSS-
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Pred. No. 1.2e-94;
'2; Mismatches 343;
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shi. Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-936 <STO>
A;Cross-references: GB:BA000008; NID:g8978817; PIDN:BAA98653.1; GSPDP.^w^^-
A;Sterimental source: strain J138
C;Genetics:
A;Gene: pmp_7
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Matches 399;
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                                             VIMDAGTTLKASTEEVTLTGLSIPVDSLGEGKKVVIAASAASKNVALSGPILLLDNQGNA 528
                                                                                      IEYGGAIVFSGEKLSPTEKAIAANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQSPGSR
                                                                                                          --TNGSTSTRNAINIIDTAKVTSIRAATGQSIYFYDPITNPGTAASTDTLNLNLADANSE
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polymorphic membrane protein G family CP0308 [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: B81591
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hic, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salz Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR A;Reference number: A81500; MUID:20150255
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A; Residues: 1-936 < REA>
A; Cross-references: GB: AE002193;
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42.0%; Pred. No. 1.4e-94;
tive 172; Mismatches 343
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A;Molecule type: DNA
A;Residues: 1-772 <570>
A;Cross-references: GB:BA000008; NID:g8978389;
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_3_2
                                                                                                                                                                                           C;Accession: H86492
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuch
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences
A;Reference number: A86491; MUID:20330349
A;Accession: H86492
                                                                                                                                                                                                                                                                                                                                                                   Pmp_3 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_
                                                                                                                                                                       A; Status: preliminary
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ILFKQDYCEENGGAISTKNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAP 217
                                            Similarity 48.79; Conservative
                                                      38.1%; Score 1827.5; DB 2;
48.2%; Pred. No. 3.1e-93;
                                            Mismatches
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polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: H86546
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shib Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Accession: H86546
A;Status: preliminary A;Molecule type: DNA
A;Residues: 1-928 <STOO
A;Cross-references: GB:BA000008; NID:g8978822; PIDN:BAA98658.1; GSPDB:GN00142
A;Experimental source: strain J138
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WKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF
                                                             SDGRGESIGRLLNLSIPYGAKEYQGDIGDSYTYDLSGFFYSDYYRNNPQSTATLYMSPDS
                                                                                TEGRSFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPDLIRNDPKCTTALVISGAS
                                                                                                                                SLPESEGSWSNECIAGGIGLDLPFVLSNPHP----LFKTFIPQMKVEMVYVSQNSFFESS
                                                                                                                                                               AYPEVKGSWGNNAFNMMLGAS----SHSYPEYLHCFDTYAPYIKLNLTYIRODSFSEKG
                                                                                                                                                                                                TLFFKHSHTLQPQNYLRLGRAKFSESAIEKFP---REIPLALDVQVSFSHSDNRMETHYT
                                                                                                                                                                                                                                AFYIQHITEC------SGFIGCLLDKLPGSWSHKPLVLEGQLAYSHVSNDLKTKYT
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RESULT D72077

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A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Recession: D72077
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <ARN>
A;Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:AAD18593.1; PID:g437673
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: pmp_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphic outer membrane protein g family - Chlamydophila pneumoniae C:Species: Chlamydophila pneumoniae. Chlamydia pneumoniae C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-: C:Accession: D72077 C:Accession: S: Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, Nature Genet. 21, 385-389, 1999
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                                                                                                                                      FSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTAT--NTK
                                                                                                                                                                                                                                          LGKTQDFSFVQLSA-LGTATTTDVPA---VPTVATPTHYGYQGTWGWTWVDDTASTPKTK 589
                                                                                                                                                                                                                                                                          GTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHM
                                                                                                                                                                                                                                                                                                         GTTLKASTEEVTLTGLSIPVDSLGEGKKVVIAASAASKNVALSGPILLLDNQGNAYENHD
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                                       AFYIQHITEC ---
   TLFFKHSHTLQPQNYLRLGRAKFSESAIEKFP---REIPLALDVQVSFSHSDNRMETHYT
                                                                     FLHKTGDENRKGFRHTSGGYVIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNNSRTYGG
                                                                                                      FLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENLISFAFCQLFGSDKDFLVAKNHTDTYAG
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                                                     TILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTLESTSFSQEAGSLLGMDS
                                                                        SIVFSGEKLSEDEAKVADNLTSTLKQPVTLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDA
                                                                                                                      DTPKRNAINIGSNGKFTELRAAKNHTIFFYDPITSE--GTSSDVLKINNGSAGALNPYQG
                                                                                                                                        QTTKRNSIDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLNKADAGNSTDYSG
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40.4%; Pred. No. 9e-91;
tive 173; Mismatches 344;
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52;

Gaps

18;

77

137

252

195

473 424

413 366 353 309

484

Length Indels

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polymorphic membrane protein G family CP0302 [imported] - Chlamydophila pneumoniae (sc;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c;Species: Glamyzophila pneumoniae, Chlamydia pneumoniae (c;Species: Glamyzophila pneumoniae) (c;Species: Glamyzophila pneumoniae) (c;Species: Glamyzophila pneumoniae) (c;Species: Glate: 31-Mar-2000 #text_change l1-May-2000 C;Accession: F81591 R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe, Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae Ar39 A;Reference number: A81500; MUID:20150255 A;Accession: F81591 A;Accession: F81591 A;Accession: F81591 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-949 < REA> A;Experimental source: SB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38159.1; PID:g718 A;Gene: CP0302
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949;
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A.Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606

A;Reference number: A72000; MUID:99206606

A;Reference number: A72000; MUID:99206606

A;Reference number: A72000; MUID:99206606

A;Residues: 1-841 <ARN>
A;Residues: 1-841 <ARN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE002235; GB:AE002161; NID:g7189672; PIDN:AAF38561.1; PID:g71896; A;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-841 < REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: pmp_2; CP0761
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 330; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   896
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112 TTDKNLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGA 171
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                                                                           FKDSVVIENVPKTGETQSTS--CFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSE 117
                                                                                                                   SLPESEGSWSNECIAGGIGLDLPFVLSNPHP----LFKTFIPQMKVEMVYVSQNSFFESS 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYPEVKGSWGNNAFNMMLGAS-----SHSYPEYLHCFDTYAPYIKLNLTYIRQDSFSEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFYIOHITEC-----SGFIGCLLDKLPGSWSHKPLVLEGQLAYSHVSNDLKTKYT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EATATWTKTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTN 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTAT--NTK 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGKTQDFSFVQLSA-LGTATTTDVPA---VPTVATPTHYGYQGTWGMTWVDDTASTPKTK 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHM 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEGRSFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPDLIRNDPKCTTALVISGAS
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                                                                                                                                                                                                                                                                                                                                                                          29.3%; Score 1406.5; DB 2; Length 841; ilarity 34.3%; Pred. No. 5.5e-70; Conservative 162; Mismatches 314; Indels 157;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874
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Search completed: October 2, 2001, 03:28:49
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Result
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Sequence:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-446-677B-4
4795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93435 seqs, 34255486 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKSQFSWLVLSSTLACFTSC.....FEVRGSSRIYNVDLGGKFQF 928
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length DB
   OMPB RICTY
YDBA ECOLI
EGT2_YEAST
Y109_YEAST
AG43_ECOLI
FHAB BORPE
AIDA_ECOLI
MSB2_YEAST
YJH8_YEAST
YJH8_YEAST
YJH8_YEAST
YJH8_YEAST
FIBP_CAMFE
SAPUL_PIG
SACULI
                                                                                                                                                                                                                                                                                                                                                                                                               OMPB_RICPR
120K_RICRI
OMPB_RICRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLAP_CAUCR
YFAL_ECOLI
OMPB_RICJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMPE_CHLTR
OMPF_CHLTR
190K_RICRI
                   ICEN_XANCT
YS89_CAEEL
ICEV_PSESX
ICEN_PSESX
ICEN_PSESY
CHPA_CLOCL
TROP_HUMAN
YDEK_ECOLI
ICEA_PANAN
YDJA_ECOLI
HLYA_SERMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ü
     YEJO_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us4877 chlamydia t
P38008 chlamydia t
P15921 rickettsia
P35828 caulobacter
P45508 escheria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93435
P40442 saccharomyc
P39180 escherichia
P12255 bordetella
P12255 bordetella
P12255 bordetella
P12255 bordetella
P12255 bordetella
P12255 bordetella
P12334 saccharomyc
P47033 saccharomyc
P47033 saccharomyc
P36711 human adeno
P36871 human adeno
P368712 sus scrofa
P18127 xanthomonas
P18127 xanthomonas
P18127 xanthomonas
P18127 xanthomonas
P18128 caenorhabdi
O33479 pseudomonas
P18128 pseudomonas
P30469 pseudomonas
P30469 pseudomonas
P30469 pantoea ana
P52143 escherichia
P15320 serratla ma
P33924 escherichia
                                                                                                                                                                                                                                                                                                                                                             006653 r outer mem
Q53020 r outer mem
P14914 rickettsia
Q53047 r outer mem
P96989 r outer mem
P33666 escherichia
P42835 saccharomyc
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AC P38008; 084878;
DT 01-0CT-1994 (Rel. 30, Created)
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DT 30-MAY-2000 (Rel. 39, Last annotation update)
DF 9UTATIVE OUTER MEMBRANE PROTEIN F PRECURSOR.
GN PMPF OR CT870.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamyd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
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MEDLINE=99000809; PubMed=9784136;
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IMDAGTTL---KASTEEVTLTGLSIPV---
: :| || | :| :|:
                                                     GAVVFSYNOMSSDIRTLMGKEHNYIKEAPTTLKFGTLAIEDDAELEIFNIPFTONPTSLL
                                                                                      GSIVFSGEKLSEDEAKVADNLTSTLKQ-PVTLTAGNLVLKRGVTLDTKG--FTQTAGSSV
                                                                                                                        FHINNNEITPYTLSLGAKKDTRIYFYDLFQWERVKENTSNNPPSPTSRNTITVNPETEFS
                                                                                                                                                       IDIGS---TAKITNLRAISGHSIFFYD-----PITANTAADSTDTLNLNKADAGNSTDYS 412
                                                                                                                                                                                            GPVYFLNN----SAAWGAAFNLSKPRSATNYIHTGTGDIVFNNNVVFTLDGNLLGKRKL
                                                                                                                                                                                                                           GGISFSNNIVQGTTAGNGGAISILAAGECS--LSAEAGDITFNGNAIVATTPQTT-KRNS
                                                                                                                                                                                                                                                               NNSSLGWSQSSSASNGGAIQTTQGFTLRNNKGSIYFDSNTATHAGGAINCGYIDIRD--N
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                                                                                                                                                                                                                                                                                                                                                                    --SATGKKGGAICATGTV-DITNNTAPTLFSNNIAEAAGGAINSTGNCTITGNTS-LVFS
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                                                                                                                                                                                                                                                                                                                                                                                                                          ASDNANLLFC-NNYCTHNKGGGAIRSGGPIRFLNNQDVLFYNNISAGAKYVGTGDHNEKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIVLSNLQSNG--TGACTISGNTQTQTFSNS----VNTTADSGGAFDMVTT----SFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Santucci A., Magi B., Marzocchi
M., Christianen G., Birkelund
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 1034 PUTATIVE OUTER MEMBRANE PROTEIN 34 35 RR -> FH (IN REF. 2). 1034 AA; 112392 MW; 445FF4C35D463AE7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.4%; Score 544.5;
23.7%; Pred. No. 1.10
:ive 148; Mismatches
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_RICRI

190K_RICRI

P15921;

P15921;

O1-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
190 KDA ANTIGEN PRECURSOR (CELL SURFACE ANTIGEN).
Rickettsia rickettsii.
                          This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                MEDLINE=90354033; PubMed=2117568;
Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
"A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";
Infect. Immun. 58:2760-2769(1990).
-!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
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EMBL; M31227; AAA26380.1;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=783;
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                                                                                                                                                                                PTM: GLYCOSYLATED (POSSIBLE).
DISEASE: PROBABLY PLAYS AN IMPORTANT ROLE IN THE PATHOGENESIS
                                                                                                                                                                  AND IMMUNITY TO ROCKY MOUNTAIN SPOTTED FEVER.
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                                             (See http://www.isb-sib.ch/announce/
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                                                                                               restrictions
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SEQUENCE
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VIKATTTKLTNAASVLTLTN
                       ---ATTTDVPAVPTVATPTH
                                                 KFTNPVVVTGAIDSTGNANNG---IVTFTGNSTVTGDIGNTNALATVNVGA-GTATLGGA
                                                                         GEGKKYVIAASAASKNVALSGPILLLDNQGNAYENHDLGKTQDFSFVQLSALGT-----
                                                                                                  TTGGDNVGVLNLNGALSQVTGDIGNTNSLATISVGAGTATLGGAVIKATTTKITNAVSAV
                                                                                                                          DTKG-----FTQTAG-----SSVIMDAGT-TLKASTEEVTLTGLSIPVDSL
                                                                                                                                                   GDIGNTNSLATISVGAGTATLGGAVIKATTTKLT-NAASVL----TLTNANAVLTGAIDN
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13 X APPROXIMATE T
A (TYPE I).
B (TYPE II).
C (TYPE II).
E (TYPE II).
E (TYPE II).
F (TYPE II).
G (TYPE I).
G (TYPE I).
J (TYPE I).
I (TYPE II).
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Pred. No. 2.5e
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A9D6646C089DF087 CRC64;
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RESULT

STANDARD;

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                                                                                                                                                                               Query Match
Best Local
                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLAP_CAUCR STAN
P35828; Q46015;
01-JUN-1994 (Rel. 2
01-OCT-1994 (Rel. 3
30-MAY-2000 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Caulobacter crescentus paracrystalline S-layer protein is secreted by an ABC transporter (type I) secretion apparatus.";
J. Bacteriol. 180:3062-3069(1998).
-i- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
-i- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
                                                                                                                                                                                              Cell
INIT_
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89008089; PubMed-3049545; Fisher J.A., Smit J.K., Agabian N.; "Transcriptional analysis of the major Caulobacter crescentus."; Dacteriol. 170:4706-4713(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilchrist A., Fisher J.A., Smit J.K.;
"Nucleotide sequence analysis of the generocation paracrystalline surface layer can. J. Microbiol. 38:193-202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-313 FROM N.A., STRAIN=ATCC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
STRAIN-ATCC 19089 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caulobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93007489; PubMed-1393820;
                                                                                                                                                                                                                        PRINTS; PR00313; CABNDNGRPT
                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                  HSSP; P01549;
                                                                                                                                                                                                                                                                            EMBL; AF062345; AAC38665.1; -.
                                                                                                                                                                                                                                                   InterPro;
299
                                                   242
                         87
                                                                                \frac{3}{3}
                                                                                                                                                                                                                                                                                                                                                                                                                S-LAYER WITH HEXAGONAL SYMMETRY.
MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
                                                                          PSDSFDGST ---NTGTYT---PKNTTTGIDYTLTGDITLQNLGDSAALTKGCFSDTTESL
                                                                                                                                                                                                         wall; S-layer; Calcium-binding
QAAAVTALPTGVTISGIETMNVTSGAAITLNTSS---GVTGLTALNTNTSGAAQTVTAGAG
                        SFAG-----KGYSLSFLNIKSSAEGAALSVTTDKNLSLTGFSSL-TFLAAPSSVITTPSG
                                                     PSSGVSGSTLSLTTGTDTLTGTANNDTFVAGEVAGAATL-TVGDT--LSGGAGTDVLNWV
                                                                                                            187;
                                                                                                                                                                                                                                     PF00353; hemolysinCabind;
                                                                                                                         Similarity
                                                                                                                                                                                                                                                IPR001343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smit J.K.;
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                                                                                                            Conservative
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(See http://www.isb-sib.ch/announce/
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SEQUENCE FROM N.A.

STRAIN-K12 / MG1655;

MEDLINE-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna i Blattner F.R., Plunkett G. III, Bloch C.A., Perna i Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K. Riley M., Collado-Vides J., Glasner J.D., Rode C.K. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M., Mau B., Shao Y.;

Mau B., Shao Y.;

The complete genome sequence of Escherichia coli i Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFAL_ECOLI STANDARD; PRT; 1250 AA. P45508; P45508; P45506; P39441; P76468; P77487; O1-FEB-1995 (Rel. 31, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-OCT-2000 (Rel. 40, Last annotation update) HYPOTHETICAL 131.2 KDA PROTEIN IN UBIG-NRDA INTERGENIC
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                             gamma
                                        of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                             subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae;
                                                                                              C.K., Mayhew
n M.A., Rose I
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three gene classes.";
Nucleic Acids Res. 23:3554-3562
-!- SIMILARITY: TO E.COLI YDEK.
-!- CAUTION: REF.3 SEQUENCE DIF
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parD-mutant of Escherichia
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Microbiol. 1:259-273(1987).
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AAV -> RGRS (IN REF. 3).

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30-MAY-2000 (Rel. 40, Last sequence update)
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                                                                                                                                      STANDARD;
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Pred. No. 2.5e-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uchiyama T.;
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749
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                                                                                                                                                          GSSKTTLNGGNVAINELVI--GNNGSVQFAHNTYLITRTTNAAGQGKIIFNPVVNNNTTL
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                                                                AAGTNLGSAANPLAEINFGSKGARADTVLNVGEGVNLYATNITTTDANVGSFVFNAGGKN 748
                                                                                                  VQGTTAGN----
IVSGTVGGQQGNKFNTVALDNGTTVKFLGNATFNGNT-----TIAANSTLQISGNY 799
                                IVATT----PQTTKRNSI--DIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLN- 401
                                                                                                                                                                                                       GTIKLTSTQNNIVVDCDLAIATDQTGVVDASSLTNAQTLTISGTIGIIGANNTTLGQFNI 630
                                                                                                                                                                                                                                                                                                        ISFEGNKSSATGK--KGGAICATGTVDITNNTAPTLF--SNNIAEAAGGAINSTGNCTIT
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528
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533
                                                                                                32 KDA BETA PEPTIDE. POLY-GLY.
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[2] SEQUENCE STRAIN-BR MOTON C.G MOTON C.G "Sequence Submitted SUDENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SERAIN-MA MEDLINE-9 Andersson Sicheritz Eriksson Sicheritz	30-MAY-2000 (Rel. 30-MAY-2000 (Rel. 30-MAY-2000 (Rel. 30-MAY-2000 (Rel. 30-MAY-2000 (Rel. COUTER MEMBRANE PRO (SURFACE PROTEIN A (CONTAINS: 120 KDA (120 KDA OUTER MEM (120 KDA OUTER MEM OMPB OR SPAP OR SP Rickettsia prowaze Bacteria; Proteoba Rickettsiaceae; Ri (120 KDA OUTER MEM OMPB OR SPAP OR SP RICKETSIA PROTEOBA RICKETSIACEAE; RI NCBI_TAXID-782; [1] SEQUENCE FROM N.A. STRAIN-BREINL; MEDLINE-91045972; Carl M., Dobson M. "Characterization surface-layer prot truncated identica	1078 1078 750 1138 1138 2T 7 2RICPR	1006 664 1018	545 963 604	493 915	402 800 452 855
[2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-BREINL; MOTON C.G., Yu X.J "Sequence analysis submitted (JUN-199 [3] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM SEQUENCE FROM SEQUENCE FROM SEG. E.; MEDLINE-99039499; Andersson S.G.E.; Sicheritz-Ponten T SICHESSON A.S., Wi SICHERIA GENOME SEG.	30-MAY-2000 (Rel. 39, Las 30-MAY-2000 (Rel. 30, Las 30-MAY-2000 (Rel. 30, Las 30-MAY-2000 (Rel. 30, Las 30-MAY-2000 (Rel. 30, Las 30	ETICHTEC	HKSGG         VTTGG	LSALG	VDS     SGVDS	KADAG
	100 (Rel. 3) 100 (	FIGER  FY LOWING COMMENT  FINANCIAL TRANSPORT  FROM STREET  FROM STREE	:   -IATN- YAIGGA       IAAGGI	TATTT-DVP	-LGEGKKV : : : :	NSTDY.
	92CMU; 92CMU; 90 (Rel. 39, L 00 (Rel	DTPVASVRETG TAYPEVKGSWG: :     CTFAGGTSTWG	GGYAIGGAAQTCS	GTATTT-DVPAVPT 	KKV : : QVIGDQ	KADAGNSTDYSGSIVFSGE
ಸಪಕ್ಷಣೆ ಆಲ್ಲ ;	39, Create 39, Last; 39, Last; 39, Last; NTIGEN) (( SURFACE-I BRANE PRO); A OR RP70; kii. cteria; al ckettsieae ckettsiea		ENLIS :  : DGKIT	AVPTVAT	VIA :: NNIVG	ADAGNSTDYSGSIVFSGE         ;   ;
ker D.H.; pB of Rickett the EMBL/GenB the EMBL/GenB the LACATE A., An mark U.C.M., MH.H., Kurland	Jreated) Last seque Last annot B pRECURS EN) (CELL ACCETYOS FROTEIN RP704.  RP704.  RP704.  PARTIAL D) PARTIAL	Sc :   NGAG 771 115	ו אי מו	PTHYGYQGTWGM	VVIAASAASKNV : ;     IGDQNNIVGLGLGSDNG	KLSEDEAKVA  ::   INVTLNKQAVPV- IMDAG :     LFLPSGIPFNDAG
H.; H.; Rickett BL/GenB G.C.M., Kurland	yuence upda; notation up nsoar (168) IRSOR (268) ISSOR PROTE; OOSED PROTE; IN OMPB); 3: IN OMPB); 3: IN SEQUENCE A: Dasch ( encoding the strike prowastical prowas	<u> </u>	NANVA	YQGTWG         GTGIG	KNVALS   :   ONGIIV	SEDEAK :: NKQAVE E GIPFNE
ittsia pr inBank/DD Andersso , Podows n, C.G.;	30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 00TER MEMBRANE PROTEIN OMPB); 32 KDA SURFAC (SURFACE ANTIGEN) (SURFACE ANTIGEN) (SURFACE (120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA RICKETTSIA PROWAZEKII. RICKETTSIA PROWAZEKII. RICKETTSIA PROWAZEKII. RICKETTSIA; Proteobacteria; alpha subdivision; Ricke RICKETSIA; PROME N.A., AND PARTIAL SEQUENCE. STRAIN-BREINL; REDLINE-91045972; PubMed-2122457; MEDLINE-91045972; PubMed-2122457; Carl M., Dobbon M.E., Ching W.M., Dasch G.A.; "Characterization of the gene encoding the protect surface-layer protein of Rickettsia prowazekii: protruncated identical homolog in Rickettsia typhi."; Proc. Natl. Acad. Sci. U.S.A. 87, 8237-8241(1990).	IYSQVIDF	TTIND-	TWVD	ALSGPILLLDNQGNAYENH ;       IIVNATTLYAGIGTINNO	KVADNL
TOWAZEK DBJ dat on J.O. Ski R.M	(SURFACE KDA BETA BETA KDA BETA BETA KDA BETA BETA KDA BE	TDFGTYNLG	LFGSDKI	DTASTI	LDNQGI   YAGIG	TSTLKQP:     - NALKQITLKAS    :  :: PLTIKST
T CALL S	URFACE-L EN) (SCA URFACE P BETA PE Ricketts Rickettve i: prese i: prese	IV :	DKDFLV	PKTKTA	NAYENH       NNNC	DPVTLI DITVSG ASTEEV ::
eslu	AYER 5) (R ROTEI PTIDE iales iales nce o	: ::    ::  EGULAX	TTINDGYTAKNHTDTYAG	TASTPKTKTATLAWTNTG	VIAASAASKNVALSGPILLLDNQGNAYENHDLGKTQDF ::	ADAGNSTDYSGSIVFSGEKLSEDEAKVADNLTSTLKQPVTLTAGNLVLK-
D ⊅ f ×	φ z <del>i</del>	SSTTAI	TDTYAG	NTGYLPN     : NLGNI	33	IG
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EMBL; AF161079; AAD42234.1; -.
EMBL; AJ235273; CAA15140.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hackstadt T., Messer R., Cieplak W. Jr., Peacoc) 
"Evidence for proteolytic cleavage of the 120-ki 
membrane protein of rickettsiae: identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments
the S-layer protein antigens of Rickettsia typhi and Rickettsia
prowazekii.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION OF CLEAVAGE SITE. MEDLINE-92104668; PubMed-1729180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92114896; PubMed=1370573; Ching W.M., Carl M., Dasch G.A.;
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Nature 396:133-140(1998).
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ect. Immun. 60:159-165(1992).

ett. Immun. 60:159-165(1992).

STRUCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE A SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                             TTGIDYTLTGDITLQNLGDSAALTKGCFSDTT--------
                                                                                                                                                                                                                                 SWLVLSSTLACFTSCSTVFAATAE----NIGPSDSFDGS------TNTGTYTPKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. 29:95-105(1992).
AICATGTVDITNNTAPTLFS--NNIAEAAGGAINSTGNCTITGNTSLVFSEN---
                             GTTVKFLGDTTFNGGTKIEGKSILQISNNYTTDHVESADNTGTLEFVNTDPITVTLNKQG
                                                           NGTILFKQDYCEENGGAISTKN-LSLKN-----
                                                                                       ILNVGKGVNLYANNITTNDANV-----GSLHFRSGGTSIVSGTVGGQQGHKL-NNLILDN
                                                                                                                   FLNIKSSAEGAALSVTT-DKNLSLTGFSSLTFLAAPSSVIT-TPSGKGAVKCGGDLTFDN
                                                                                                                                                   T----YLITKTINAANQGQIIVAADPLNTNTTLADGTNLGSAENPLSTIHFATKAANADS
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329 1643 32 KDA BETA PEPTIDE.
257 V -> A (IN STRAIN BREINL).
010 1010 Y -> D (IN STRAIN BREINL).
450 1450 A -> S (IN STRAIN BREINL).
179 AA -> VC (IN REF. 1).
191 201 TTOCAPLICA -> INSRSSSYHLVS (IN REF. 1).
191 212 T -> I (IN REF. 1).
193 313 Q -> L (IN REF. 2).
193 1123 T -> S (IN REF. 2).
194 AN; 735FDF392E6346CC CRC64;
                                                                                                                                                                                                                                                                     5.2%; Score 248.5; DB 1; 21.9%; Pred. No. 3.6e-06; live 118; Mismatches 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wall.
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MEDLINE=90136087; PubMed=2515418;
              SEQUENCE FROM N.A. STRAIN=R;
                                                       Rickettsiaceae;
NCBI_TaxID=783;
                                                                                      Bacteria; Proteobacteria; alpha
                                                                                                     Rickettsia rickettsii.
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01-FEB-1996 (Rel. 33, Last sequence up
01-CCT-2000 (Rel. 40, Last annotation
120 KDA SURFACE-EXPOSED PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the ENE European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content by non-profit institutions as long as its content if the content is not removed. Usage by and this statement is not removed. Usage by and the content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS:
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          PSGKGAVKCGG-----DLTFDNNGTILFKQDYCEENGGAISTKNLSLKNSTGSISFEGNKS
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                                              CFSDTTESLSFAGKGYSLSFLNIKSSAEGAALSVTTDKNLSLTGFSSLTFLAAPSSVITT
                                                                  TTAFKTAASKVTITQDSNFGNTDFGNLAAQIKVPNA-ITLTGNFTGDASNPGNTAGV---
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                                                                                                                  Similarity
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OMAY-2000 (Rel. 39, Last sequence update)

OMAY-2000 (Rel. 39, Last annotation update)

OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)

(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)

(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)

TOAN KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                                   Rickettsiaceae;
NCBI_TaxID=783;
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MEDLINE=92167802; PubMed=1724278;
Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;
Gilmore R.D. kilodalton outer membrane protein (rOmp B) of Rickettsia
rickettsii is encoded by an unusually long open reading frame:
evidence for protein processing from a large precursor.";
Mol. Microbiol. 5:2361-2370(1991).
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onling, expression and sequence analysis of the gene encoding the surface-exposed protein of Rickettsia rickettsii.";
kD surface-exposed protein of Rickettsia rickettsii.";
. Microbiol. 3:1579-1586(1989).
. PUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVEREIN AND CONTRACTORY.
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een the Swiss Institute of Bioinformatics and the EM
European Bioinformatics Institute. There are no restr
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 GQQGNKFNTVALENGTTVKFLGNATFNGNT----
                                                              SATNPLAEINEGSKGVNVDTVLNVGEGVNLYATNITTTDANVGSFVFNAGGTNIVSGTVG
                                                                                                                             VLSNGNVAINELVIGNDGAVQFAHDTYLITRTTNAAGQGKIIFNPVVNNGTTLAAGTNLG
                                                                                                                                                             VTFSGNQA-----VANGGAI-----YAKKLTLASGGGGGISFSNNIVQGTT--AGN---
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                              -PQTTKRNSIDI--GSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLN-KADAGNS
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32 KDA BETA PEPTIDE.
POLY-THR.
PW; D7AB70FB7087F61E
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l; Mismatches
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Pred. No. 5.4e-06;
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Ching W.M., Carl M., Dasch G.A.;
Ching W.M., Carl m., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on
"Mapping of monoclonal antibody binding sites on
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0UTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-WILMINGTON; PubMed=8224886; MEDLINE-94040787; PubMed=8224886; Hahn M.-J., Kim K.-K., Kim I., Chang "Cloning and sequence analysis of the surface layer protein of Rickettsia t Gene 133:129-133(1993).
                                                        MEDLINE-92104668; PubMed-1729180;
Hackstadt T., Messer R., Cieplak W., I
"Evidence for proteolytic cleavage of
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Rickettsiaceae; Rickettsi
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-I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE
-I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED S-LAYER WITH HEXAGONAL SYMMETRY.
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KLSEDEAKVADNLTSTLK--QPVTLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDAGTTLK
                                              LGGGTTAINGEIDLLTNNLIFANGTSTWGNNTSLSTTLNVSNGNVGQIVIAEGAQV-NAT
                                                                                               ----AISG-----
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MEMBRANE ANCHOR (POTENTIAL).

H -> N (IN REF. 2).

V -> I (IN REF. 2).

G -> A (IN REF. 2).

G -> S (IN REF. 2).

MW; OCB5641C7EB185EE CRC64;
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                                                                      MEDILINE-PALANCE P., Danchin A.,
MOSZET I., Glaser P., Danchin A.,
"Multiple IS insertion sequences near the replic
"Multiple IS insertion sequences near the replic
Escherichia coli K-12.";
Biochimie 73:1361-1374(1991).
Biochimie 73:1361-1374(1991).
Biochimie 73:1361-1374(1991).
CAUTION: THIS IS A CONCEPTUAL TRANSLATION;
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2
                                                                                                                                                                                                                                                                                         MEDINE-97251357; PubMed-9097039;
MEDINE-97251357; PubMed-9097039;
Aiba H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamanoto Y., Horiuchi T.;
Ta 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P33666; P76087; P76088; P76856; P76857; P76859;
01-FEB-1994 (Rel. 28, Created)
01-CCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 205.9 KDA PROTEIN IN PAAY-ACPD INTERGENIC
             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                               MEDLINE=92190338; PubMed=1665988;
                                                                                                                                                                                                                                                                  SEQUENCE OF 464-2003 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shao Y.;
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ode C.K., Mayhew
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THE GENE CODING
                                 and the EMBL outstation
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOJ. Cell. Biol. 16:3264-3274(1996).

-I- FUNCTION: SEEMS TO BE INVOLVED IN THE CORRECT TIMING OF CELL SEPARATION AFTER CYTOKINESIS, AS SEPARATION OF MUTANT DAUGHTER CELLS IS DELAYED. COULD EITHER BE AN ENZYME NECESSARY FOR GLUCANS-DEGRADATION OF THE CELL WALL'AT THE NECK REGION BETWEEN MOTHER AND DAUGHTER CELLS OR A REGULATORY PROTEIN CONTROLLING THIS METABOLIC STEP. EXCLUSIVELY EXPRESSED BETWEEN THE END OF MITOSIS AND EARLY GI; INACTIVATED BEFORE CELLS PASS START.
                    1028 AGMAAYGASNTVINQGTINL---EKNGNYDDSLAA----NTLVGMAVYEHGTAINDQTGV 1080
666 SGGYAIGGAAOTCSENLISFAFCOLFGSDKDFLVAKNHTDTYAGAFYIQHITECSGFIGC 725
                                                                                                                                                                                                                                                                                                                                                                                                 Maftahi M., Nicaud J.-M., Levesque H., Gaillardin C.; "Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the RPD3, PASB and KREI loci, five new open reading
                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle; Cell division; Mitosis
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NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "EGT2 gene transcription is induced predominantly by
                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update
EGT2 PROTEIN PRECURSOR (EARLY GI TRANSCRIPT:
EGT2 OR YNL327W OR N0320.
                                                                                                                                                                   PRT; 1041 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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POLY SER.
POLY SER.
POLY SER.
POLY-SER.
POLY-THR.
11-1.
11-2.
11-3.
11-4.
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                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kovacech B., Nasmyth K., Schuster T.;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-S288C / FY1676;
MEDLINE-95373280; PubMed=7645347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND FUNCTION. MEDLINE-96251274; PubMed=8668141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z46259; CAA86371.1; -. EMBL; Z71603; CAA96259.1; -. SGD; S0005271; EGT2. Glycoprotein; Repeat; Signal;
                                                                                                                                                                   STANDARD;
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P42835;
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            (See http://www.isb-sib.ch/announce/
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modified and this statement is not removed.
                                                                                                                                                                                                                                                                                       Matches 171; Conservative 125; Mismatches
              tities requires a license agreement (send an email to license@isb-sib.ch)
                                                       EMBL; AE000237; AAC74483.1; ALT_SEQ.
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                                                                                                                                                                                                                                                                         Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones I. Louls E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         Saccharomycetes;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
F63E287A03F137EC CRC64;
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                                                                     30-MAY-2000 (Rel. 31, Last sequence update)
HYPOTHETICAL 99.7 KDA PROTEIN IN SDL1 5'REGION PRECURSOR
YILL69C OR Y19402.07C.
                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccl
Saccharomycetales; Saccharomycetaceae; Saccharomyces
NCBI_TaxID=4932;
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99735 M
                                   STANDARD;
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Hypothetical protein; S
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695 AA;
RESULT 13
YIQ9_YEAST
ID YIQ9_YEAST
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CARBOHYD
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Query Match
 Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                             424
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314 IS----GDLTLTGKVIATEGVVVAAGAKLTLLDGDKYSFSA---DLKVYGDLLVKKSKET 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINSHIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                  425 FSPYSNSGAFSFSNAILNGGSVSGLQRRDDTEGSVNNGEINLDNGSTYVIVEPVSGKGTV
                                                                                                                                                                                                              542 --FVQLSALGTATTTDVPAVPTVATPTHYGYOGTWGMTWVDDTASTPKTKTATLAWTNTG
                                                                                                                                                                                                                                    593 NGVVATSAASSTASGASASVTGST-----SFGASVTGSTASTSFGASVTGSTASTS
                                   367 YPGTEFDISGENFDVTGNFNAEESAATSASIYSFTPSSFDNSGDI--SLSLSKSKKGEVT
                                                                                                                                        485 NIISGNLYLHYPDT----FT---GOTVVFKGEGVLAVDPTETNAT----PIPVVGYTGK
                      356 TKRNSIDI-GSTAKIT----NLRAISGHSIFFYDPITANTAADSTDTLNLNKADAGNST
                                                                   --DYSGSIVF-----SGEKLSED-----EAKVADNLTSTLKQPVT----
                                                                                                                   - LTAGNLVLKRGVTLDTKGFTQTAGSSVIMDAGTTLKASTEEVTLTGLSIPVDSLGEGKK
                                                                                                                                                               502 VVIAASAASKNVALSGPI-LLLDNQGNAYENHDLG---KTQDFS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ML 308-225;
Henderson I.R., Owen P.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                        AG43_ECOLI STANDARD; PRT; 1039 AA. P39180; P76360; P75614; P97241; Q46771; O1-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 31, Last sequence update) 01-NOV-1997 (Rel. 40, Last annotation update) ANTIGEN 43 PRECURSOR (AG43) (FLUFFING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97251358; PubMed=9097040;
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MEDLINE=89291704; PubMed=2661530;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
"Purification and N-terminal sequence of the alpha subunit of antigen 43, a unique protein complex associated with the outer membrane of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEMS Microbiol. Lett. 149:115-120(1997).
--- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAX FUNCTION AS AN ADHESTN.
--- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                determines colony morphology and autoaggregation in Escherichia coli K-12.";
                                                                                                                                                                                                                                       properties of proteins encoded
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ANTIGEN 43 BETR CHAIN.

SL -> FF (IN STRAIN ML 308-225).

T -> K (IN STRAIN ML 308-225).

T -> K (IN STRAIN ML 308-225).

V -> L (IN STRAIN ML 308-225).

V -> E (IN STRAIN ML 308-225).

ATN -> STI (IN STRAIN ML 308-225).

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A -> T (IN STRAIN ML 308-225).

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                                                                                                                                                                                                                                                                                                                                                                                           Henderson I.R., Meehan M., Owen P.; "Antigen 43, a phase-variable bipartite outer membrane protein,
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-!- SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETELLA PERTACTIN.
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QGT -> LGA (IN STRAIN ML 308-225)

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S -> I (IN STRAIN ML 308-225)

ETV -> TIT (IN REF 5)

WW; 5170D647C8DEEBEG CRC64;
                                                                                                                                                                                                            Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed prol
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
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EMBL; D90838; BAA15825.1; ALT_INIT.
EMBL; D90839; BAA15832.1; ALT_INIT.
EMBL; U244.29; AAB47869.1; -.
ECOGENE; EG12686; flu.
                                                           cherichia coli.";
Bacteriol. 171:3634-3640(1989).
                                                                                                                                                           STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
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                                                                                     ---TLTGDITLQNLGDSAALT-----KGCFSDTTESLSFAGKGYSLSFLNIKSS 103
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                                                                                                                                                                                                                                                        215 TAPTLFS-----NNIAEAAGGAINSTGNCTITGNTS------LVFSENSVTATA-- 257
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                                                                                                                                                                                                                                                                                                                                                                                                                  437 NGGLFTARGGTLAGTTTLNNGAILTLSGKTVNNDTLTIREGDALL--QGGSLTGNGSVEK 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSGTLTVSNTT---LTQKAVNLNE-----GTLTLNDSTVTTDVI----AQRGTAL 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 DYSGSIVFSGE-----KLSE-----DEA---KVADNL------TSTLK---QPVT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTAGNLVLKRG-VTLDTK-GFTQTAGSSVIMDAG-----TTLKASTEEVTLTGLSIPVDS 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGEGKKVVIAASAASKNVALSGPILLLDNQGNAYE----NHDLGKTQDFSFVQLSALGTA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGKGIQVVEAINGATTE---EGAFV----QGNRLQAGAFNYSLNRDSDESWYLRSE--NA 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTDVPAVPTVATPTHYGYQGTWGMTWVDDTASTPKTKTATLAWTNT------GYLPNP 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 YRAEVPL-----YASMLTQAMDYDRIVAGSRSHQTGVNGENNSVRLSIQGGHLGHD 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              605 ERQG---PLVPNSLWGSFSDIQAIQGVIERSALTLCSDRG--FWAAGVANFLDKDKKGEK 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       757 NNGGIARGATPESS-GSYGFVR-LEGDLMRTEVAGMSVTAGVYGAAGHSSVDVKDDDGSR 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                660 RKYRHKSGGYAIGGAAQTCSENLISFAFCQLFGSDKDFLVAKNHTDTYAGAFYIQHITEC 719
             Gaps
                                                     36 VAVALSLAAVTSLPVLAADIV--VHPGETVNGGTLANHDNQIVFGTTNGMISTGLEYGP 93
                                    LVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNT------GTYTPKNTTTGIDY-- 57
                                                                                                                                                                                                               207 VRGDAVRTTINKNGRQIVRAEGTANTTVVYAGGDQTVHGHALDTTLNGGYQYVHNGGTAS
                                                                                                                                                                                                                                                                                                                                         -GNGGALSGDADVTISGNQS----VTFSGNQAVANGGAIYAKK---LTLASG------
                                                                                                                                      104 AEG------AALSVTTDKNLSLTGFSSLTFLAAPSSVITTPSGKG------
           Mismatches 344; Indels 260;
                                                                                                                                                                                         ---AVKCGGDLT----
0.00012
Pred. No.
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          Conservative 126;
Best Local Similarity
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           Matches 199;
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PRT; 3591 AA

FHAB\_BORPE. STANDARD; P12255; 01-0CT-1989 (Rel. 12, Created)

RESULT 15 FHAB\_BORPE ID FHAB\_B AC P12255 DT 01-0CT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1071 ARRALRODFFTPGSVVVRAQGNVTVGRGDPHQGVLAQGDIIMDAKGGTLLLRNDALTENG 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1191 SGRQIDVVDGRPQITDAVTGEARKDESVVSDAALVADGGPIVVEAGELVSHAGGIGNGRN 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDVNGTGDVRVAKLVSDAGADLQAGRSMTLG-IVDTTGDLQARAQQKLELGSVKSDGGLQ 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1251 KENGASVTVRTTGNLV---NKGYISAGKQGVLEVGGALTNEFLVGSDGTQRIEAQRIENR 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PSSVITTPSGKGAVKCG------GDLTFD-NNGTILFKQDYCEENG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-AISTKNLSLKNSTGSISFEGNKSSATGKKG-----GAICATGTVDITNNTAPTL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TFSGNQAVANGGAIYAK---------KLTLASGGGGGISFSNNIVQGTTAGN- 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-3261 FROM N.A.
MEDLINE-80202384; PubMed-2539596;
Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow S.
"Filamentous hemagglutinin of Bordetella pertussis: nucleotide sequence and crucial role in adherence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90355839; PubMed=2388559;
Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow
"Genetic characterization of Bordetella pertussis filamentous
haemagglutinin: a protein processed from an unusually large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3591;
                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 86:2637-2641(1989).
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   (Rel. 33, Last sequence update) (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M60351; AAA22974.1; -.
EMBL; M60351; AAA22975.1; ALT_INIT.
EMBL; M60351; AAA22976.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SUBCELLULAR LOCATION: SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 4:787-800(1990)
01-FEB-1996 (Rel. 33, Last
01-FEB-1996 (Rel. 33, Last
FILAMENTOUS HEMAGGLUTININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 181; Conservative
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3591 AA; 30
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                                                                                                                                Bordetella pertussis
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                                                                                                                                                                                                                               NCBI_TaxID=520;
                                                                                                                                                                                                        Bordetella.
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SEQUENCE
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321	358 1423	404	456	502 1585	547	598
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Search completed: October 2, 2001, 03:32:05 Job time: 240 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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SPTREMBL_16:*

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Sp_archea:*

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9: sp_ph'
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Gapop 10.0 , Gapext 0.5
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4795
1 MKSQFSWLVLSSTLACFTSC.....FEVRGSSRIYNVDLGGKFQF 928
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   sp_plant:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                                                                                                            sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
                                                                                 sp_organelle:*
sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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28.1	29.1	29.2	29.3	29.3	35.5	36.4	37.2	37.2	37.3	38.1	38.7	38.7	40.1	42.3	42.4	42.5	98.5	100.0	Query Match I	đ
973	922	922	922	841	846	847	949	928	839	772	936	936	928	930	930	926	914	928	ength D	
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Q9Z896	Q9Z4H9	Q9K1Y9	Q9Z9G5	Q9Z3A1	P71133	P71132	Q9K299	086164	P77792	Q9RB71	Q9JS42	Q9Z898	Q9Z398	Q9RB66	Q9Z393	P71135	086163	Q9RB65	ID	
Q9z896 chlamydia p	Q9z4h9 chlamydia p	Q9k1y9 chlamydia p	_		P71133 chlamydia p	P71132 chlamydia p	Q9k299 chlamydia p	086164 chlamydia p		Q9rb71 chlamydia p	Q9js42 chlamydia p					P71135 chlamydia p	086163 chlamydia p	Q9rb65 chlamydia p	Description	
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                                                                                                             LPNPERQGPLVPNSLWGSFSDIQAIQGVIERSALTLCSDRGFWAAGVANFLDKDKKGEKR
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Pred. No. 9.7e-266;
; Mismatches 0;
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SEQUENCE
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Bacteria;
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Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkel "Identification of two novel genes encoding outer membrane associated surface layer proteins in Chlamydia pneumoniae." Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001311; CAA04671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O86163 PRELIMINARY; PRT; 914 AA.
O86163;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence upda-
01-MAR-2001 (TrEMBLrel. 16, Last annotation up-
01TER MEMBRANE PROTEIN 5 PRECURSOR (FRAGMENT).
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InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145;
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  KLSEDEAKVADNLTSTLKQPVTLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDAGTTLKAS
                    KLSEDEAKVADNLTSTLKQPVTLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDAGTTLKAS
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es; Chlamydiaceae; Chlamydophila
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Pred. No. 1.6e-261;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE 98 KDA OUTER MEMBRANE PROTEIN.
Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
MCBI_TaxID=83554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-OVINE ABORTION $26/3;
Longbottom D., Russell M., Dunbar S.M., Jones
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ
EMBL; U72499; AAB18188.1; -.
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P71135;
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Local Similarity
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                                                                                                                               GIDYTLTGDITLONLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKSSAEGAALSV-T
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    ADKILTLTDFSKLSFKECPSSLVNT-
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; DUF145; 1.
6 AA; 98439 MW;
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46.2%; Pred. No. 1.9e
tive 137; Mismatches
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-GKGAMKSGGALNLANNASILFDQNYSAENGGAI
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Q9Z393 PRELIMINARY; PRT; Q9Z393; Q9Z393; O1-MAY-1999 (TrEMBLrel. 10, Created) O1-MAY-1999 (TrEMBLrel. 16, Last seque O1-MAR-2001 (TrEMBLrel. 16, Last annot OUTER MEMBRANE PROTEIN 11 PRECURSOR. OMP11 OR PMP_8. Chlamydia pneumoniae (Chlamydophila protectia; Chlamydiales; Chlamydiaceae;
MEDLINE-99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Olinger L., Grimwood J., Davis R.W., Stephens I "Comparative genomes of Chlamydia pneumoniae at Nat. Genet. 21:385-389(1999).
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SEQUENCE FROM N.A.
STRAIN=CWL029;
                                                                                                          NCBI_TaxID=83558
                                                                                                                     (Chlamydophila pneumoniae)
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                        WASGTANFFHKDKSGTNQAFRHKSYGYIVGGSAEDFSENIFSVAFCQLFGKDKDLFIVEN
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
POLYMORPHIC OUTER MEMBRANE PROTEIN G FAMILY (POLY
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PMP_8 OR CP0307.
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Umayam L.A., Utterba Berry K., Bass S., Linher K., Weidman J., Khouri H., Cra Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kol McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chla
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Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa
"Comparison of whole genome sequences of Chlamydia p
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
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Bacteria; Chlamydiales;
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CP0307; -.
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MEDLINE=99206606; PubMed=10192388;
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rEMBLrel. 16, Last annotation update)
PROTEIN PRECURSOR (POLYMORPHIC MEMBRANE
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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Christiansen G., Birkelund S.;
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ATYAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITFNGNAIV
                                                        ASSFISSNKAISFINNSVTATSATGGAIYCSSTSAPKPVLTLSDNGELNFIGNTAITSGG
                                                                                          GNCTITGNTSLYFSENSYTATAGNGGAL---SGDAD---YTISGNQSYTFSGNQAVANGG
                                                                                                                                                                 SISL-SLNPNLTFAKNKAT---QKGGALYSTGGITINNTLNSASFSENTAANNGGAIYTE
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Q1-MAY-1999
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Kalman S., MitChell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae (Chlamydophila pneumoniae) Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila pneumoniae) Chlamydophila pneumoniae)
  Pfam; PF02385; OMP;
Pfam; PF02415; DUF1
SEQUENCE 936 AA;
                                                                       Nat. Genet. 21:385-389(1999).
EMBL; AE001627; AA018589.1; -.
InterPro; IPR003357; -.
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Best Local S
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InterPro; IPR003357; -.
InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
ProDom; PD004552; -; 1.
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Nucleic Acids Res. 28:1397-1406(2000).

EMBL; AP002546; BAA98653.1; -

EMBL; AE002193; AAF38165.1; -

TIGR; CP0308; -
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T. Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B. Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20330349; PubMed=10871362; Shirai M., Hirakawa H., Kimoto M.,
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PMP_7 OR CP0308.
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                VATTPQTTKRNSIDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLNKADAGNS
                                                      TGNCTITGNTSLVFSENSV-TATAGNGGAL---SGDADVTISGNQSVTFSGNQAVANGGA
                                                                                                                                                                                                                                        KNLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGAIST
                                                                                                                                                                                                                                                                                 SLLSDVSFQNAGALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSSAGTVASTSAAD
                                                                                                                                                                                                                                                                                                            TLTGDITLQNLGD-SAALTKGCFSDTTESLSFAGKGYSL--SFLNIKSSAEGAALSVTTD
                                                                                                                                                                                                                                                                                                                                      MKSSVSWLFFSS-IPLFSSLSIV-AAEVTLDSSNNSYDGSNGT-TFTVFSTTDAAAGTTY
                                                                                                                                                                                                                                                                                                                                                                   MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNTT---TGIDY
--TNGSTSTRNAINIIDTAKVTSIRAATGQSIYFYDPITNPGTAASTDTLNLNLADANSE
                                                                                                             TDNCSITDNFQVIFDGNSAWEAAQAQGGAICCTTTDKTVTLTGNKNLSFTNNTALTYGGA
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es; Chlamydiaceae; Chlamydophila.
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Last annotation update)
PROTEIN G FAMILY (POLYMORPHIC
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7.2e-98;
hes 343;
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RESULT Q9RB7LT ID P9RB7LT Q9RB7LT Q9RB
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Matches 379;
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InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
SEQUENCE 772 AA; 82931
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Q9RB71;
01-MAY-2000
01-OCT-2000
01-MAR-2001
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PMP_3_2.
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EMBL; AP002545; BAA98226.1; -.
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Bacteria; Chlamydiales;
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                                              158
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MLFSKNFSTDNGGAITAKTLSLTGTTMSALFSENTSS---KKGGAIQTSDALTITGNQGE 57
                        ILFKQDYCEENGGAISTKNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAP
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                                                                                                   Conservative
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AA; 82931
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48
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es; Chlamydiaceae; Chlamydophila.
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8.2%; Pr
ve 117;
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                                                                                                Score 1827.5; DB 2
Pred. No. 1.8e-96;
7; Mismatches 260;
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RESULT 10
P77792
ID P77792
AC P77792
AC P77792
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-MAP90
OS Chlamy
OC Bacter
OX NCBI-T
RN [1]
RN [1]
RP SEQUEN
RC STRAIN
RA Longbo
RL Submit
RN [2]
RP SEQUEN
RC STRAIN
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01-FEB-1997 (TrEMBLrel. 02, Last sequence upon the control of th
                                                                    STRAIN-OVINE ENZOOTIC ABORTION ISOLATE S26/3;
Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
    STRAIN-OVINE ENZOOTIC
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                       KYTAYPEVKGSWGNNAFNMMLGASSHSYPEYLHCFDTYAPYIKLNLTYIRQDSFSEKGT-
                                                 NIYAGSLYYQHISYWSAWQNLLQNTI---GAEAPLVLNAQLTYCHASNDMKTNMTTTYAP
                                                                                                  SGLANFLHKSGSDTKRKFRHNSAGYALGVYAKTPSDDIFSAAFCQLFGKDKDYLVSKNNA
                                                                                                             ---TKTATLTWEQTGYSPNPERQGPLVPNTLWGAFSDLRAIQNLMDISVNGADYHRGFWV
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T "Comparison of whole genome sequences of Chlamydia pneumonia(
I from Japan and CWL029 from USA.";

Nucleic Acids Res. 28:2311-2314(2000).

EMBL; AJ001311; CAA04672.1; -.

EMBL; AJ133034; CAB37072.1; -.

EMBL; AF002546; BAA98658.1; -.

InterPro; IPR003357; -.

InterPro; IPR003357; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knudsen K. Madsen A.S., Mygind P., Christiansen G., Birkelu "Identification of two novel genes encoding outer membrane cassociated surface layer proteins in Chlamydia pneumoniae."; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
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                                                      SDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDS
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Nucleic Acids Res. 28:1397-1406(2000).
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                                                  EATATWTKTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTN
                                                                                                                                              FSHDQLFSLLKITYDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTAT--NTK
                                                                                                                                                                                           LGKTQDFSFVQLSA-LGTATTTDVPA----VPTVATPTHYGYQGTWGMTWVDDTASTPKTK
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Best Local S
Matches 402
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MEDLINE=98187897; Pubmed=9529048;
Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.
"Molecular cloning and characterization of the genes coding fo
highly immunogenic cluster of 90-kilodalton envelope proteins
Chlamydia psittaci subtype that causes abortion in sheep.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia psittaci (Chlamydophila psittaci). Bacteria; Chlamydiales; Chlamydiaceae; Chlam.NCBI_TaxID-83554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003368; -. Pfam; PF02385; OMP; 1. Pfam; PF02415; DUF145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infect. Immun. 66:1317-13:
EMBL; U65942; AAC15921.1;
InterPro; IPR003357; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.; "Identification of a multigene family coding for the 90 kDa proteins of the ovine abortion subtype of Chlamydia psittaci."; FEMS Microbiol. Lett. 142:277-281(1996).
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                                                                                                             NLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGAISTK
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AA; 90694 MW;
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                                        STRAIN-OVINE ENZOOTIC ABORTION ISOLATE $26/3;

MEDLINE-96406378; Pubmed-8810511;

Longbottom D., Russell M., Jones G.E., Lainson F.A., H

"Identification of a multigene family coding for the 9

of the ovine abortion subtype of Chlamydia psittaci.";

FEMS Microbiol. Lett. 142:277-281(1996).
                                                                                                                                                                                                                                        Chlamydia psittaci (Chlamydophila psittaci). Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiacea
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FYSKNSSTIYAGSIYYQHISYWNTW-NTLLQNTLG--AEAPLYLNAQLTYCHASNNMKTN
                           LVAKNHTDTYAGAFYIQHITECSGFIGCLLDKLPGSWSHKPLVLEGQLAYSHVSNDLKTK
                                                                    SDRGFWAAGVANFLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENLISFAFCQLFGSDKDF
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                                                       YSRGFWVSSLANFLNKSGSDTKRKFRHHSAGYALGVYAQTPSDDVCSAAFCQLFGKDKDY
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Q9Z3A1;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2001
                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                         pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AE001586; AAD18172.1; -.
EMBL; AJ33335; CAB37083.1; -.
EMBL; AE002235; AAF38561.1; -.
                                                                                                                                                                                                                                                                                                      Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelbe White O., Hickey E.K., Peterson J., Umayam L.A., Utte Berry K., Bass S., Linher K., Weidman J., Khouri H., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99206606; pubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; "Ast. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMP7 OR PMP_2 OR CP0761.
Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLRE) (POLYMORPHIC MEMBRANE PROTEIN
                                                                                                                                                                                             TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Chlamydia proteins containing the GGAI-repeat belong to of autotransporting pathogenicity factors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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A., Utterback T.,
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                                 TALVISGASWETYANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGSSRIYNVDLGGK
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                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
October 2, 2001, 00:43:56; Search time 18674.8 Seconds (without alignments) 2527.870 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1344157 segs, 7733874588 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-446-677B-5
3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGCGATTTTCGCTCTGCGG......GTTCCTTGAGTCCTTTGGCA 3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                    9b_pat1:*
9b_pat2:*
9b_ph:*
9b_pl::*
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9b_pl3:*
9b_pl4:*
em_ba1:*
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gb_ba2: *
gb_ba3: *
gb_in1: *
gb_in2: *
gb_om: *
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Description	400/00/00/00/00/00/00/00/00/00/00/00/00/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	O		O					Result
ω	7	6	ഗ	4	w	ν	_	17.4
271	272.6	1192	3044.4	3045.6	3047.2	3052	3052	Score
8.9	8.9	39.1	99.8	99.8	99.8	100.0	100.0	Query Match
16448	12127	1200	10044	299650	10766	26920	3052	Query Match Length DB
Н	-	9	_	N	<u>, , , , , , , , , , , , , , , , , , , </u>	Ŋ	9	BB
AE001587	AE002235	A81853	AE002237	AP002545	AE001585	CPN133035	A81831	DB ID
AE001587 Chlamydia	AE002235 Chlamydop	A81853 Sequence 27	AE002237 Chlamydop	AP002545 Chlamydop	AE001585 Chlamydia	AJ133035 Chlamydia	A81831 Sequence 5	Description

Query Match 100.0%; Score 3052; DB 9; Length 3052; Best Local Similarity 100.0%; Pred. No. 0; Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 ATGCGATTTTCGCTCTGCGGATTTCCTCTAGTTTTTTTTT	ERENCE UTHORS ITLE OURNAL TURES SOUR	3052 bp com Patent W	47.8 1.6 11781 1 AE002248 AE002248 47.8 1.6 11781 1 AE001676 AE00167 47.8 1.6 325865 2 AP002548 AP002548 45 1.5 180354 61 AC009689 AC00968 46 1.5 180354 61 AC009689 AC009687 47.8 1.5 1141 10 AX083744 AX08374	178 5.8 2838 9 A81849 159.4 5.2 10574 1 AE001586 150.4 4.9 2526 9 A81843 138.6 4.5 6110 2 CPU65942 126.6 4.1 6234 2 CPU65942 106 3.5 10695 1 AE001629 106 3.5 15789 1 AE002191 106 3.4 1839 9 A81855 64.6 2.1 14477 1 AE002393	9 270 8.8 2787 9 A81835 10 264.8 8.7 4926 2 CPU72499 11 260.8 8.5 10026 1 AE002193 260.8 8.5 10026 1 AE002193 260.8 8.5 300650 2 AP002546 13 260.8 8.5 300650 2 AP002546 14 252.6 8.3 3200 9 A81827 15 252.6 8.3 10757 1 AE001628 16 252.6 8.3 112576 1 AE002192 18 252.6 8.3 112576 1 AE002192 252.6 8.3 112576 1 AE002192 252.6 8.3 112576 1 AE002192 252.6 8.3 12576 1 AE002192 252.6 7.6 300650 2 AP002546 252.8 7.6 300650 2 AP002546 252.8 7.6 10757 1 AE001628 252.8 7.6 10757 1 AE001628 252.8 7.6 10757 1 AE001629 262.8 7.6 10757 1 AE001629 272.8 7.6 10757 1 AE001629 273.1 AE001629 274. 2757 9 A81837 275 9 A81837 276 18184 6 6 0 2787 9 A81837 277 18184 6 6 0 2787 9 A81837 278 18185 1 Sequence 11
Qy 1021 GGAACAATTACATTCCAAGGAAACCGGACGAGCTTACCGTTTTTGAATGGCATCCATC	841 TRAGTCTTTGAAAGAAACCATTCCATTAATGGGTGGCGAGCCATTTATGCTAGGAAACTT	Qy 661 GGTTCTGGAAGGGGCTTTGTACTCCGATGGTGATATTGATATTGATATTGATAAGATGCTTATGTT 720	Qy 541 GATTCCGTCTGTTTCTATCAGAATGCAGCCACTTTTGGAGGTGCTATCCATTCTTCAGGT 600	Oy 361 TCTGGGTTCTCCACGCTCTTTTATTCAGAGCCCCGGAGATATTAAAGAACAGGATGT 420	Qy 61 GACACTTCTTTGAGTGCTACTACGATTTCTTTAACCCCAGAAGATAGTTTTCATGGAGAT 120

2280	GGTCATGCCACCAATGATATGAAAACAGACTACGCAAATTTCCCTATGGTGAAAAACAGC	2221	Qy
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2160 2160	ACAACCTCCCTAGGGAATATTTTCCGTTATGCTTCGGGTAACCCTAATGTAAACGTCGGG	2101 2101	Db 04
2100 2100	GACTATGCGGTTTCCAACAACGAATACAGAATGTATTTAGGATCGTATCTCTATCAATAT	2041	рь
2040	GAGATCACACCTAAGCACTATACTTCGATGGCATTTTCCCAACTCTTTAGTAGAGACAAG	1981 1981	B 64
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1740 1740	CAAGGCAATTGGAAATTAGCTTGGACAGGAACTGGAAACAAAGTTGGAGAATTCTTCTGG	1681 1681	дь Q
1680 1680	GGGGGTAGTGTGACTGTAACTGCTGGAGATTTCCTACCGGTAAGTCCCCATTATGGTTTT	1621 1621	ОУ
1620 1620	GAAGATCTCAGAATGAGAAATTCACAGACGTTCCCTCTGCTCTCTTTAGAGCCTGGAGCC	1561 1561	D 04
1560 1560	AATAAACAGATATCCGTGACGGACTCTATAGAACTTATCTCGCCTACTGGCAATGCCTAT	1501 1501	DЬ
1500 1500	ATAGATATAGATAGCTTAAGCTCATCCTCAACAGCAGCTGTTATTAAAGCAAACACCGCA	1441 1441	DP 6A
1440 1440	TTAGATTTAGGAACCAAACTGATAGCCTCTAAGGAAGACATTGCCATCACAGGCCTCGCG	1381 1381	υ
1380 1380	AAAGAGGGGCCGAAGTCACAGTTTCAAAATTCACGCAGTCTCCAGGATCGCATTTAGTT	1321 1321	Qу Дъ
1320 1320	AGGGATTTTAAATCTACAATCCCTCAGAACGTCAACCTGTCTGCAGGATACTTAGTTATT	1261 1261	Db Qq
1260 1260	L AATAAAGAGTACACAGGGACCATACTCTTTTCTGGAGAAAAGAGTCTAGCAAACGATCCT	1201 1201	DP dd
1200		1141	Ф

SOURCE ORGANIS REFERENCE AUTHORS JOURNAL	CES RSI YWO	RESULT CPN133039 LOCUS DEFINITIO	Оу 3001	Qy 294: Db 294:	Qy 288: Db 288:	Qy 282: рь 282:	Qy 276: Db 276:	Qy 270: Db 270:	Qy 264: Db 264:	Qy 258: Db 258:	Оу 252: Db 252:	Qy 2460 Db 2460	Qy 240: Db 240:	Qy 234: Db 234:	Qy 228: Db 228:	Db 222:
Chlamydophila pneumoniae.  M Chlamydophila pneumoniae  Bacteria; Chlamydiales; Chlamydiaceae; Chlamyd  1 (bases 1 to 26920)  Daugaard, L., Hjerno, K., Knudsen, K., Madsen, A.:  and Birkelund, S.  Unpublished	AJ133035 AJ133035.1 GI:445 AJ133035.1 GI:445 HB1 gene; HB2 gene; gene; omp15 gene; membrane protein 6	2 35 CPN133035 26920 bp DNA BCT 27-FEB-2001 TON Chlamydia pneumoniae GGAI-protein family cluster B, genes omp6, hb1, hb2, hb3, hb4, hb5, hb6, hb7, omp7, pseudogenes omp8, omp9, omp15, strain VRI310.	1 TCTCTAACGAATCATAGGGATTCCAGGGTTCTGTTCCTTGAGTCCTTTGGCA 3052	1 CTAAACTTCGTATTTTATCGAGAATCCTTTACGTTCTTGGTTTGCTTGTCTCCGAGGAGT 3000	1 TAACGGAATACTCGTATCACCTCAGCCCCTAGAGACATTCTTTAGGGGTTCTTTATTTGT 2940	1 ATGGATCATAGGCATTGGGTTTCTCGAACTTGTGTGGAGAATAACGACATTTTATATGCA 2880 	1 CGTTTTAGAAGGTTTCCATTGCCTGTGTGGGTTCCGGATCTTAACTATAAATCCTGGACT 2820 	1 GGAAGTATAGAATGCCGCCCCCATGCTAGGAATTATAATATAAACTGTGGAAGCAAATTT 2760 	1 TTTGTAGGGAGTGGAACGGGTCGGTATCACTTTAACGACTATACTGAGCTCTTATGTCGA 2700	1 GCTCTGGTGATTAGCGGAGACTCCTGGCTTGTTCCGGCAGCACACGTATCAAGACATGCT 2640 	1 TATGACTTTAGTTTCTCCTATATTCCTGATATTTTCCGTAAGGATCCCTCATGTGAAGCT 2580	1 TCGATTTCTGTACCTCTAGGCATACGCTTTGAGAAGCTGGCACTTTCTCAGGATGTACTC 2520	1 CAGGGAGATTTCAAAGAGACGACTGCAGATGGCCGTAGATTTAGTAATGGGAGTTTAACA 2460 	1 AACGGAAGACTTTTCCAAGGTGCCATCCCATTTATGAAACTACAATTAGTTTATGCTTAT 2400	1 TGGAGAAACAATTGTTGGGCTATAGAGTGCGGAGGGAGGATGCCTCTATTGGTATTTGAG 2340 	1 GGTCATGCCACCAATGATATGAAAACAGACTACGCAAATTTCCCTATGGTGAAAAACAGC 2280

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FEATURES
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      CDS
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Boesen,T.
Birect Submission
Submitted (21-JAN-1999) Boesen T., Department of Medical
Microbiology and Immunology, University of Aarhus, The Bartholin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Building,
                                                                                                                                                                LDEGHPOSMRKLRILATVLIVESIILIASGVVLLTVAIPGLSSVISSPACMGACALGC
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'note="hypothetical"

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                                                                             TCAGGAAGTGTGACGTTCGCAGGAAATCATCATGGGTTATATTTTAATAATATTTCCTCA
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 AATAAACAGATATCCGTGACGGACTCTATAGAACTTATCTCGCCTACTGGCAATGCCTAT
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Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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1 (bases 1 to 10766)
Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S. Comparative genomes of Chlamydia pneumoniae and C. trackers (Comparative Genet. 21 (4), 385-389 (1999)
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Chlamydia pneumoniae
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Kalman,S., Mitchell,W.,
Grimwood,J., Davis,R.W.
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ATFEFVACKOCKNFRSLSNWYTVEFGGRKTLGYKLPSGGIFPEGVAQLVNAIDGGVI
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                        TCTGGGTTCTCCACGCTCTCTTTATTCAGAGCCCCGGAGATATTAAAGAACAGGGATGT 420
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  TCTGGGTTCTCCACGCTCTTTTATTCAGAGCCCCGGAGATATTAAAGAACAGGGATGT
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VMLALGIDVLLKKREVPIVLASVTTTPGTGSPRSGISISGADSTIRSLPTYPLDEGHP
QSMRKLRILAIVLIVESIILIASGVVLLTVAIPGLSSIISSPAGMGACALGCVMLALG
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VESHLENNKSLPYDGHGLEEKTKHQIRVVRSSLKAMVPEFLDIRRIFEEMESAFEGYIKV
VESHLENNKSLPYDGHGLEEKTKHQIRVVRSSLKAMVPEFLDIRRIFEEMESFFFISAR
KRLIDLATTLVERKILTEQLERNNLRAFSYLVQDSIFKKIIDHEFLAMKFMILSKS
ICRETIIFEHHEHGVAKSLLHKNAVLLEKVIYRSLQKSYRDIGMSSAKMKILHGNPFF
SLEDNKKTIMKEHAEMLESLSSYRKVFLALSDENVVDTPSDPKKWDLSGIPCRDALSE
ISRDEQWQKKAHLKHQESLYTQARDRLTDQSSKENQKELEKAEGDYISSMERVKKEI
ERVQERIRRAIGKLPWILEREETTGGETTPTPVGGTTASSDLTDLIGRIEVSSREDN
QNQESCVKVLRSHEVEMSWEVKQEYGPKKKEFQDQMGSLERFFTEHIEELEVLQKDYS
KHLSYFKKVNNKKEYQYAKFRLKVLESDLEGILAOTESAESLLTQEELDILATRGALE
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	21 TATGACTTPAGTTTCTCCTATATTCCTGATATTTTCCGTAAGGATCCCTCATGTGAAGCT 2	TOGATTTCTGTACCTCTAGGCATACGCTTTGACAAGCTGGCACTTTCTCAGGATGTACTC	CAGGGAGATTTCAAAGAGACGACTGCAGATGGCCGTAGATTTAGTAATGGGAGTTTAACA	AACGGAAGACTTTTCCAAGGTGCCATCCCATTTATGAAACTACAATTAGTTTATGCTTAT	11 TGGAGAAACAATTGTTGGGCTATAGAGTGCGGAGGGAGCATGCCTCTATTGGTATTTGAG 2	21 GGTCATGCCACCAATGATATGAAAACAGACTACGCAAATTTCCCTATGGTGAAAAACAGC 2	IL ATTCTCTAAGAAGGTTTCTTCAAAATCCTCTTATGATTTTTCATTTTTGTGTGCTTAT 2 	)1 ACAACCTCCCTAGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGG 2 	11 GACTATGCGGTTTCCAACAACGAATACAGAATGTATTTAGGATCGTATCTCTATCAATAT 2 	GAGATCACAC	TCCGAAGACA           TCCGAAGACA	I TTACAGACAGATCGAGGGCTGTGGATCGATGGAATTGGGAATTTCTTCCATGTATCTGCC 1 	01 TGGGGGAATGCTGTAAATGTCAGATCCTTAATGCAGGTTCAAGAGACCCATGCATCGAGC 1 	41 GATAAAATAAATTATAAGCCTAGACCTGAAAAAGGAAGGA	81 CAAGGCAATTGGAAATTAGCTTGGACAGGAACTGGAAACAAAGTTGGAGAATTCTTCTGG 1 	21 GGGGGTAGTGTGACTGTAACTGCTGGAGATTTCCTACCGGTAAGTCCCCATTATGGTTTT 1	SI GAAGATCTCAGAATGAGAAATTCACAGACGTTCCCTCTGCTCTCTTTAGAGCCTGGAGCC 1 	

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                      source
                                               Mutsunori Shirai, Yamaguchi University School of Medicine,
Mutsunori Shirai, Yamaguchi University School of Medicine,
Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
75-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-227, Fax:81-836-22-2415)
On Aug 31, 2000 this sequence version replaced gi:6172316 gi:6172318
gi:6172328 gi:6172310 gi:6172312 gi:6172314 gi:6172316 gi:6172318
gi:6173320 gi:6173322 gi:6172324 gi:635158 gi:6635160 gi:6635162
gi:6635164 gi:6635166 gi:6635168 gi:6635170 gi:6635172 gi:8547422
gi:8635164 gi:635166 gi:6635168 gi:6635170 gi:6635172 gi:8547422
gi:8547426 gi:8547430 gi:8978373
AB033780-AB033781, AB033792-AB033799: Submitted (14-Feb-2000)
AB038345-AB038347: Submitted (18-Dec-2000).
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Chlamydophila pneumoniae
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Chlamydophila pneumoniae J138
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Direct Submission
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573. .
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NGKTKALGFLVGQIMKRTAGKAPPKRVNELLLLELDKG"
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ATFFEVACKDCKNFRSLSNWVSVEFGGRCKTLGVKLPSSGIFPEGVAQLVNAIDQGVI
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LKRSVKEVMDRFMRVTWKSWEASVMLDHSYGVARELFKKAVGVLEESVYKILFKSYRD
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DFKMALEAMQFNEEALLQEELSIQAPSE"
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GHATNDMKTDYANFPMVKNSWRNNCWALECGGSWPLLVEENGRLEQGAIPEWKLQLVY
AYQGDFKETJADGRRESGGSLTSISVPLGIREKKLALSQOVLYDDFSFSYLPDIFRKDY
SCEAALVISGDSWLVPAAHVSRHAFVGSGTGRYHFNDYTELLCRGSIECRPHARNYNI
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Best Local Similarity
Matches 3048; Conserv
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CTTCCCACTTCAGGAAGTAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAAAAAACAG
                                   GGTTCTGGAGGGGCTTTGTACTCCGATGGTGATATTGATATTGATCAGAATGCTTATGTT
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QRTKKVNLENLYADIEKKYHHCVREQEHYWKEVENKEAEYERUGKVLSAEEVSECLQ
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EIEMTLAWELPLLFMKNTFEKASLQYNSCKEMLAKVEDQCKESPTYRSQERLERLN
QDLQTAYTNCQERLQGFSDLSSKVRTCHDHLREQMKHFEVGGLMFINEELLWGAELF
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	1920	TTACAGACAGATCGAGGGCTGTGGATCGATGGAATTGGGAATTTCTTCCATGTATCTGCC	1861	γQ
	1860 5986	TGGGGGAATGCTGTAAATGTCAGATCCTTAATGCAGGTTCAAGAGACCCATGCATCGAGC	1801 5927	Db Qy
····	1800 5926	GATAAAATAAATTATAAGCCTAGACCTGAAAAAGAAGGAAATTTAGTTCCTAATATCTTG 	1741 5867	g Q
	1740 5866	CAAGGCAATTGGAAATTAGCTTGGACAGGAACTGGAAACAAAGTTGGAGAATTCTTCTGG 	1681 5807	B 84
	1680 5806	GGGGGTAGTGTGACTGTAACTGCTGGAGATTTCCTACCGGTAAGTCCCCATTATGGTTTT	1621 5747	DЬ
	1620 5746	GAAGATCTCAGAATGAGAAATTCACAGACGTTCCCTCTGCTCTCTTTAGAGCCTGGAGCC	1561 5687	p 64
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	1500 5626	ATAGATATAGATAGCTTAAGCTCATCCTCAACAGCAGCTGTTATTAAAGCAAACACCGCA	1441 5567	D 89
	1440 5566	TTAGATTTAGGAACCAAACTGATAGCCTCTAAGGAAGACATTGCCATCACAGGCCTCGCG	1381 5507	B 8
	1380 5506	AAAGAGGGGCCGAAGTCACAGTTTCAAAATTCACGCAGTCTCCAGGATCGCATTTAGTT	1321 5447	ДУ
	1320 5446	AGGGATTTTAAATCTACAATCCCTCAGAACGTCAACCTGTCTGCAGGATACTTAGTTATT	1261 5387	B 8
	1260 5386	AATAAAGAGTACACAGGGACCATACTCTTTTCTGGAGAAAAGAGTCTAGCAAACGATCCT	1201 5327	Db 09
	1200 5326	GATCCTATTACTTCTGAAGCAĞATGGGTCTACCCAATTGAATATCAACGGAGATCCTAAA	1141 5267	дь VQ
	1140 5266	TTACAAAATGCTAAATTCCTGAAATTACAGGCGAGAAATGGATGCTCTATAGAATTTTAT	1081 5207	P 99
	1080 5206	GGAACAATTACATTCCAAGGAAACCGGACGAGCTTACCGTTTTTGAATGGCATCCATC	1021 5147	B 6
	1020 5146	AATTTAGGTGGAGCTATTGCCATTGATACTGGAGGGGAGATCAGTTTATCAGCAGAGAAA	961 5087	P 68
	960 5086	. AGCATCTCTTCAGGAGGTCCTACTCTATTTATCAATAATATATCATATGCAAATTGCAAATTGGCAA 	901 5027	Db Qy
	900 5026	TTAGTCTTTGAAAGAAACCATTCCATAATGGGTGGCGGAGCCATTTATGCTAGGAAACTT	841 4967	Db Qy
<del></del>	4966	CTTCCCACTTCAGGAAGTAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAATAAACAG	4907	рь

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CTAAACTTCGTATTTTATCGAGAATCCTTTACGTTCTTGGTTTGCTTGC	TAACGGAATACTCGTATCACCTCAGCCCCTAGAGACATTCTTTAGGGGTTCTTTATTTGT 29	ATGGATCATAGGCATTGGGTTTCTCGAACTTGTGTGGAGAATAACGACATTTTATATGCA 28	CGTTTTTAGAAGGTTTCCATTGCCTGTGTGGTTCCGGATCTTAACTATAAATCCTGGACT 28	GGAAGTATAGAATGCCGCCCCCATGCTAGGAATTATAATATAAACTGTGGAAGCAAATTT 27	TTTGTAGGGAGTGGAACGGGTCGGTATCACTTTAACGACTATACTGAGCTCTTATGTCGA 27	GCTCTGGTGATTAGCGGAGACTCCTGGCTTGTTCCGGCAGCACGCATCAAGACATGCT 26	TATGACTITAGTITCTCCTATATICCTGATATTTTCCGTAAGGATCCCTCATGTGAAGCT 25	TCGATTTCTGTACCTCTAGGCATACGCTTTGAGAAGCTGGCACTTTCTCAGGATGTACTC 25	CAGGGAGATTTCAAAGAGACGACTGCAGATGGCCGTAGATTTAGTAATGGGAGTTTAACA 24	AACGGAAGACTITTCCAAGGTGCCATCCCATTTATGAAACTACAATTAGTTTATGCTTAT 24	TGGAGAAACAATTGTTGGGCTATAGAGTGCGGAGGAGCATGCCTCTATTGGTATTTGAG 23	GGTCATGCCACCAATGATATGAAAACAGACTACGCAAATTTCCCTATGGTGAAAAACAGC 22	ATTCTCTCAAGAAGGTTTCTTCAAAATCCTCTTATGATTTTTCATTTTTGTGTGCTTAT 22	ACAACCTCCCTAGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGG 21	GACTATGCGGTTTCCAACAACGAATACAGAATGTATTTAGGATCGTATCTCTATCAATAT 21	GAGATCACACCTAAGCACTATACTTCGATGGCATTTTCCCAACTCTTTAGTAGAGACAAG 20	TCCGAAGACAATATAAGGTACCGTCATAACAGCGGTGGATATGTTCTATCTGTAAATAAT 19 
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Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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Read, T.D., Brunham, R. C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weldman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J.,
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DNKQLVFERNIS IMGGGAIYARKLSISSGFILFIGNISYANSQNIGGAIAIDTGGEI
SLSAEKGTIFPGGNRTSLPFLMGIHLLQNAKFILFILARNGYSIEFYDPITSEADGSTO
LNINGDPKNKEYTGTILFSGEKSLANDPRDFKSTIPQNVNLSAGYLVIKEGAEVTVSK
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/db_xref="GI:7189685"
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/codon_start=1
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                                                                                                         AYQGDFKETTADGRRFSNGSLTSISVPLGIRFEKLALXQDVLYDFSFSYIPDIFRKDP
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AR39, section 65 of 94 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identified by sequence
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/note="conserved hypothetical protein; identified
Glimmer2; putative"
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LAIEIDDADSCESLEMHVVNVEDLREDSVTSDFNREEFLRNVPESLGGLVKVPAVIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDVALMMDVESGRDRKDATSREFERDSEMSKLSTEVPKVIGVPETFLEGLRDDIRENF
FSSLAIFEGEGTHLVDVELDILSHAVSIYYILASAEAATHLARFDGVRYGYRSPOAHT
ISQLYDLSRGEGFGKEVMRRILLGNVYVLSAERQNVYYKKATAVRAKIVKAFRTAFEKC
EILAMPVCSSPAFEIGEILDPVTLYLQDIYTVAMNLAYLPAIAVPSGFSKEGLPLGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="myrySaleLakavTlGeLTaTGVTQHFFHRIEEAEGQVGAFISL
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ATVVERIKKEDGIILGKLNMDEFAMGSTTLYSAFHPTHNPWDLSRVPGGSSGGSAAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:AL009126; identified by sequence
similarity; putative"
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TGKIAKEIADLMMESPGKNPEEILKEKPELLPMSDEGELQKIIAEVVLANPESIVDYK
NGKTALGFLVGQIIKKRTAGKAPPKRVNELLLLELDKG"
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/gene="CP0773"
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/gene="CP0772"
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/gene="CP0772"
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MNSFAFMAQALEAEKQRQIDEYLNQPNKDPKLVIPAATYRWDPEKKKTVLMRLKESAE
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PIIRGGRIKAIVQGEERYFELAQTHIEDDAGMLKHFGEFAGVDYNRAGVPLIEIVSKP
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/gene="CP0771"
                                                                                6968. .7249
/gene="CP0775"
                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="AAF38573.1"
/db_xref="GI:7189688"
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/protein_id="AAF38572.1"
/db_xref="GI:7189687"
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/db_xref="Gl;7189686"
/translation="MSAVYADWESVIGLEVHVELNTASKLFSSALNRFGDEPNTNIST
                                                                                                                                      /gene="CP0775"
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                                                                                                                                                                                                                      translation="MFKKFLNCKQLPVFMIRETVQNKNFNFLSLDNLSLLALRKEHIF/
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                                                                                                                                                                                                                                                                                                                                                                                                                   'note="hypothetical protein; identified
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    AGTCAGAATGCAGAACGTTCTTATAATGTTCAAGCTGGGGATGTCTATAGCCTTACTGGT
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/gene="CP0778"
complement(9764.
/gene="CP0778"
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NIEDTYVFFKOMVGQSAMLYRRELDLKTTLSEEQAREQAFLEMKGISELVDYELVSAN
LRNVLITGLSLKRSWVLGISQRPVHLIKNTLRILRSFNIDFTSCPAICEDGMLSHPTKD
TTFDQAMAIEKNILFVGSLKNQPMDAALEVLLSGISSPPSQIIYVDQDAERLRSIGA
FCKKANIYFIGMLYTPAKQRVESYNPKLTAIQMSQIRKNLSDEYYESLLSYVKSKG"
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/protein_id="AAF38576.1"
/db_xref="GI:7189691"
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/gene="CP0777"
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/gene="CP0777"
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/protein_id="AAF38575.1"
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Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CP0776"
                                                                                                                                                                                                                                          /translation="MHYFMGLTLFRLKMVRKSIKSFFLKSTEFKKLLDNDVES'
2186 c 1911 g 2926 t 3 others
                                                                                                                                                                                                                                                                      /product="hypothetical protein"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                               putative
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ATQITYIIIGIAGVICLLSFCPFCSKKSRHSHGDSCSSGGCHSHHSDKN"
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                                                                           GATCCTATTACTTCTGAAGCAGATGGGTCTACCCAATTGAATATCAACGGAGATCCTAAA
                                                                                                         TTACAAAATGCTAAATTCCTGAAATTACAGGCGAGAAATGGATACTCTATAGAATTTTAT
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Madsen, A. and Birkelund, S.
Madsen, A. and Birkelund, S.
Madsen, A. and Birkelund, S.
Madsen Anna Sofie (DK); BIRKELUND SVEND (DK)
Location/Qualifiers
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GTAAATAATGAGATCACACCTAAGCACTATACTTCGATGGCATTTTCCCCAACTCTTTAGT 2031
                                                                                                                             AATATCTTGTGGGGGAATGCTGTAAATGTCAGATCCTTAATGCAGGTTCAAGAGACCCCAT
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/translation="DPKNKEYTGTILESGEKSLANDPRDFKSTIPQNVNLSAGYLVIK
EGAEVTYVKFTQSFGSHLVLDLGTKLLASKEDIAITGLAIDLDSLSSSSTAAVIKANT
ANKQISVTDSIELISPTGNAYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPH
GFQGNWKLAWTGTGNKYGEFFYNDKINYK PRPEKEGNLVPNILMGNAVNVRSLMQVQE
THASSLOTDGILWIDGIGNEFHYSASEDNIRVEHNSGGYLVSVNNEITPKHYTSMAFS
THASSLOTDGILWIDGIGNEFHYSASEDNIRVEHNSGGYLVSVNNEITPKHYTSMAFS
OLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGILSRRFLQNPL
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                                                                                                                                                                                                                                                                                                    McClarty G., Salzberg, S.L., Elsen, J. and rraser, c. Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA on Jun 1, 2000 this sequence version replaced g1:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M. Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
Nucleic Acids Res. 28 (6), 1397-1406 (2000)
                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 12127)

Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., White, O., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
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Chlamydophila pneumoniae
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                                  sequence similarity; putative;polymorphic membrane
G family authentic point mutation"
complement(3003. .3191)
                                                                                           /note="This region contains an authentic point mutation, causing a premature stop, and is not the result of a sequencing artifact; similar to GP:4455886; identified b
                                                                                                                                                                         /note="synonym: Chlamydia complement(150. .2987)
                                                                                                                                    /note="This region contains
                                                                                                                                                       /gene="CP0757"
                                                                                                                                                                                                                    /db_xref="taxon:115711"
                                                                                                                                                                                                                                  /organism="Chlamydophila
/strain="AR39"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                CGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGGACTGTA---GCAGGGGCTGCTGT
TGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAG
                                              TCAGAGCCCCGGAGATATTAAA-----GAACAGGGATGTCTCTATTCAAAAAAATGCA 438
                                                                                                                                                                                                                       CACAGCAATCACAAAAAGCTGTTTTAACAACACTAAGGGCGATTTGACTTTCACAGGTAA
                                                                                                  TAACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTAT
                                                                                                                                            TTGTTGCCAAGATCCTCAAGCAACGGCACGTTTTTCTGGGTTCTCCACGCTCTCTTTAT 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGIVQASGFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF"
2722 c 2431 g 3441 t 1 others
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GGYVWAGELGTRVAVENTSGRGFFQEYTPFVKVQAVYARQDSFVELGAISRDFSDSHL
YNLAIPLGIKLEKRFAEQYYHVVAMYSPDVCRSNPKCTTTLLSNQGSWKTKGSNLARQ
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ILELDAGKDIVISADSRSIDAVGSPYGYQKWFINWSTDDKKAFYSWAKQSFUNFRAEQ
LEAPLVPNLLWGSFIDVRSFQNBIELGTBGAPVEKRFWVAGISNVLHRSGRENQRKFR
EAPLVPNLLWGSFIDVRSFQNBIELGFARDKDYFMNTNFAKTYAGSLRLQHDASLYSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     **Translation="MKIPLRFILISLYPTLSMSNLLGAATTEELSASNSFDGTTSTTS
FSSKTSSATDGTNYVRDSVVLENYPKTGETGSTSCFKRDAAAGDLNFLGGGFSFTFS
NIDATTASGAAIGSEBAKTYVTLSGFSALSFLKSPASTYVNGLGAINVRGHULSLLDUB
KVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTRGGAIHTKNLTLSSGGETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATGTVSHSAIDLGTSAK
ITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKEYTGTIVFSGEKLTEAE
AKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDLGTSLVANTESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"This region contains an authentic frame is not the result of a sequencing artifact; si GP:4455886; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity; putative"
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/gene="CP0761"
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/gene="CP0761"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="polymorphic membrane protein
/protein_id="AAF38561.1"
/db_xref="GI:7189674"
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Kalman,S., Mitchell,W., Marathe,R., Lammel,C.,
Grimwood,J., Davis,R.W. and Stephens,R.S.
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Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
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/note="CPn0016"
3196. .5953
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/note="Polymorphic contains frame ships fr
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172. 705
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172. .2957
complement(9380./gene="CPn0020"
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/note="CPn0017"
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ILKKYHGCVYNVQGLPIQTLKYLLEELNIDLWDYSI"
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LFVRPHPCWNYRLSLRYGWHRQDTPNYLEYQMILGTKIFEHWQLYGVYERREADSRFF
FFLKLDKPKKPPF"
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SLLSIGKTTLRVGRIPLLPPFSIMPMEIPKPDIMFRGGTGGFIGGSYLGMSYSPLSR
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                                                                                                                                    RVLLCQALFGHPEALLLDEPTNHLDLYSINWLGNFLKDYEGTVIVVSHDRHFLNTITT
HIADIDYDTIIIYPGNYDDMVEMKTASREQEKADIKSKEKKISQLKEFVAKFGAGSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(13791.
/gene="yjjK"
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LLELGCDTPKLLEYITERLVOPHYNETLALSFSKGRTLOWKRRVNIIVPODPOERERL
LSTTRGLEEOILTFLERLPKEAYLPCIYKLLASOKTOLATTALSFLSHTSHOEALDL
LSTTRGLEEOILTFLERLPKEAYLPCIYKLLASOKTOLATTALSFLSHTSHOEALDL
FQAAKLPGEPIIRAYADLAIYNLTKDPEKKRSLHDYAKKLIQETLLFVDTENQRPHPS
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SYIQRRHIIEPFVTFITETRPLAKNEDHYIFSIQDAFHSLNLLKAGIDTSVLSKTNPR
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/protein_id="AAD18173.1"
/db_xref="GI:4376272"
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/transl_table=11
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/protein_id="AAD18175.1"
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/protein_id="AAD18174.1"
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/gene="xerC"
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/protein_id="AAD18177.1"
/db_xref="GI:4376276"
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No. 6.9e-55;
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/translation="MIASIYSPLDYLKMVKSASPHTLRNYCLDLNGLKIFLEERGNLA PSSPLOLATEKKKYSELPFSLFTKEHVRNYLAKLIENGAKTKKCLGSIKSFAHYC VIQKILLENPARTIHGPRELPKELPSMYTAQVEVLMATPDISKYHGLENGCLMELFYS SGLRISEIVAVNKQDFDLSTHLIRIRGKGKKERIIPVTSNAIQMIQIYLNHPDRKRLE KDPQALTFLNRFGRRISTRSIDRSFQEYLRRSGLSGHITPHTIRHTIATHWLESGMDLK TIQALLGHSSLETTTVYTQVSVKLKKQTHQEAHPHA"

13330 C 3665 g 4743 t
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CTCTGCATTAAATAAAGCCTGCTTCAATGTGACCTCAGGAAGTGTGACGTTCGCAGGAAA Length 16448; Indels 9; Gaps 266 14;

TCAGAGCCCCGGAGATATTAAA-----GAACAGGGATGTCTCTATTCAAAAAATGCA TAACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTAT 438 614 554

CTTATGCTCTTAAACAATTATGTAGTGCGTTTTGAACAAAACCAAAGTAAGACTAAAGGC

GGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTTTCT GGAGCTATTAGTGGGGCGAATGTTACTATAGTAGGCAACTACGATTCCGTCTCTTTCTAT

734 558 674 498

GAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACT 794 615

GTAAATCAGGCAGAGATAAGATTTGCACAAAATACTGCCAAGAATGGTTCTGGAGGGGCT 851 675

TTGTACTCCGATGGTGATATTGATATTGATCAGAATGCTTATGTTCTATTTCGAGAAAAT 911

735

GAGG----CATTGACTACTGCTATAGGTAAGGGAGGGGCTGTCTGTTGTCTTCCCACTTCA 971 792

GGAAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAATAAACAGTTAGTCTTTGAA 852

AGAAACCATTCCATAATGGGTGGCGGAGCCATTTATGCTAGGAAACTTAGCATCTCTTCA 912 TATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGC 103:

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                                                      TTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGGTTTCGCCATTTGAGT
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                 TATAATATAAACTGTGGAAGCAAATTTCGTTTTTAGAAGGTTTCCATTG
                                                                                   AACGACTATACTGAGCTCTTATGTCGAGGAAGTATAGAATGCCGCCCCCATGCTAGGAAT
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1 (bases 1 to 2787)
1 (bases 1 to 2787)
Madsen,A. and Birkelund,S.
MOYEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
PATENT: WO 9858953-A 9 30-DEC-1998;
PADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
Location/Qualifiers
1. .2787 A81835 Sequence S A81835 A81835.1 unidentified unclassified unidentified 9 from Patent GI:6731868 2787 bp W09858953 PAT PNEUMONIAE 21-JAN-2000

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1101 AGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCCATCTACTTCTA
                            1080 TTTACAAAATGCTAAATTCCTGAAATTACAGGCGAGAAATGGATGCTCTATAGAATTTTA 1139
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                                                          CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATCGACTT
                                                                                                                        AGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTATCCGCCGATAGTGGTGACATTGT
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2133 TTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTCAAGAAGGTTTCTTCAAAATCCTCT 2192	Qy 21 Db 21
2073 GTATTTAGGATCGTATCTATCAATATACAACCTCCCTAGGGAATATTTTCCGTTATGC 2132	Qy 20 Db 21
2013 ATTTTCCCAACTCTTTAGTAGAGACAAGGACTATGCGGTTTCCAACAACGAATACAGAAT 2072 	Qy 20 Db 20
1953       CGGTGGATATGTTCTATCTGTAAATAATGAGATCACACCTAAGCACTATACTTCGATGGC       2012         1	Qy 19
1893 AATTGGGAATTTCCTTCCATGTATCTGCCTCCGAAGACAATATAAGGTACCGTCATAACAG 1952 	Qy 18 рь 19
1833       GCAGGTTCAAGAGACCCATGCATCGAGCTTACAGACAGATCGAGGGCTGTGGATCGATGG       1892	Qy 18 Db 18
1773 AGAAGGAAATTTAGTTCCTAATATCTTGTGGGGGAATGCTGTAAATGTCAGATCCTTAAT 1832	Qy 17 Db 18
1713 TGGAAACAAAGTTGGAGAATTCTTCTGGGATAAAATAAA	Qy 17 Db 17
1656 ACCGGTAAGTCCCCATTATGGTTTTCAAGGCAATTGGAAATTAGCTTGGACAGGAAC 1712	Qy 16 Db 16
1599 GCTCTCTTTAGAGCCTGGAGCCGGGGGTAGTGTGACTGTAACTGCTGGAGATTTCCT 1655	Qy 15 Db 16
1539 CTCGCCTACTGGCAATGCCTATGAAGATCTCAGAATGAGAAATTCACAGACGTTCCCTCT 1598 	Qy 15 Db 15
1479 TGTTATTAAAGCAAACACCGCAAATAAACAGATATCCGTGACGGACTCTATAGAACTTAT 1538 	Qy 14 Db 15
1419 CATTGCCATCACAGGCCTCGCGATAGATATAGATAGCTTAAGCTCATCCTCAACAGCAGC 1478	ОУ 14 рь 14
1359 GTCTCCAGGATCGCATTTAGATTTTAGATTTAGGAACCAAACTGATAGCCTCTAAGGAAGA 1418	Qy 13 Db 14
1299 GTCTGCAGGATACTTAGTTAATAAGAGGGGGCCGAAGTCACAGTTTCAAAATTCACGCA 1358 	Оу 12 Db 13
1241 AGAGTCTAGCAAACGATCCTAGGGATTTTAAATCTACAATCCCTCAGAACGTCAACCT	Оу 12 Db 12
1194 TCCTAAAAATAAAGAGTACACAGGGACCATACTCTTTTCTGGAGAAA 1240	Qy 11 Db 12
1140 TGATCCTATTACTTCTGAAGCAGATGGGTCTACCCAATTGAATATCAACGGAGA 1193 	Qy 11 Db 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTCCGTAAGGATCCCTCATGTGAAGCTGCTCTGGTGATTAGCGGAGACTCCTGGCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAGGAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGCTGGCACTTTCTCAGGATGTACTCTATGACTTTAGTTTCTCCTATATTCCTGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGTGAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPU72499 4926 bp DNA BCT 13-MAY-1999 Chlamydophila abortus putative outer membrane protein gene, partial cds; and putative 98 kDa outer membrane protein gene, complete cds.
                                                                                                                                                                                                                Submitted (25-SEP-1996) Moredun Research Institute, Road, Edinburgh EH17 7JH, Scotland, UK
                                                                                                                                                                                                                                                                                                                                                   Longbottom,D., Russell,M., Dunk
98kDa protein genes from ovine
                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydophila abortus
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                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                               (bases 1 to
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<1. .1950</pre>
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                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                              .4926
                                                                                                                                                                                                                                                                                               4926)
                                        as Chlamydia psittaci"
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Best Local
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TGATATTGATCAGAATGCTTATGTTCTATTTCGAGAAAATGAGGCATTGACTACTGCTAT
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                                                                                                                                                                                                              TTTTTCTCTAACCGGCTCGAGCAAAGAAATCAGCTTCACCACTAACTCTACTGCGAAAAA 2674
                                                                                                                                                                                                                                                     TGTTACTATAGTAGGC----AACTACGATTCCGTCTCTTTCTATCAGAATGCAGCCACTTT 575
                                                                                                                                                                                                                                                                                           CAGTATTCTGTTTGATCAGAACTATTCCGCTGAGAATGGTGGAGCCATCTCTTGCAAAGC
                                                                                                                                                                                                                                                                                                                 TGTAGTGCGTTTTGAACAAAACCAAAGTAAGACTAAAGGCGGAGCTATTAGTGGGGCGAA
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48.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 264.8; DB 2;
Pred. No. 2.1e-53;
0; Mismatches 1162;
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Indels Length 4926;

87;

Gaps

13;

695 2791

2734 635

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AUTUM AUGUST
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    1033 c    1031 g    1390 t
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TTCTGGGATAAAATAAATTATAAGCCTAGACCTGAAAAAGAAGGAAATTTAGTTCCTAA 1793	1734 C	Qy
TCAAAGATAATAACTCTGATCCTAAAACACAAACAGCAATCTT 3	794 C	Дb
. سر	689	Qy
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	614	В
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TAGCTTAAGCTCATCCTCAACAGCAGCTGTTATTAAAGCAAACACCGCAAATAAACAGAT 1511	1452 T 1 3557 T	оу Оу
	497	B &
GGAAGTAGAAGCAAAAACAGTCGTGCAAACAGCAGGATCTTTGATTCTGATAGATGCATGC	3437 G	D D
CGAAGTCACAGTTTCAAAATTCACGCAGTCTCCAGGATCGCATTTAGTTTTAGATTTAGG 1391		Qy
ATCTACAATCCCTCAGAACGTCAACCTGTCTGCAGGATACTTAGTTATTAAAGAGGGGGC 1331 	1272 A 3377 G	Оу
CAIRCTTTTTTTGGRAPARAGASTTTRACARACGATCCTRAGGRIT*******TTRA 12/1		pb dg
	257	망
ANTGGGTCTACCCAATTGAATATCAACGGAAGATCCTAAAAATAAAGAGTACACAGGGAC 1220	1161 A	Qy
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RESULT AE00219: LOCUS	Qу	Qу	Оу	рь	Ф	Фр	Qу Дъ	Ф	Фр	Qу ДЪ	Оy	Оу	Qy Db	ДУ	Qу	Qy	Qy Дъ
ILT 11 12193/c	2751 4856	2691 · 4796 ·	2631 . 4736 .	2571 4676	2511 · 4616 ·	2451 ·	2391	2331 ( 4439 (	2271 ( 4379 (	2211 ( 4319 )	2151 ; 4262 (	2091 ( 4214 )	2031	1971	1911 : 4034 :	1854 ; 3974 ;	1794 : 3914 :
AE002193	AAGCAAATT      CGCTAAGGT	CTTATGTCG	AAGACATGO	ATGTGAAGC      CTGTATGAC	GGATGTACT   GAGAAGTGC	GAGTTTAAC     CGATCTTCT	TTATGCTTA	GGTATTTGA	GAAAAACAG      GAAAGGTTC	STGTGCTTA 	AAACGTCGGGATTCTCTCAAG 	CTATCAATAT          TTATCAGCAT	TAGAGACAA          AAAAGATAA	TGTAAATAA 	TGTATCTGC	ATCGAGCTT       GATAGTAT	PATCTTGTG
3	TCGTTT	AGGAAG    GTTTGG	GCTTTTGI	TGCTCI      AGGATI	CTATGA             TATGA	ATCGAT	TCAGGG	GAACGO   -AGTTO	CTGGAG         TTGGGG	TGGTCA	GATTCI	TACAAC	GGACTA       AGACTA	TGAGAT     AAATAC	CTCCGA   GAATGO	ACP	TGGGGGAP       TGGGGATC
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DNA	TTCC 2778	CCGCCCCA     ACGAAGCTC	AACGGGTCG             	CGGAGACTC           TGACGTTTC	CTCCTATAT        GATGTATAT	TCTAGGCAT           TATAGGTAT	AGAGACGAC          AGAACCAAC	CCAAGGTGC      TGATAGTTA	TTGGGCTAT	TGATATGAA        CAACATGAC	GTTTCTTCA          GTTTTCTAA	GAATATTTT          GAGCAAGTT	CAACAACGA          CAAGAACGC	GCACTATAC 	AAGGTACCG         CAAATTCCG	AGGCTGTG          GGTTTGTG	TGTCAGATC
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вст		GAATTATAAT          AAATTATAAC	CTTTAACGAC         CTTAACCTCT	TGTTCCGGCA      AACCACAGCT	TATTTTCCGT	TGAGAAGCTG         TGAGAAACTC	TGGCCGTAGA       AGGCCGGGTC	ATTTATGAAA         GTTTGCAAAA	CGGAGGGAGC     GTCTACTAGC	CTACGCAAAT          CTATACAGAC	TCTTATGATI	TGCTTCGCGT	AATGTATTTA       CGTCTATGCG	GGCATTTTCC          GGCTTTCTGT	CAGCGGTGGA      AGTTCGGGA	TGGAATTGGG             TGGAATTGGG	GCAGGTTCAA      AGATGTCTTG
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2000		3 2750 1 3 4855		2630	2570	1 2510 1 4615	3 2450 3 4555	2390	2330	r 2270 r 4378	r 2210 1 4318	1 2150 3 4261	2090 4 4213	2030	1970	1910 1 4033	1853

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COMMENT
FEATURES
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On Jun 1, 2000 this sequence version replaced gi:7189234.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 10026)
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Chlamydophila pneumoniae AR39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-MAR-2000) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 10026) Read, T.D., Brunham, R.
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ALKGNVLETUVAGTTQTEGSTLLMQPGTKLKADTEAISLTKLVVDLSALEGNKSYST ET
AGANKTITLTSPLVFODSSGNEYESHTI INQAFTYPDLVFDTAATAASDT IDALLTSPV
QTPEPHYGYQGHWEATMADTSTAKSGTMTWVTTGYNDNEERRASVVDDSLMASFTDIR
TLQQIMTSQANSIYQQRGLMASGTANFFHKDKSGTNQAFRHKSYGYIVGGSAEDFSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFMNNKGETGGGALGFEASSSITQNSSLFFSGNTATDAAGKGGAIYCEKTGETPTLTI
SGNKSLTFAENSSVTQGGAICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIAIADSGS
LSLSANQGDITFLGNTLTSTSAPTSTRNAIYLGSSAKITNLRAAQGQSIYFYDPIASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mkiplhkllisstlytpillsiatygadaslsptdsfdgaggst
ftpkstadangtnyvlsgnvyindagkgtaltgccftettgdltftgkgysfsfntyd
agsnagaaasttadkaltftgfsnlsfiaapgttvasgkstlssagalnltdngtilf
                                                                                                                 /note="similar to GP:4376728;
similarity; putative"
                                                                                                                                                                                                                                                                                                     GSAHIYNVDCGLRYSF"
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similarity; putative"
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/gene="CP0307"
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                                                                                                                                                                                                                                                                                                                                                                                       ILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNNSGALELGGSLALYLPKEAPFFQGYFF
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/protein_id="AAF38164.1"
/db_xref="GI:7189235"
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837 ACAGTTAGTCTTTGAAAGAAACCATTCCATAATGGGTGGCGGAGCCATTTATGCTAGGAA 896

4954 TTGC----

Query Match
Best Local Similarity Matches 1055;

48.8%;

Score 260.8; DB 1; Pred. No. 2e-52; Mismatches 1032;

Length 10026; Indels 75; Gaps

10;

Conservative

0;

5074 GAAAGGATCTGGCGGTGCTCTGTACAGCACTGACTGTTCGATTACAGATAACTTTCA 5015

657 GAATGGTTCTGGAGGGGCTTTGTACTCCGATGGTGATATTGATATTGATCAGAATGCTTA 716

TTGTCTTCCCACTTCAGGAAGTAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAATAA 836

----ACTACGACAGATAAAACAGTGACTCTTACTGGGAACAA

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BASE COUNT
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TSGGLK ISGDLKFHNNEGSFYDNPGLKANLKLFFLDLSSTSGTVNLDDENPIBSSMAA
PDYGYGGSMTLYPKVGAGGKVTLDAEMQALGYTPKPEDLASTLVPNSLMAVVNIHSI
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VAFSQLFGKSKDYVVSDIKSQYYAGSLCAQSSYVIPLHSSLRRHYLSKVLPELFGETP
LVLHGQYSYGRNHHNMTTKLANNTQGKSDMDSHSFAVEVGGSLPVDLNYRYLTSYSPY
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SLSGNTATVSGGAIYATKCALHGNTTLTFDGNTATTAGGAIYTTEDFTLTGSTGTVT
FSTNTAKTAGALHTKNISTFKNKALVFSGNSATATATTTDQEGCGGALYSES
IATKSLTLTENESLSFINNTAKRSGGCIYAPKOVISGSESINFDGNTAETSGGAIYSES
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LGAGAKITKLAAAPGHTIYFYDPITMEAPASGGTIEELVINPVVKAIVPPPQPKNGPI
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SSNTARDKGGIYSKEKDSTLDANTGVVTFKSNTAKTGGANSDNTALTGNTQVLFQ
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TKCTLDGNTTLTFDQNTATAGCGGAIYTETEDESLKGSTGTVTFSTNTAKTGGALYSK
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SINQLIETKSSGEPFERELWLSGIANFFYRDSMPTRHGFRHISGGYALGITATTPAED
QLTFAFCQLFARDRNHITGKNHGDTYGASLYFHHTEGLFDIANFLWGKATRAPWVLSE
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TAASTDTLNLMLADANSEIEYGGAIVESGEKLSPTEKAIAANVTSTIRQPAVLARGDL
VLRDGVTVTFKDLTOSPESRILMDGCTTLSAKEANLSLNGLAVRLSSLDGTNKAALKT
EAADKNISLSGTIALIDTEGSFYENHNLKSASTYPLLELTTAGANGTITIGALSTLTL
                                                                                                                                                                VKLQVVSVNQKGFQEVAADPRIFDASHLVNVSIPMGLTFKHESAKPPSALLLTLGYAV
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THDGAAINNTNTALSFSGFSSLLIDSAPATGTSGGKGAICVTNTEGGTATFTDNASVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="polymorphic membrane protein
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similarity; putative"
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LKEVEPFVKVQYIYAHQQDFYERYAEGRAFNKSELINVEIPIGVTFERDSKSEKGTYD
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TGNKNLSFTNNTALTYGGAISGLKVSISAGGPTLFQSNISGSSAGQGGGGAINIASAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 15068)
Kalman, S., Mitchell, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10192388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAKKESIQNLELKITECQNKLAQKQPKRKSSQKSFMRSIKHLSKNPVILFDC*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae CWL029
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gene

CDS

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gene

CDS

CDS

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BASE COUNT
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Best Local Similarity
                                                   10397
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1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDVYRKNPRSRTSLMVSGASWTSLCKNLARQAFLASAGSHLTLSPHVELSGEAAYELR
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LTLMYTLDAYRRNPKCQTSLIASDANMMAYGTNLARQGFSVRAANHFQVNPHMEIFGQ
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/protein_id="AAD18590.1"
/db_xref="G1:4376729"
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Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases. Mutsunori Shirai, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi 75-8505, Japan (E-mail:mshirai@po.cc. yamaguchi-u.ac.jp, Tel:81-836-22-2227, Fax:81-836-22-2415)
                                                                                                                                                                                                                         Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T. Comparison of whole genome sequences of Chlamydia pneumon from Japan and CWLD29 from USA
Nucleic Acids Res. 28 (12), 2311-2314 (2000)
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Chlamydophila pneumoniae J138
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APO02546 AB033782 AB033783 AB033784 AB033785 AB033800 AB033801 APO02546 AB033782 AB033804 AB033805 AB033806 AB033807 AB033803 AB033804 AB033805 AB033806 AB033807 AB033811 AB033812 AB033813 AB033814 AB033815 AB033809 AB033810 AB033811 AB033812 AB033813 AB033814 AB033815 AB036079 AB036080 AB036081 AB036082 AB038348 AB038349 BA000008 AB0025466.2 GI:10176692
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BA000008
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gi:6172386 gi:6172338 gi:6172390 gi:6172392
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gi:8547438 gi:8978640.
AB033782-AB033785, AB033800-AB033815: Submit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB038348-AB038349:
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)35
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gi:6172394 gi:6174666
gi:6635180 gi:8547433
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gene

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Translation-"MFNKDEIIVPKNLEEEMKESYLRYSMSVIISRALPDIRDGLKPS
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                                                                                                                                                                                                                                                                                                                                                              GVRSTLTNERNGNVLGATPVTDHDSTLLMSSQGQATRTNMQDVRVMGRSTQGVRLVHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YHNRIREGFLSLASADPSRYLVLDARESLASLIDKVMLHTQLGLCT"
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/protein_id="BAA98482.1"
/db_xref="GI:8978646"
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DELFDVDLETPKEALEELILNLNRPYNEIIIGGFSQGAILATHLVLTSQNPYAGALIF
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/protein_id="BAA98481.1"
/db_xref="GI:8978645"
                                                                                                                                                          'codon_start=1
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MDPKEKNYDASAITVLEGLQAVRERPGMYIGDTGITGLHHLVYE
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TGGAGAAAAGAGTCTAGCAAACGA---
                                                         GAACTTAAACTTAGCAGATGCGAACAGTGAGATCGAGTATGGGGGTGCGATTGTCTTTTC
                                                                                                               --AATTGAATATCAACGGAGATCCTAAAAAATAAAGAGTACACAGGGACCATACTCTTTTC 1232
                                                                                                                                                                        ATCTATCTATTCTATGATCCCATCACAAATCCAGGAACCGCAGCTTCTACCGACACATT
                                                                                                                                                                                                                                  CTCTATAGAATTTTATGATCCTATTACTTCTGAAGCAGATGGGTCTACCC------
                                                                                                                                                                                                                                                                                        AAACGCAATAAATATCATTGATACCGCTAAAGTCACATCGATACGAGCTGCTACGGGGCA 195627
                                                                                                                                                                                                                                                                                                                                                       GAATGGCATCCATCTTTTACAAAATGCTAAATTCCTGAAATTACAGGCGAGAAATGGATG 1124
                                                                                                                                                                                                                                                                                                                                                                                                                TACTTCTGGAGATATTACCTTCAATAACAACCAAGTCACCAACGGAAGCACAAGTACAAG
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QAREAAKKARELTLRKSALDSARLPGKLIDCLEKDPERKCEMY TVEGDSAGGSAKOGRD
RREQAILPIRGKILNVEKARLOKIFONQEIGTIAALGCGIGADNFNLSKLRYBRII
MTDADVDGSHIRTLLLTFFYRHMTALIENECVYIAQPPLYKVSKKKDFRYILSEKEMD
SYLLMLGTNESSILFKSTERELRGEALESFINVILDVESFIRTLEKKALPSEFLEMY
KEGIGYPLYKLAAPATGNGGRYLYSDEEKEBALAQEETHKFKIIELYKYAPVFVDIONQ
KEYGLDISSYLLPGKNEIVIGNEDSPSCNYSCYTLEEVINYLKNLGRKGIEIQRYKG
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/protein_id="BAA98486.1"
/protein_id="BAA98486.1"
/db_xref="G1:8978650"
/translation="MFLKRKKRGGSQVQNKRTASPIKHAKHYLHNYLQELQKIMAARP
/translation="MFLKRKKRGGSQVQNKRTASPIKHAKHYLHNYLQELQKIMAARP
HDAIDAWNQVFRDKYKGMSQAIGFRDHILLVKVYNSSLYALLKQTPQNDLIMSLYQVA
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SFDKVTFFYEGGIQSFVSYLNQNKESLFSEPIYICGTRVGDDGEIEFEAALQWNSGYS
ELVYSYANNIPTRQGGTHLTGFSTALTRVINTYIKAHNLAKNNKLALTGEDIREGLTA
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CAATTGTTGGGCTATAGAGTGCGGAGGGAGCGTCTATTGGTATTTGAGAACGGAAG
                                                                     AGACAACCACATGAAGACATATTATACCGATAACTCTATCATCAAGGGTTCTTGGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                       ACCTAAGCACTATACTTCGATGGCATTTTCCCAACTCTTTAGTAGAGACAAGGACTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAGATCTCCCAGATCATTCCTTTATCG---TTCGATGCTAAATTCAGTTATCTCCATAC
                                                                                                                                                                              AAGAAGGTTTCTTCAAAATCCTCTTATGATTTTTCATTTTTGTGTGCTTATGGTCATGC
                                                                                                                                                                                                                                                       CCTAGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGGATTCTCTC
                                                                                                                                                                                                                                                                                           TACAGGTAAGAACCACGGAGATACTTACGGTGCCTCTTTGTATTTCCACCATACAGAAGG
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                                                                                                         CACCAATGATATGAAAACAGACTACGCAAATTTCCCCTATGGTGAAAAAACAGCTGGAGAAA
                                                                                                                                                                                                                                                                                                                              GGTTTCCAACAACGAATACAGAATGTATTTAGGATCGTATCTCTATCAATATACAACCTC
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Madsen, A. and Birkelund, S.
NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
Patent: WO 9858953 A 1 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
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TSGGAIDDEGTSILSNNKFLYEEGNAAKTTGGAICNTKASGSPELLISNNKTLIEASN
VAETSGGAILDEGTSILSNNKFLYEEGNAAKTTGGAICNTKASGSPELLISNNKTLIEASN
VAETSGGAILBAKKLALSSGGTEELRANKVSSATPKGAAISIDASGELSLSAETGNITF
VRNTLITTGSTDTPKRNAINIGSNGKFETELRAAKNTIFFYDPITSEGTSSDVLKINN
GSAGALNPYQGTILESGTSTTADELKVADNLKSSFTQPVSLGGKELLDKGVTVSGK
LNLIDIEGNIYESHMESHDQLFSLLKITDADUDTNVDISSLIPVPAEDPNSEYGFOG
QWNVNWTTDTAINTKEATATWTKTGFVESPERKSALVCWTLWGVFTDIRSLQQLVEIG
ATGMEHKQGFEVSSWENELHKTGDENRKGFRTSGGYVIEGSAHTPKDLFTFRECHL
FARDKDCFIAHNNSRTYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIPIAL
DVQVSFSHSDNAMETHYTGLPSEGSWSNECIAGGIGLDLFFVLSNHPLFKTFIPOM
KVEMVYVSQNSFFESSSDGRGFSIGRILNLSIPVGAKFVQGDIGDSYTYDLSGFFVSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTTAACGACTATACTGAGCTCTTATGTCGAGGAAGTATAGAATGCCGCCCCCATGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTCGCGGTGGCAATCTTTCAAGACAGGCATTTTTACTGAGGGGTAGCAACAACTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTCTATCGTAACAATCCCCAATCTACAGCGACTCTTGTGATGAGCCCCAGACTCTTGGAA 2831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACGCAAATTTCCCTATGGTGAAAAACAGCTGGAGAAACAATTGTTGGGCTATAGAGTG
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Chlamydophila pneumoniae.
Chlamydophila pneumoniae
Bacterila; Chlamydiales; Chlamydiaceae; Chlamydophila
1 (bases 1 to 6030)
  2 (bases 1 to 6030)
Knudsen,K., Madsen,A.S.,
Birkelund,S.
                                                         Submitted (29-AUG-1997) Knudsen K., Department of Medical Microbiology and Immunology, University of Aahus, The Bartholin building, University of Aahus, DK-8000 Aarhus C, DENMARK
                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae
AJ001311
                                                                                                                         Direct Submission
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                      Mygind, P.,
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                      Christiansen, G.
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MEDLINE
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outer membrane proteins of Chlamydia pneumoniae
Infect. Immun. 67 (1), 375-383 (1999)
                                                                                                                                  2905. ...../gene="omp4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFSNNIAEAAGGAINSTGNCTITGNTSLVFSENSVTATAGNGGALSGDADVTISGNOS
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                                                                                                                                                                                                                                                                                                                                                                               complement (2799.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="outer membrane complement(2698. .2742)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Chlamydophila pneumoniae"
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2905. .2955
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/gene="omp4"
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LIRNDPKCTTALVISGASWETYANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative"
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Best Local Similarity
Matches 1292; Conserv
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                                                                                                                                                                          ATCAACAAAGGGAGGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACACAGG 3527
                                                                                                                                                                                                                                                                                                                                                                                                                  AAATATTCGTAAACTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAA 3407
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                                                                                                                                                                                                                                                                                                                                                       TGGGGCGAATGTTACTATAGTAGGCAACT---ACGATTCCGTCTCTTTCTATCAGAATGC 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACAATTATGTAGTGCGTTTTGAACAAAACCAAAGTAAGACTAAAGGCGGAGCTATTAG 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGCTGGGGATGTCTATAGCCTTACTGGTGATGTCTCAATATCTAACGTCGATAACTC 209
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/note="putative"
1341 c 1195 g
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KVEMVYVSQNSFFESSSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSD
VYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
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FARDKDCFIAHNNSRTYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIPLAL
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1710 AACTGGAAACAAAGTTGGAGAATTCTTCTGGGATAAAATAAAT	Qy
4575 TCCTAATTCAGAATACGGATTCCAAGGACAATGGAATGTTAATTGGACTACGGATACAGC 4634	Ъ
1662AAGTCCCCATTATGGTTTTCAAGGCAATTGGAAATTAGCTTGGACAGG 1709	Qy
	Db !
614 TGGAGCCGGGGGTAGTGTGACTGTAACTGCTGGAGATTTCCTACCGGT 16	Q !
1554 TGCCTATGAAGAATCAGAAAATTCAGAAGATCTCTCTCTC	D Q
98 TGCTTCAAATAAAGTGATCGTATCTGGGAAGCTCAACCTGATTGATATTGAAGGGAA 4	Db
1494 CACCGCAAATAAACAGATATCCGTGACGGACTCTATAGAACTTATCTCGCCTACTGGCAA 1553	Qy
TITLE	р Б 2
278 CCTCGCATGGATTCAGGAACGACATTATCAACTACAGCTGGGAGTATTACAATCACGAA	2 B
374 TTTAGTTTTAGGTATCACAAACTGATAGCCTCTAAGGAAGACATTGCCATCACAGG 1	Qy
4218 ATTGCTACAAAAGGGAGTCACTTTAGAGAGCACGAGCTTCTCTCAAGAGGCCCGGTTCTCT 4277	Db
1314 AGTTATTAAAGAGGGGGCCGAAGTCACAGTTTCAAAATTCACGCAGTCTCCAGGATCGCA 1373	Qy
4158 AGTTGCTGACAATTTAAAATCTTCATTCACGCAGCCAGTCTCCCCTATCCGGAGGAAAGTT 4217	Дb
TTAAATCTACAATCCCTCAGAACGTCAACCTGTCTGCAGGATAC	Qy
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C	Qу
038 C	DЬ
149 T	Qy
3978 CGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATACAATTTTCTTCTATGATCCCAT 4037	В
1089 TGCTAAATTCCTGAAATTACAGGCGAGAAATGGATGCTCTATAGAATTTTATGATCCTAT 1148	Qy
3918 CCTTACAACAACCGGAAGTACCGATACTCCTAAACGTAATGCGATCAACATAGGAAGTAA 3977	Дb
1044CCGGACGAGCTTACCGTTTTTGAATGGCATCCATCTTTTACAAAA 1088	Qy
3858 TGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAACATTACCTTTGTAAGAAATAC 3917	DЬ
GATCAGTTTATCAGCAGAGAAAGGAACA	Qy
3801 GTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAGGGGGGTGCTATCAGCATCGA 3857	DЬ
TATTGO	Qy
3741 AACAAGCGGTGGCGCCATCCATGCTAAAAAGCTAGCCCTTTCCTCTGGAGGCTTTACAGA 3800	Дb
CATTTATGCTAGGAAACTTAGCATCTCTTCA	Qy
3681 ATCTCCTGAACTGATAATCTCTAACAATAAGACTCTGATCTTTGCTTCAAACGTAGCAGA 3740	Дb
AAACAGTTAG	Qy
3645 TACTG	Db
747 TACTGCTATAGGTAAGGGAGGGGCTGTCTGTTGTCTTCCCCACTTCAGGAAGTAGTACTCC 806	Qγ
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                                                                                            GAATTATAATATAAACTGTGGAAGCAAATTTCGTTTTTAGAAGGTTTCCATTGCCTGTGT 2789
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GGTTCCGGATCTTAACT 2806
                                                          GAACTACAATGTAGATGTTGGTACCAAACTCCGATTCTAGATTGCTAAAACTCCCTAGTT 5711
                                                                                                                                                                                   CTACAACTCCAATTGTGAGCTCTTCGGACATTACGCTATGGAACTCCGTGGATCTTCAAG
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## RESULT Chlamydia pneumoniae surface exposed protein Omp6 DNA. AAX06818; AAX06818 standard; DNA; 3052 BP 26-APR-1999 (first entry)

ALIGNMENTS

Omp6; outer membrane protein 6; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma; ss.

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XX O Birkelund Mygind P; WPI; 1999-105610/09 WO9858953-A2 Chlamydia pneumoniae. (BIRK/) BIRKELUND S. (CHRI/) CHRISTIANSEN G. 23-JUN-1997; 19-JUN-1998; 30-DEC-1998 s Christiansen 97DK-0000744 98WO-DK00266 Location/Qualifiers
1..2764 /\*tag= a G, Knudsen K, Madsen

P-PSDB; AAW88419

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Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89,6-100.3 kDa and 20 about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by pCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
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Matches 3052; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This DNA sequence codes for the novel 100.3 kDa surface exposed protein Omp6 (see AAW88419) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
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                                             The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY34584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
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	720 15203	GGTTCTGGAGGGGCTTTGTACTCCGATGGTGATATTGATATTGATCAGAATGCTTATGTT 	661 15144	DP QA
	660 15143	CCCCTACAGATTGCAGTAAATCAGGCAGAGATAAGATTTGCACAAAATACTGCCAAGAAT	601 15084	Dp VQ
	600 15083	GATTCCGTCTCTTTCTAFCAGAATGCAGCCACTTTTGGAGGTGCTATCCATTCTTCAGGT	541 15024	р В
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	300 14783	TCAGGAAGTGTGACGTTCGCAGGAAATCATCATGGGTTATATTTTAATAATATTTTCCTCA	241 14724	Db Qy
	240 14723	GATGTCTCAATATCTAACGTCGATAACTCTGCATTAAATAAA	181 14664	ОУ ОБ
	180 14663	AGTCAGAATGCAGAACGTTCTTATAATGTTCAAGCTGGGGATGTCTATAGGCCTTACTGGT 	121 14604	Оy
	120 14603	GACACTTCTTTGAGTGCTACTACGATTTCTTTAACCCCAGAAGATAGTTTTCATGGAGAT	61 14544	₽ <b>Q</b>
	60 14543	ATGCGATTTTCGCTCTGCGGATTTCCTCTAGTTTTTTCTTTAACATTGCTCTCAGTCTTC	1 14484	B 8
0;	ps ;;	atch 99.5%; Score 3037.8; DB 20; Length 1230025 cal Similarity 99.7%; Pred. No. 0; 3042; Conservative 0; Mismatches 10; Indels 0; Ga	Query M Best Lo Matches	> m 0

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                                                                                                                                                                                                                           The present sequence is that of Chlamydia pneumoniae genomic DNA including an open reading frame that codes for CPN100877 RY-61 (see AAY95548), a putative 98 kba outer membrane protein. It is an example of C. pneumoniae polynucleotide molecules of the invention (see AAA50030-42) that encode antigenic polypeptides (see AAY95543-55) useful in the diagnosis, treatment and prevention of Chlamydia infection. The polynucleotides can be utilised: in the recombinant production of Chlamydia antigens using transformed unicellular host cells; in vaccines or live vaccine vectors; in naked form or formulated with a delivery vehicle for therapy and prophylaxis of Chlamydia infection; and as probes or primers for diagnosis of Chlamydial
                                                                                                                                                                                              Sequence 2950
                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                           prevention
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        AGTCAGAATGCAGAACGTTCTTATAATGTTCAAGCTGGGGATGTCTATAGCCCTTACTGGT
                                                      GACACTTCTTTGAGTGCTACCTACGATTTCTTTAACCCCAGAAGATAGTTTTCATGGAGAT
                                                                                                    gacacttctttgagtgctactacgatttctttaaccccagaagatagttttcatggagat
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20	AGGGATTTTAAATCTACAATCCCTCAGAACGTCAACCTGTCTGCAGGATACTTAGTTATT 13	1261
	ataaagagtacacagggaccatactcttttctggagaaaagagtctagcaaacgatcct 13	·ω
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00	GATCCTATTACTTCTGAAGCAGATGGGTCTACCCAATTGAATATCAACGGAGATCCTAAA 12 	1141 1241
40	TTACAAAATGCTAAATTCCTGAAATTACAGGCGAGAAATGGATGCTCTATAGAATTTTAT 11 	1081 1181
80	GGAACAATTACATTCCAAGGAAACCGGACGAGCTTACCGTTTTTGAATGGCATCCATC	1021 1121
20	AATTTAGGTGGAGCTATTGCCATTGATACTGGAGGGGGAGATCAGTTTATCAGCAGAGAAA 10	1061
60	AGCATCTCTTCAGGAGGTCCTACTCTATTTATCAATAATATATCATATGCAAATTCGCAA 96 	901
00	TTAGTCTTTGAAAGAAACCATTCCATAATGGGTGGCGGAGCCATTTATGCTAGGAAACTT 90	. 841 941
• •	CTTCCCACTTCAGGAAGTAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAATAAACAG 84 	781 881
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0 0	GGTTCTGGAGGGGCTTTGTACTCCGATGGTGATATTGATATTGATCAGAATGCTTATGTT 72 	661 761
	CCCCTACAGATTGCAGTAAATCAGGCAGAGATAAGATTTGCACAAAATACTGCCAAGAAT 66 	701
	GATTCCGTCTCTTTCTATCAGAATGCAGCCACTTTTGGAGGTGCTATCCATTCTTCAGGT 60	541 641
	CAAAGTAAGACTAAAGGCGGAGCTATTAGTGGGGCGAATGTTACTATAGTAGGCAACTAC 54 	481
0 0	CTCTATTCAAAAAATGCACTTATGCTCTTAAACAATTATGTAGTGCGTTTTGAACAAAAC 48 	, 421 521
• •	TCTGGGTTCTCCACGCTCTCTTTATTCAGAGCCCCGGAGATATTAAAGAACAGGGATGT 42 	361 461
0 0	GGAACTACAAAGGAAGGGGCTGTACTTTGTTGCCAAGATCCTCAAGCAACGGCACGTTTT 36 	301
• •	TCAGGAAGTGTGACGTTCGCAGGAAATCATCATGGGTTATATTTTAATAATATTTCCTCA 30 	341
• •	GATGTCTCAATATCTAACGTCGATAACTCTGCATTAAATAAA	181

Qy 234	ν	Оу 228	ОУ 22 Db 23	Oy 216 Db 226	Qy 2101 Db 2201	Qy 204 Db 214	20	Qy 19 Db 20	Qу 18 дь 19	Qy 180 Db 190	Qy 1741 Db 1841	Qy 16 Db 17	Qy 16 Db 17	15 16	Qy 15 Db 16	Qy 14 Db 15	Qy 13 Db 14	Qy 13 Db 14	Db 13
41 AACGGAAGACTTTTCCAAGGTGCCATCCCATTTATGAAACTACAATTAGTTTATGCTTAT		1 TGGAGAAACAAT	21 GGTCATGCCACCAATGATATGAAAACAGACTACGCAAATTTTCCCTATGGTGAAAAACAGC 	61 ATTCTCTCAAGAAGGTTTCTTCAAAATCCTCTTATGATTTTTCATTTTTTTGTGTGCCTTAT	01 ACAACCTCCCTAGGGAATATTTTCCGTTATGCTTCGCGTAACCCTAATGTAAACGTCGGG 	41 GACTATGCGGTTTCCAACAACGAATACAGAATGTATTTAGGATGGTATCTGTATCAATAT 	1 GAGATCACACCTAAGCACTATACTTCGATGGCATTTTCCCAACTCTTTAGTAGAGACACIIIIIIIIII	921 TCCGAAGACAATATAAGGTACCGTCATAACAGCGGTGGATATGTTCTATCTGTAAATAAT	61 TTACAGACAGATCGAGGGCTGTGG 	.801 TGGGGGAATGCTGTAAATGTCAGATCCTTAATGCAGGTTCAAGAGACCCATGCATCGATCG	1741 GATAAAATAAATTATAAGCCTAGACCTGAAAAAGAAGGAAATTTAGTTCCTAATATCTTG	81 CAAGGCAATTGGAAATTAGCTTGGACAGGAACTGGAAACAAAGTTGGAGAATTCTTCTGG 	21 GGGGTAGTGTGACTGTAACTGCTGGAGAGTTTCCTACCGGTAAGTCCCCATTATGGTTTT	61 GAAGATCTCAGAATGAGAAATTCACAGACGTTCCCTCTGCTCTCTTTAGAGCCTGGAGCC	501 AATAAACAGATATCCGTGACGGACTCTATAGAACTTATCTCGCCTACTGGCAATGCCTAT	441 ATAGATATAGATAGCTTAAGCTCATCCTCAACAGCAGCTGTTATTAAAGCAAACACCGCA 	381 TTAGATTTAGGAACCAAACTGATAGCCTCTAAGGAAGACATTGCCATCACAGGCCTCGCG 	1321 AAAGAGGGGGCCGAAGTCACAGTTTCAAAATTCACGCAGTCTCCAGGATCGCATTTAGTT	
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                                 Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific outer membrane proteins of C. pneumoniae or nucleic acids encoc
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(CHRI/) CHRISTIANSEN
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> This DNA sequence encodes the novel surface exposed protein Omp6 (see AAW88430) of Chlamydia pneumoniae, a human respiratory pathogen. It is described as a subsequence of a claimed nucleic acid fragment (see AAX06818) encoding omp6 (see AAW88419). The invention provides a new species specific test for identifying mammals (including humans) infected with C. pneumoniae. The test comprises detecting antibodies specific for surface exposed proteins Omp4-Omp15 (see AAW88417-28) or detecting nucleic acid fragments encoding them (see AAW88417-28), especially by PCR. The proteins are also used in the diagnosts of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.

Sequence 1200 BP; 378 A; 243 C; 247 ດ; 332 T; 0 other;

Query Match
Best Local Similarity

39.18;

Score 1192; Pred. No. 0;

DB

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Length 1200;

δÃ δÃ δõ δÃ Q ğ Q δÃ 밁 δÃ 밁 δÃ 밁 B 밁 δõ ₽ В 밁 망 В 밁 ρy 밁 Ş Matches 1195; 1912 GTATCTGCCTCCGAAGACAATATAAAGGTACCGTCATAACAGCGGTGGATATGTTCTATCT 1252 AACGATCCTAGGGATTTTAAATCTACAATCCCTCAGAACGTCAACCTGTCTGCAGGATAC 1192 GATCCTAAAAATAAAGAGTACACAGGGACCATACTCTTTTCTGGAGAAAAGAGTCTAGCA 1251 121 481 361 61 L GCATCGAGCTTACAGACAGATCGAGGGCTGTGGATCGATGGAATTGGGAATTTCTTCCAT aatatcttgtgggggaatgctgtaaatgtcagatccttaatgcaggttcaagagacccat AATATCTTGTGGGGGAATGCTGTAAATGTCAGATCCTTAATGCAGGTTCAAGAGACCCCAT CCTGGAGCCGGGGGTAGTGTGACTGTAACTGCTGGAGATTTCCTACCGGTAAGTCCCCAT aatgcctatgaagatctcagaatgagaaattcacagacgttccctctgctctctttagag AATGCCTATGAAGATCTCAGAATGAGAAATTCACAGACGTTCCCTCTGCTCCTCTTTAGAG AACACCGCAAATAAACAGATATCCGTGACGGACTCTATAGAACTTATCTCGCCTACTGGC ggcctcgcgatagatatagatagcttaagctcatcctcaacagcagctgttattaaagca GGCCTCGCGATAGATATAGATAGCTTAAGCTCATCCTCAACAGCAGCTGTTATTAAAGCA catttagttttagatttaggaaccaaactgatagcctctaaggaagacattgccatcaca CATTTAGATTTAGGAACCAAACTGATAGCCTCTAAGGAAGACATTGCCATCACA aacgatcctagggattttaaatctacaatccctcagaacgtcaacctgtctgcaggatac gatcctaaaaataaagagtacacagggaccatactcttttctggagaaaagagtctagca gcatcgagcttacagacagatcgagggctgtggatcgatggaattgggaatttcttccat TATGGTTTTCAAGGCAATTGGAAATTAGCTTGGACAGGAACTGGAAACAAAGTTGGAGAA cctggagccgggggtagtgtgactgtaactgctggagatttcctaccggtaagtccccat aacaccgcaaataaacagatatccgtgacggactctatagaacttatctcgcctactggc tatggttttcaaggcaattggaaattagcttggacaggaactggaaacaaagttggagaa Conservative 0 Mismatches 5; Indels 0; 1491 1311 1911 1731 1671 1551 660 540 480 420 1611 300 180 120 60 1851 360 0

Disclosure; Page

80-82; 115pp;

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01-MAR-1999;
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              Claim
                                Novel Chlamydia 98 kDa putative outer membrane protein antigen, for vaccination and protection against Chlamydia infection
                                                                                                                                                                                                                         29-OCT-1999;
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and intranssally into mice, which were subsequently inoculated with Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice were lower than those of the controls. Thus the 98kba putative outer membrane protein can be used as a vaccine to provide protection against Chlamydia infections, especially Chlamydia pneumoniae infections. The polypeptide may also be administered orally to treat Chlamydia infection. The present sequence may also be used in the construction of attenuated Chlamydia strains that can over-express the gene or express it in a non-toxic form. The present sequence is the 98kDa putative outer membrane protein gene from Chlamydla pneumoniae. The genomic sequence was amplified using two PCR primers. The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence close to the 5' end of the 98kDa putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BarGl restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame c-terminal fusion with the Histidine tag. The PCR product was cloned into a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with NotI and BamHl and performing a ligation reaction. This expression vector was injected intramuscularly and intramascularly into mice which were enhancemently incrulated with

Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 other;

Query Match
Best Local Similarity

9.0%; 48.2%;

Score 273.2; DB 21; Length Pred. No. 1e-67;

3000

γ 밁 20 밁 δÃ 밁 Š 문 Š 밁 δÕ 밁 Ş 밁 Š 망 20 밁 δÃ 멍 Qy Matches 1267; 781 724 604 484 544 387 424 207 CTCTGCATTAAATAAAGCCTGCTTCAATGTGACCTCAGGAAGTGTGACGTTCGCAGGAAA AGGAAGTAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAATAAACAGTTAGTCTTTGA ACTTATGCTCTTAAACAATTATGTAGTGCGTTTTGAACAAAACCAAAGGTAAGACTAAAGG ttataaaactagtacagatactaaggtcaccctcactggaaatcagatgttactcttcag taaggtcacaggagcgagctcctcaacaacgggggatatgtcaggaggtgctatctgtgc TGAGG----CATTGACTACTGCTATAGGTAAGGGAGGGGCTGTCTGTTGTCTTCCCACTTC aatttttacagaagcctcggtgactatttctaataatgctaaagtttcctttattgacaa TTTGTACTCCGATGGTGATATTGATATTGATCAGAATGCTTATGTTCTATTTCGAGAAAA tggaaaccaaggggaagtctctttttctgacaatacttcttcg---gattctggagctgc AGTAAATCAGGCAGAGATAAGATTTGCACAAAATACTGCCAAGAATGGTTCTGGAGGGGC tgaaaatacctcctcaaagaaaggcggagccattcagacttccgatgcccttaccattac TCAGAATGCAGCCACTT - - - TTGGAGGTGCTATCCATTCTTCAGGTCCCCTACAGATTGC cggtgctatcaccgcaaaaactctttcattaacagggactacaatgtcagctctgttttc CGGAGCTATTAGTGGGGCGAATGTTACTATAGTAGGCAACTACGATTCCGTCTCTTCTA cttgagtttgacaaaaatgtcagtttgctcttcagcaaaaacttttcaacggataatgg tgcgtctcctggaagttcgataactaccggcaaaggagccgttagctgctctacgggtag TCAGAGCCCCGGAGATATTAAA------GAACAGGGATGTCTCTATTCAAAAAATGC taacagcagcgtggtagataaatctaccacgtttatagggttttcttcgctatctttat TTGTTGCCAAGATCCTCAAGCAACGGCACGTTTTTCTGGGTTCTCCCACGCTCTCTTTTAT cgggaactctctattgttccaaacggtggatgcagggactgta---gcaggggctgctgt cacagcaatcacaaaaagctgttttaacaacactaagggcgatttgactttcacaggtaa Conservative 0; Mismatches 1273; Indels 90; Gaps 960 900 79T 840 780 674 723 614 663 557 603 497 543 437 483 386 423 366 266 14;

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1952	AATTGGGAATTTCTTCCATGTATCTGCCTCCGAAGACAATATAAGGTACCGTCATAACAG	1893	~;
1892 2034	GCAGGTTCAAGAGACCCATGCATCGAGCTTACAGACAGATCGAGGGCTGTGGATCGATGG	1833 1975	0 ~
1974	tatoggctctttagtccctaatagcttatggaatgcatttatagatattagctctctcca	1915	U
1832	AGAAGGAAATTTAGTTCCTTAATATCTTGTGGGGGAATGCTGTAAATGTCAGATCCTTAAT	1773	~
1772 1914	TGGAAACAAAGTTGGAGAATTCTTCTGGGATAAAATAAA	1713 1855	٠ ~
1712 1854		1795	0~
1794	gctcaaagcttctggaactgtaacaagcaccgcagtgactccagatcctataat	1735	0
1655		1599	~
1598 1734	CTCGCCTACTGGCAATGCCTATGAAAATTCACAAATTCACAAATTCACAGACGTTCCTCT	1539 1675	Ų ·~
1538 1674	TGTTATTAAAGCAAACACCGCAAATAAACAGATATCCGTGACGGACTCTATAGAACTTAT	1615	0 ~
1614.	TAITUCEATCHEAGACTAGACHAGATHAGATHAGCTHAGACTCATCCTCAACAGCAGC	1555	
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1139 1260	AATTTTA         acttcta	1080	9
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                                                                    taactcaaattttgaagcctttagccaattttcttttgaattgcgtgggtcatctcgcaa
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AAX06820 standard; DNA; 2787 ВP

AAX06820

26-APR-1999 (first entry)

Chlamydia pneumoniae surface exposed protein Omp8 DNA.

RESULT
AAXO6820
ID AAXC
XX AAXC
AC AAXC
XC AAXC
XX CAAXC
XX CALA
XX CALA
XX CALA
XX CMD8
KW Omp8
KW infe Omp8; outer membrane protein 8; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma; ss.

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody was used to identify the genes (see AAX06816-27) encoding Omp4-Omp15 proteins (see AAW88417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This DNA sequence codes for the novel 90.0 kDa surface exposed protein Omp8 (see AAW88421) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
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Mygind P;
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ACTTATGCTCTTAAACAATTATGTAGTGCGTTTTGAACAAAACCAAAGTAAGACTAAAGG
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                                                                                            TCAGAGCCCCGGAGATATTAAA-----GAACAGGGATGTCTCTATTCAAAAAATGC
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                                                                                                                                          tactagcaccataaacaatttggtcattaacatcagttctatagacggtgcaaagaaggc
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; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE:
US-08-728-470-2
                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-617-697-2
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                                                                                                                                                                                                                                                                     Sequence 2, Application US/08617697 Patent No. 5977336
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Hest Local Similarity 21.1%;
Matches 134; Conserva+***
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                               APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1110
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                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                     STREET:
COUNTRY: U.S.A. 7TP: 22202-0286
                                                CITY: Arlington
STATE: Virginia
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                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                            AT-----TGEANVTSATGTIGGTISGNTVNVTA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                               AEDPNSEYGFQGQWNVNWTTDT----ATNTKEATA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIKG-TESVTTSSQSG--DIGGTISGG-----TVEVKATESLTTQSNSKIK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAKGASNKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGS 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STS----FSQEAGSLLG---MDSGT-TLSTTAGSITITNLG----INVDSLGLKQPVSL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDSSDNNAGL-----TIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTIN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTLE 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSILS------NNKFLY 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGNIVNIAGNLTVESNANFKAITNFTFNVGGLEDNKGNSNISIAKGGARFKDIDNSKNLS
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                                                                                     2001 Jefferson Davis
Bldg. 1
                                                                                                    Shoemaker and Mattare, Ltd.
Shoemaker and Mattare, Ltd.
101 Tefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSET, JETRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            851 VTINNNANVTLIGSDFDNHQKPL-----
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495 TAKGASNKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        736 SFNGNISVSGGGSVDFTLLASSSNVQTPGVVINSKYFNVSTGSSLR----FKTSGSTKTGF 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 SFNGNID-----SGTFTPKTSATTYSLTGDVF---FYEPGKGTPLSDSCFKQT------ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/302,832 FILING DATE: 05-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                  STS----FSQEAGSLLG---MDSGT-TLSTTAGSITITNLG----INVDSLGLKQPVSL 494
                                                                                                                                                                       LKINNGSAGALNPYOGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTLE 447
                                                                                                                                                                                                                    SDLTIGNTNSAD-----GTNAKKVTFNQVKDSKISADGHKVTLHSKVETSGSNNNT 1109
                                                                                                                                                                                                                                                                                                       ----NITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITAKDG 1058
                                                                                                                                                                                                                                                                                                                                                TEFLRNNVSSATPKGGA----ISIDASGELSLSAETGNITFVRN-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSILS------NNKFLY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIEKDLTLNATGGNITLLQVE-GTDGMIGKGIVAKKNITFEGGN-ITFGSRKAVTEIEGN 850
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                                           ATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGS 1216
                                                                                                                                EDSSDNNAGL-----TIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTIN 1156
                                                                                                                                                                                                                                                              ---TLTTTGSTDTPKRNAINIGSNGK---FTELR----AAKNHTIFFYDPITSEGTSSDV 387
                                                                                                                                                                                                                                                                                                                                                                                            ITTNSSSTYRTIISGNITNKNGDLNITNE-----GSDTEMQIGGDVSQKEGNLTISSDKI 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGNIVNIAGNLTVESNANFKAITNFTFNVGGLFDNKGNSNISIAKGGARFKDIDNSKNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTLSSAGGVNL-----ENIRKLVVAGNESTADGGAIKGASFLLTGTSGDALFSNNSSSTK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1536 amino acids
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16-MAR-1993
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415-0813
40: 2:
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US-08-719-641-2
; Sequence 2, Application US/08719641
; Patent No. 6218141
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US PFILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1260 AT-----TGEANVTSATGTIGGTISGNTVNVTA 1287
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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137 GTLSSAGGVNL-----ENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTK 191
                                               793 SIEKDLTLNATGGNITLLQVE-GTDGMIGKGIVAKKNITFEGGN-ITFGSRKAVTEIEGN 850
                                                                                                                                                                                 34 SENGNID-----SGTFTPKTSATTYSLTGDVF---FYEPGKGTPLSDSCFKQT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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STREET: Bldg. 1
CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 22202-0286
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                                                                                                                                      SFNGNISVSGGGSVDFTLLASSSNVQTPGVVINSKYFNVSTGSSLR---FKTSGSTKTGF 792
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                                                                                       --TDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQ 136
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 6218141-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                5.0%; Score 238; DB 4; Length 1536; 21.1%; Pred. No. 2.6e-09;
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                                                                                                                                                                                                                             Indels 168;
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US-08-614-377A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Smit, John
APPLICANT: Bingle, Wade H.
APPLICANT: No. 5976846ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF
TITLE OF INVENTION: HETEROLOGOUS
TITLE OF INVENTION: POLYPEPTIDES FROM CAULOBACTER
                                                                                                                                                                                                                                                                     COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                 CLASSIFICATION: 435
                                                                                                              APPLICATION NUMBER: FILING DATE: 09-FEB: CLASSIFICATION: 435
                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 12-MAR-1996
                                                               APPLICATION NUMBER: US 07 FILING DATE: 09-JUNE-1992
                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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TELEPAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER:
NRKGFRHTSGGYVIGGS----AHTPKDDLFT 676
                                     TGTAPAVTFVSA---NTTVGEVVTIR-----GGAGADSLTG---
                                                                          TGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGDE
                                                                                                             VNIAATDTNTTAHVDTLTLQATSAKSIVVTGNAGL----NLTNTGNTAVTSFDASAV---
                                                                                                                                               VD-ADVDTN----VDISSLIPVPAED--PNSEYGFQGQWNVNWTTDTATNTKEATATWTK
                                                                                                                                                                                                                           VSLT-----AKG-----ASNKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKIT 536
                                                                                                                                                                                                                                                                 AFGGFETLRVAGAAAQG----SHNANGFTALQ----LGATAGATTFTNVAVNVGLTVLAAP 746
                                                                                                                                                                                                                                                                                                      SLSGGKLLLQKGVTLESTSFSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQP 491
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APPLICANT: Bingle, Wade H.

APPLICANT: No. 6210948ellini, John F.

TITLE OF INVENTION: EXPRESSION AND SECRETION OF HET FILE OF INVENTION: EXPRESSION AND SECRETION OF HET FILE OF INVENTION: UNMBER: US/09/142,648B

CURRENT APPLICATION NUMBER: PCT/CA97/00167

PRIOR APPLICATION NUMBER: PCT/CA97/00167

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: US 07/614,377

PRIOR FILING DATE: 1996-03-12
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LENGTH: 1026
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Best Local Similarity
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APPLICANT:
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  492 VSLT----AKG---
                                           694 AFGGFETLRVAGAAAQG----SHNANGFTALQ----LGATAGATTFTNVAVNVGLTVLAAP
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                                                                                      SLSGGKLLLQKGVTLESTSFSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQP 491
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                                                                                                                                                                            YDPITSEGTSSDVLKINN---GSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPV 431
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  -- ASNKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKIT 536
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Pred. No. 8.8e-09;
D7; Mismatches 273
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Sear Job 1	ОУ	Оy	Qy Db	Db
Search completed: October 2, 2001, 03:27:12 Job time: 7194 sec	650 NRKGFRHTSGGYVIGGSAHTPKDDLET 676  : :	590 TGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGDE 649	537 VD-ADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWITDTATNTKEATATWTK 589	747 TGTTTVTLANATGTSDVFNLTLSSSAALAAGTVALAGVE

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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GenEmbl:*
1: gb_bal:
2: gb_ba2:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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A81837	CPOMP54	A81851	AE001628	AP002546	AE002192	CPN133034	A81829	DB ID
A81837 Sequence 11	AJ001311 Chlamydia	A81851 Sequence 25	AE001628 Chlamydia	AP002546 Chlamydop	AE002192 Chlamydop	AJ133034 Chlamydia	A81829 Sequence 3	Description

- FILORIBLE COVERSE A SUCLOUI A FIDA DUA CARA A COMPAÑA A DOVERSO A CARA A FIDA DO CARA A COMPAÑA A COMPAÑ	ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTCTCGACATTGGCATGTTTTACTAGTAGT 	Query Match 100.0%; Score 2815; DB 9; Length 2815; Best Local Similarity 100.0%; Pred. No. 0; Matches 2815; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	### ASE COUNT	MADSEN ANNA	REFERENCE 1 (bases 1 to 2815) AUTHORS Madsen, A. and Birkelund, S. TITLE NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE TOTINAL PATENT: WO 9858057-A 3 OLDEC-1998.	S . unidentified. ISM unidentified	LOCUS A81829 2815 bp DNA PAT 21-JAN-2000 DEFINITION Sequence 3 from Patent WO9858953. ACCESSION A81829 CT.6731865	RESULT 1	50.6 1.8 1141 10 AX083744 A	77.4 2.7 10908 1 AE002294 AE00	125.8 4.5 1200 9 A81853	1830 9 A81855 A81855 10695 1 AE001629 AE0016 15789 1 AE002191 AE0021 1840 9 A81843 A81843	309.4 11.0 2526 9 A81833 A81833 Sequence 235.6 8.4 10044 1 AE002237 AE002237 Chlamyc 236.6 8.3 10766 1 AE001585 AE001585 Chlamyc 237.6 8.3 2062 6 A81831 AE001585 Chlamyc	456 16.2 6030 2 CPOMP54 398.8 14.2 6110 2 CPU65942 375 13.1 6234 2 CPU65943 309 8 11 0 10574 1 ABO01586	21 535 19.0 2787 9 22 521.8 18.5 2787 9 23 518.2 18.4 2889 24 456 16 2 3200 9	641.8 22.8 12127 1 AE002235 594.4 21.1 4926 2 CPU72499 536.2 19 0 12676 1 AE002192	649.4 23.1 300650 2 AP002546 AP002546 Ch1 647.8 23.0 17280 2 CPN133034 AJ133034 Ch1 646.4 23.0 273 9 A81841 A81841 Seque 642.2 22.8 299650 2 AP002545 AP002545 Ch1	663 23.6 16448 1 663 23.6 26920 2 649.4 23.1 10026 1 649.4 23.1 15068 1
Qy 1141 TTTTTCTACGATCCGATTACTGCTAATACGGCTGCGGATTCTACAGATACTTTAAATCTC 1200	Qy 1081 ATTGACATAGGATCTACTGCAAAGATCACGAATTTACGTGCAATATCTGGGCATAGCATC 1140	Qy 1021 ATTACCTTCAATGGGAATGCCATTGTTGCAACTACACCACAAACTACAAAAAGAAATTCT 1080	Qy 961 GGTGGAGCCATTTCTATACTGGCAGCTGGAGAGTGTAGTCTTTCAGCAGAAGCAGGGGAC 1020	Qy 901 GGGGGGGGGGGGTATCTCCTTTTCTAACAATATAGTCCAAGGTACCACTGCAGGTAAT 960	Oy 841 GGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCTAAGAAGCTTACACTGGCTTCC 900	Qy 781 GGAGCTCTTTCTGGAGATGCCGATGTTACCATATCTGGGAATCAGAGTGTAACTTTCTCA 840	Qy 721 ACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGGACCGCAGGAAATGGA 780	Qy 661 TCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACAGGAAACTGTACAATT 720	Oy 601 GGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACGGCTCCTACCCTCTTC 660	Qy 541 AACAGCACGGGATCGATTTCTTTGAAGGGAATAAATCGAGCGCAACAGGGAAAAAAAGGT 600	Qy 481 AAACAAGATTACTGTGAGGAAAATGGCGGAGCCATTTCTACCAAGAATCTTTCTT	Qy 421 AAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATTTTATTT 480	Qy 361 GGATTTTCGAGTCTTACTTTGTTAGCGCCCCATCATCGGTAATCACAACCCCCTCAGGA 420	Qy 301 AAGTCTAGTGCTGAAGGGGCAGCACTTTCTGTTACAACTGATAAAAATCTGTCGCTAACA 360	Qy 241 GACACTACGGAATCTTTAAGCTTTGCCGGTAAGGGGTACTCACTTTCTTT	Qy 181 GGAGATATAACTCTGCAAAACCTTGGGGATTCGGCAGCTTTAACGAAGGGTTGTTTTCT 240	Qy 121 ACTAACACAGGCACCTATACTCCTAAAAATACGACTACTGGAATAGACTATACTCTGACA 180	Qy 61 TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGAAGT 120

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/gene= unip12 <1841		/organism="Chlamydophila pneumoniae" /strain="VR1310" /db xref="taxon:83558"	e 117280	Direct Submission  Submitted (21-JAN-1999) Boesen T., Department of Medical  Microbiology and Immunology, University of Aarhus, The Bartholin  By 2000 Archae Department	unpublished 2 (bases 1 to 17280) Boesen,T.	L Luases I CO 1/200, Daugaard, L., Hjerno, K., Knudsen, K., Madsen, A.S., Christiansen, G. Daugaard, L., Hjerno, K., Knudsen, K., Madsen, A.S., Christiansen, G. and Birkelund, S.	ydiaceae; Chlam	hypothetical protein; omp10 gene; omp11 gene; omp12 gene; omp13 gene; omp14 gene; omp4 gene; omp5 gene; ORF1; outer membrane protein; outer membrane protein 11; outer membrane protein 12; outer membrane protein 14; outer membrane protein 5.		C CPN133034 17280 bp DNA BCT 27-FEB-2001 Chlamydia pneumoniae GGAI-protein family cluster A, genes omp12 (partial), omp11, omp10, omp5, omp4, omp13 and omp14 (partial) and	GATCTTGGGGGTAAGTTCCAATTCTAGGAGCGTCTCTCATGTCTCAGAAATTCTG 2815	GATCTTGGGGGTAAGTTCCAATTCTAGGAGCGTCTCTCATGTCTCAGAAATTCTG 2815	TTTGAAGTGCTCGGCCAGTTTGTCTTTGAAGTTCGTGGATCCTCACGGATTTATAATGTA 2760	TTTGAAGTGCTCGGCCAGTTTGTCTTTGAAGTTCGTGGATCCTCACGGATTTATAATGTA 2760	~1	AACTTAGCACGACAGGCCTTGCAAGTGCGTGCAGGCAGTCACTACGCCTTCTCTCTC	GATICUCAAATIGUACHTATUCAGUGAGUCTUTTIGGGAAACTTATGUCAAT 2640   - - - - - - - - - - - - - - - - - -	2 2 2	5 6	GATGACAGCAACCTCTTCAATTTATCTTTGCCTATAGGGGTGAAGTTTGAGAAGTTCCTCT 2520	GATGACAGCAACCTCTTCAATTTATCTTTTGCCTATAGGGGTGAAGTTTGAGAAGTTCTCT 2520	AATCTGACCTATATACGTCAGGACAGCTTCTCGGAGAAAGGTACAGAAGGAAG	AATCTGACCTATATACGTCAGGACAGCTTCTCGGAGAAAGGTACAGAAGGAAG	TCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATGCTCCATACATCAAACTG 2400	TCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATGCTCCATACATCAAACTG 2400	TATCCTGAGGTGAAAGGTTCTTGGGGGAATAATGCTTTTAACATGATGTTGGGAGCTTCT 2340	TATCCTGAGGTGAAAGGTTCTTGGGGGAATAATGCTTTTAACATGATGTTGGGAAGCTTCT 2340	TTAGAAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTATACTGCG 2280

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TTAAPCQLFGKDRDHFINKNAASAYAASLHAGHLATLSSPSLTLYLGGSESBQPVLFD
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GSAHIYNVDCGLRYSF"
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885. .
                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mksslhwelissslalplslnfsafaavveinlgptnsfsgpgg
ytppagotnalgetiymltgdysitnagsptaltasckkettgnlsfoghgygytgo
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daganctffmtaanklsfsgefylsligtnakkkatokggalystggitinntlnsasfsent
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FYERHAEGRAFNKSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="outer membrane protein"
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/db_xref="GI:4455884"
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3827. .6613
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/db_xref="GI:4455883"
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VEASYIHQDSFKERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q9Z398"
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/transl_table=11
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/note="putative"
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                                                                                                        /db_xecf="Sptrend:086164"
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VAETSGGAIHAKKLALSSGGFTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITF
VRNTLTTTGSTDTPKRNAINIGSNGFTELRAAKNHTIFFDDFTSEGTSSDVLKINN
GSAGALNPYOGTILFSGETLTADELKVADDLKSSFTOPVSLSGKLLLOKGVTLESTS
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FARROKDEFIAHNNSRTYGGTLFFKHSHTLOPONYLRIGGSATVESAIRKFPREIPLAL
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FARROKDEFIAHNNSRTYGGTLFFERSGYVLGGSAHTPKDDLFTFACHL
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/gene="omp4"
11535. .11588
/gene="omp4"
/11535. .14321
/gene="omp4"
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VTFSGNQAVANGGAIYAKKLTLASGGGGGISFSNNIVQGTTAGKNGAISILAAGECSL
SAEAGDITFNGNAIVATTPQTTKRNSIDIGSTAKITNLARISGHSIFFYDPITANTAL
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ISFAFCQLFGSDKDFLVAKNHTDTYAGAFYIOHITECSGFIGGLLDKLDGSWSKFNU
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KQDYCEENGGAISTKNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDLTNNTAPT
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/db_xref="GI:4455886"
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LWIHNLVMKDRPEDLFVSLHVCRGDYQAEFFSRRAYDSIEEPLFAKTDVDSYHYYWAL
DDKYSGGAEPLAYVSGEKHVCLGLISSNHSCIEDRDAVVSRIYEAASYIPLERLSLSP
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KISVSKHDFIEHFEFVKTFEKGNAKAKQTIPSPSQFFHEMIFAPNLKNTRKFYPTNQE
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/note="ORF1"
DVQVSFSHSDNRMETHYTSLPESEGSWSNECTAGGTGLDLPFVLSNPHPLFKTFTPQM
KVEMVYVSQNSFFESSSDGRGFSTGRLLNLSTPVGAKFVQGDTGDSYTYDLSGFFVSD
VYRNNPQSTATLVMSPDSWKTRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
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/db_xref="GI:4455887"
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11535. .1432
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/protein_id="CAB37070...
/db_xref="GI:4455885"
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/transl_table=11
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                                                                                                                                               ACTAACACAGGCACCTATACTCCTAAAAATACGACTACTGGAATAGACTATACTCTGACA 180
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Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
Direct Submission
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(Dases 1 to 12676)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (6), 1397-1406 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP:4376735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   section
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete
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GP:4376733;

identified

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sequence

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TYTPKNTTTGIDYTLTGDITLQNLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKS
SAEGAALSVTTDKNLSLTGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILF
KQDYCEENGGAISTKNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGDENRKGFRHTSGGY
VIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNNSRTYGGTLFFKHSHTLQPQNYLRL
GRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLPESEGSWSNECIAGGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KASGSPELIISNNKTLIFASNVAETSGGAIHAKKLALSSGGFTEFLRUNVSSATPKGG
AISIDASGELSLSAEFGNITFVRNTLTTGSTDTPKRNAINIGSNGKTTELRAAKNHT
IFFYDDTTSEGTSSDVLKINNGSAGALNPYGGTDFKRNAINIGSNELKVADNLKSSFTQ
PVSLSGGKLLLQKGVTLESTSFSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLG
LKQPVSLTAKGASNKVIVSGKLNLIDLEGNIYSHMFSHDQLFSLLKITVDADVDTNV
DISSLIPVPAEDPNSBYGFQGQMNVMMTTDTATNTKEATATWTKTGFVPSPERKSALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein; identified by Glimmer2;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(8170. .8292)
/gene="CP0304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRGYTLDTKGFTQTAGSSVINDAGTTLKASTEEVTLTGLSIPVDSLGEGKKVVIAASA
ASKNVALSGPILLLDNOGNAYENHDLGKTQDFSFVQLSALGTATTTDVPAVPTVATPT
HYGYQGTWGMTWVDDTASTPKTKTATLAWTNTGYLPNPERQGPLVPNSLWGGSSDIQA
IQGVIERSALTLCSDRGFWAAGVANFLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LESNNIABBAAGGA I NSTGNCTITGNTSLVFSBNSVTATAGNGGALSGDADVTI SGNQS
VTFSGNQAVANGGA IYAKKLTLASGGGGI ISFSNNIVQGTTAGNGGA ISILAAGECSL
SAEAGDITENGNA IVATEOCTKRNSI DIGSTAKITMLRA ISGHISIFYDJTTAATA
DSTDTLNLNKADAGNSTDYSGS I VFSGEKLSEDEAKVADNLTSTLKQPVTLTAGNLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="polymorphic membrane protein G family"
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/db_xref="G1:7189229"
/tzanslation="MIYEFCEYIDANSSLKNKSITMKTSIPWYLVSSYLAFSCHLOSL
ANEELLSPDDSFNGNIDSGTFTPKTSATTYSLTGDVFFYEPGKGTPLSDSCFKQTTDN
LTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQGTL
                                                                                                                                                    /note="conserved hypothetical protein; identified
Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(8170. .8292)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRIYNVDLGGKFQF"
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                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="AAF38161.1"
/db_xref="GI:7189231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CP0304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIRNDPKCTTALVISGASWETYANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLNLTYIRQDSFSEKGTEGRSFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="polymorphic membrane protein G family"
/protein_id="AAF38160.1"
/db_xref="GI:7189230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGFSIGRLLNLSIPVGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSAGGVNLENIRKLYVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIAT
TAGARIANNTGYVRFLSNIASTSGGAIDDEGTSILSNNKFLYFEGNAAKTTGGAICNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity; putative"
/product="conserved hypothetical protein"
/protein_id="AAF38162.1"
                                                                        /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                     'gene="CP0305"
                                                                                                                                                                                                                                                                                                                                                                                  translation="MDLSSRWLNKLKTRKQLDQNIKYDCKSYCLRGISQILGWV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEGQLAYSHVSNDLKTKYTAYPEVKGSWGNNAFNMMLGASSHSYPEYLHCFDTYAPYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [SFAFCQLFGSDKDFLVAKNHTDTYAGAFYIQHITECSGFIGCLLDKLPGSWSHKPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CP0303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CP0303"
                                                                                                                                                                                                                                                                                                             'gene="CP0305"
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                                                                                                                                                                                                                                                                                                                         ASQTYTLSGSLSLUPPSGNNYEDVSWNNPQVFSCLTLTADDPANHTTDLAADPLEKN
PIHWGYQGNWALSWQEDTATKSKAATLTWTKTGYNPNPERRGTLYANTUKKGSFVDVRS
IQOLVATKVRQSQFTRGIWCEGISNFFHKDSTKINKGFRHISAGYVVGATTTLASDNL
ITAAFCQLFGKDRDHFINKNRASAYAASLHLQHLATLSSPSLLRYLPGSESEQPVLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAGANCTETNTAANKLLSFSGFSYLSLIQTINATTGTGAIKSTGACŠIQSNÝSCYFGQ
NESNDAGALGGSSISLSLNENLITAKKKATQKGALKTSTGGITINNTLNSASFSENT
AANNGGAITEASSFISSNKAISFINNSVTATSATGGAIYCSSTSAFKEVUTLSDNSE
LNFIGNTAITSGGAIYTDNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLSA
LGGDITEGNTVYKGASSSQTTTRNSINIGNTAKIVQLASGGOTTIYFYDFITTSIT
AALSDALNLAGPDLAGNAYQGTIVFSGEKLSEAEAAEADNLKSTIQQFLTLAGGQLS
AKSGVTLVAKSFSQSPGSTLLMDAGTTLETADGITINNLVLNVDSLKETKKATLKATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="polymorphic membrane protein G family"
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/db_xref="G1:7189233"
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YTPPAQTTNADGTIYNLTGDVSITNAGSPTALTASCFKETTGNLSFQGHGYQFLLQNI
                                                                                                                                                                                                                             VYRKNPDCTTALLINNTSWKTTGTNLSRQAGIGRAGIFYAFSPNLEVTSNLSMEIRGS
                                                                                                                                                                                                                                                            AQISYIYSKNIMKTYYIQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIK
VEASYIHQDSFKERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="memmspfQQPEQCHFDVVGSFLRPESLTRARSDFEEGRIVYEQM
RVVEDAAIRNLIKKQTEAGLIFFTDGEFRRYSWDFDFMWGFHGVDRRRDSNDPEIGVY
LKDKISVSKHPFIEHFEFVKTFEKGNAKAKQTIPSPSQFFHEMIFAPNLKNTRKFYPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQELIDDIVFYYRQVIQDLYAAGCRNLQLDDCAWCRLLDIRAPSWYGVDSHDRLQEIL
EQFLWIHNLVMKDRPEDLFVSLHVCRGDYQAEFFSRRAYDSIEEPLFAKTDVDSYHYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSPQCGFASCEGDHRMTEEEQWKKIAFVKEIAKEIWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WALDDKYSGGAEPLAYVSGEKHVCLGLISSNHSCIEDRDAVVSRIYEAASYIPLERLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="similar to GP:4376731; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="CP0306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CP0306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:7189232"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11
99.9%;
                                                                                                                                                                2890
Score 2813.4;
Pred. No. 0;
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                              DB
                              1;
                              Length 12676;
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Š δÃ В Ş Qy Ş Вþ Q 멍 멍 В δÃ 밁 밁 Q Query Match Best Local Similarity Matches 2814; 5266 5206 5146 5086 5026 ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT 421 AAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATTTTATTT 480 181 121 61 TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGAAGT 120 1 ATGAAATCGCAATTTTCCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT AAGTCTAGTGCTGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTGTCGCTAACA 360 GGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACCCCCCTCAGGA 420 AAGTCTAGTGCTGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTGTCGCTAACA GGAGATATAACTCTGCAAAACCTTGGGGGATTCGGCAGCTTTAACGAAGGGTTGTTTTTCT GGAGATATAACTCTGCAAAACCTTTGGGGATTCGGCAGCTTTAACGAAGGGTTGTTTTTCT ACTAACACAGGCACCTATACTCCTAAAAATACGACTACTGGAATAGACTATACTCTGACA ACTAACACAGGCACCTATACTCCTAAAAATACGACTACTGGAATAGACTATACTCTGACA 180 TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGAAGT Conservative 0; Mismatches ŗ Indels 0; Gaps 5385 5205 5445 5325 300 5265 5145 5085 240 60 0;

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AAAGTT	ACAGAG	TTTACT	GTAACT       GTAACT	AAGCTC        AAGCTC	AATAAG 	TTTTTC       TTTTTC	ATTGAC        ATTGAC	ATTACC       ATTACC	GGTGGA         GGTGGA	999999        	GGAAAC         GGAAAC	GGAGCT       GGAGCT	ACAGGG        ACAGGG	TCGAAC	GGGCT       GGGGCT	AACAGC        AACAGC	AAACAA         AAACAA	 AAAGGT
GTAATT	GAGGTC	CAGACC	CTAACT       CTAACT	TCTGAA        TCTGAA	GCTGAT	TACGAT	ATAGGA         ATAGGA	ATTACCTTCAATG	GCCATT       GCCATT	999999        	CAAGCT	CTTTCT	AATACG        AATACG	AATATT        AATATT	ATTTGT       ATTTGT	ACGGGA        ACGGGA	GATTAC        GATTAC	 GCAGTT
GCTGCT	ACTTTA       ACTTTA	GCGGGT	GCAGGA         GCAGGA	GATGAA         GATGAA	GCAGGT       GCAGGT	CCGATT	TCTACT        TCTACT	GGGAAT        GGGAAT	TCTATA        CTATA	GGTATC        GGTATC	GTAGCT	GGAGAT        GGAGAT	TCTCTT       TCTCTT	GCTGAA       GCTGAA	GCTACT	TCGATT	TGTGAG        TGTGAG	 AAATGT
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AAAATG	ATTCCTG	ATGGATG	VAACGTG VAACGTG	ACAACC           ACAACC	TATAGTO	CTGCGG	ATTTAC	ACTACAC	SAGTGT?        SAGTGT?	VATATAG               VATATAG	ATTTATO	ATATCTO ATATCTO	ATAGTO ATAGTO	CTATAP          CTATAP	ATTACAP         ATTACAP	VATAAAT               VATAAAT	CCATTI CCATTI	CATTTE
TAGCCC	TAGACT	TCAGACCGCGGGTTCCTCTGTTATTATGGATGCGGGCACAACGTTAAAA 	GTGTCA	TCACTT	GGTCGA	ATTCTA	GTGCAA	CACAAA CACAAA	GTCTTT	TCCAAG	CTAAGA         CTAAGA	GGAATC	TGACAG	ATAGCA         ATAGCA	ATAATA       ATAATA	CGAGCG	CTACCA	 ;ATAACA
TTAGTG	CTTTAG	CAACGT	CTCTCG.	CTACGC	TTGTTT        TGTTT	CAGATA         CAGATA	TATCTG	CTACAA        CTACGA	CAGCAG	GTACCA        GTACCA	AGCTTA       AGCTTA	AGAGTG	CGACCG	CAGGAA               CAGGAA	CGGCTC	CAACAG         CAACAG	AGAATC	 ATGGAA
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1560	1500 6525	1440 6465	1380 6405	1320 6345	1260 6285	1200 6225	1140 6165	1080 6105	1020 6045	960 5985	900 5925	840 5865	780 5805	720 5745	660 5685	600 5625	540 5565	5505
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7606	2521 GATTGTAATGACTTTTCTTATCATCTTCATTTATCCTATGTTCCTGATCTTATCCGCAAT	2461 GATGACAGCAACCTCTTCAATTTATCTTTGCCTATAGGGGTGAAGTTTGAGAAGTTCTCT  + + + + + + + + + + + + + + + + + + +	2401 AATCTGACCTAFATACGTCAGGACAGCTTCTCGGAGAAAGGTACAGAAGGTACTTTTT	2341 TCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATGCTCCATACATCAAACTG	2281 7306	2221 TTAGANGGCAGCTGGCTTATAGCCAGGTCAGTAATGATCGTGAAGACAAAGTATACTGCG	2161 GGGTTCATAGGTTGTCTCTTAGATAAACTTCCTGGCTCTTGGAGTCATAAACCCCTCGTCTT	2101 AAAANICATACIGATACCTATIGCAGGAGCCTTICTATATCCAACACATTACAAANIGTAGT 	2041 AACTTAATTAGCTTTGCCTATCCCAACTCTTTGGTAGGATAAAGATTTCTTAGTGGCTTTGGTAGGATAAAGATTTCTTAGTGCGTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGCGATAAAGATTTCTTAGTCGCTTTGGTAGCGATAAAGATTTCTTAGTCGCTTTGGTAGCGATAAAGATTTCTTAGTCGCTTTGGTAGCGATAAAGATTTCTTAGTCGCTTTGGTAGCGATAAAGATTTCTTAGTCGCTTTGGTAGCGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTTTGGTAGGATAAAGATTTCTTAGTCGCTAGTGAGATAGAT	1981 AAATACCGTCATAAATCTGGTGGATATCCTATCGGAGGTGCAGCGCAAACTTGTTCTGTA	1921 GGCTTCTGGGCTGCGGAGTCGCCAATTTCTTAGATAAAGATAAGAAAGGGAAAAACGC	TOOL ONCATCCANGCOMIT CANGGOIG CALAGROMAGAGO LI TOOL CALAGROMAGAGO CALAGROMAGO CALAGROMAGAGO CALAGROMAGO CALAGROMAGO CALAGROMAGO CALAGROMAGO CALAGROMAGO CALAGROMAGO CALAGROMAGO CALAGROM	1801 CTT	1/41 GATACUCCAAGCACTCCAAGACTAGACACGCGACATTAGCTTGGACCAATACAGGCTAC	TOOL ACAD INCLAND INCLANDED IN ICANOCIA IN SUBSTRICT SOCIETION OF THE STATE OF TH	CALLES   CONTROL   CONTR		6526 AAA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases. Mutsunori Shirai, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi 755-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-227, Fax:81-836-22-2415)
On Sep 15, 2000 this sequence version replaced gi:6172328 gi:6172390 gi:6172392 gi:6172394 gi:6172396 gi:6172398 gi:6172398 gi:6172393 gi:6172393 gi:6172394 gi:6172390 gi:6172392 gi:6172394 gi:6
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AP002546 AB033782 AB033783 AB033784 AB03378 AB033802 AB033803 AB033804 AB033805 AB033804 AB033802 AB033804 AB033811 AB033812 AB033812 AB036079 AB033810 AB033811 AB035081 AB035080 AB036081 AB036082 AB038381 AB036082 AB038381
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Chlamydophila pneumoniae J138
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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144. .935
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3656. .4387
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ILCSKETFSYLFRYAQCEIPVTEVSQIIKESSETDKQVLRDKVQRFMEVLLELYRDRY
                                                                                                      LVSLQYKEKELVSVSPGQDLSN"
                                                                                                                                    TLNLGLKASALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4359. .5255)
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DGPCSHGLESTVVASDPLYIYREGLISRSVIENIAGTEAKIFHRTSHAFSKHIKIYTV
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/gene="ywlC"
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complement(1495.
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KGV I GLNLVRS Y VGDSLGDLEKHVLHAENLG I LSS I VLGSDFFYANEDENFFFNECSS
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/translation-workernydasaitylegiqavrerpkokkoryomesskilevy
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                                                                                                                                                                                                                                                                                     /gene="CPj0276"
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                                                                                                       GGGGGGGGGGGGTATCTCCTTTTCTAACAATATAGTCCAAGGTACCACTGCAGGTAAT
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                                                                                                                                                                                                                                                                                     GGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACCCCCTCAGGA
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                       ATTACCTTCAATGGGAATGCCATTGTTGCAACTACACCAAAACTACAAAAAAATTCT
                                                                                             GGGGGGGGGGGGGTATCTCCTTTTCTAACAATATAGTCCAAGGTACCACTGCAGGTAAT
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Kalman,S., Mitchell,W., Marathe,
Grimwood,J., Davis,R.W. and Step
Direct Submission
Submitted (01-DEC-1998) Program
of California, 235 Earl Marren F
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/organism="Chlamydophila
/strain="CWL029"
/db_xref="taxon:115713"
                                                                              1. .10757
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:4376730
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                                                                                                                                                                                                       Marathe, R., Lammel, C., and Stephens, R.S.
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                                                                                                                              Hall,
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l, Berkeley,
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                                                                                                                                                       University
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/translation="MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTF
TPKTSATTYSLIGDVFFYEPGKOTPLBDSCFKQTTDNLTFLGHKHSLIFGFIDAGTHA
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TSGGAIDDEGTSILSNNKFLYFEGNAKTTGGAICNTKASGSPELIISNNKTLIFASN
VAETSGGAIHAKKLALSGGFTEFLRNNVSSATPKGGAISIDASGELSLSAFTGNITF
VRNTLITTGSTDTPKRNAINIGSNGKFTELRAKNHTIFPDITSEGTSSDLKANING
GAGALMPYQGTILFSCETLTADELKVADNLKSSFTQPVSLSGKKLLAKGSNKVVVSGK
FSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVVVSGK
LNLIDIEGNIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6715.
/gene="pmp_10.2"
/note="CPn0450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Polymorphic Outer Membrane contains frame shift"
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NQELIDDIVFYYRQVIQDIYAAGCRNLQLDDCAMCRLLDIRAPSWYGVDSHDRLQFIFI

EQFLMIHNLYMKDRPEDLFVSLHVCRGDYQAEFFSRRAYDSIEEPLFAKTDVDSYHYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="pmp_10.1
/note="CPn0449"
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/gene="pmp 10.1"
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/gene="yxjG_2"
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LOGDITFEGNTVVKGASSSQTTTRNSINIGNTAAKIVQLRASGONTIYTYDPITTSIT
AALSDALNLNGPDLAGNPAYQGTIVESGEKLSEAEAAEADNLKSTIQQPTLAGGQLS
LKSGVTLVAKSFSQSPGSTLLMDAGTTLETADGITINNLVLNVDSLKETKKATLKATQ
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NFSNDNGGAIQGSSISLSLNPNLTFAKNKATQKGGALYSTGGITINNTLNSASFSENT
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                                                                                                                                                                                                                                                                                              /product="Polymorphic Outer Membrane
/protein_id="AAD18593.1"
/db_xref="GI:4376733"
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LSPQCGFASCEGDHRMTEEEQWKKIAFVKEIAKEIWG"
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/protein_id="AAD18592.1"
/db_xref="GI:4376732"
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/transl_table=11
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YTPPAQTTNADGTIYNLTGDVSITNAGSPTALTASCFKETTGNLSFQGHGYQFLLQNI
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/protein_id="AAD18591.1"
/db_xref="GI:4376731"
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/note="CPn0451"
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                       TCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACAGGAAACTGTACAATT
                                                                                                                                                         GGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACGGCTCCTACCCTCTTC
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ATGMEHKQGFWVSSMTWPLHKTGDENIKGFRHTSGGVVIGGSAHTPKDDLFTFAFCHL
FARDKDCFIAHINSRTYGGTLFFKHSHTLQPQNVLTHLGRAKFSESAIEKFPREIPLAL
DVQVSFSHSDINMETHYTSLPESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPAL
DVQVSFSHSDINMETHYTSLPESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPAL
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SRNYNVDVGTKLRF"
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1980 5672	1 GGCTTCTGGGCTGCGGGAGTCGCCAATTTCTTAGATAAAGATAAGAAAGGGGAAAAACGC 	192 573	Db Qy
1920 5732	1 GACATCCAAGCGATTCAAGGTGTCATAGAGAGAGTGCTTTGACTCTTTGTTCAGATCGA 	186 579	Оy
1860 5792	CTTCCGAATCCTGAGCGTCAAGGACCTTTAGTTCCTAATAGCCTTTTGGGGATCTTTTTCA	1801 5851	g 49
1800 5852	GATACCGCAAGCACTCCAAAGACTAAGACAGCGACATTAGCTTGGACCAATACAGGCTAC	1741 5911	Qy Db
1740 5912	ACAGTAGCAACTCCTACGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGTTGAT	1681 5971	Ωy
1680 5972	TCATTTGTGCAGCTCTCTGCTCTGGGTACTGCAACAACTACAGATGTTCCAGCGGTTCCT	1621 6031	р <i>Q</i>
1620 6032	CTTTTGGATAACCAAGGGAATGCTTATGAAAATCACGACTTAGGAAAAACTCAAGACTTT 	1561 6091	90 VQ
1560 6092	1 AAAGTTGTAATTGCTGCTGCTGCAGCAAGTAAAAATGTAGCCCTTAGTGGTCCGATTCTT 	150	g dg
1500 . 6152	ACAGAGGAGGTCACTTTAACAGGTCTTTCCATTCCTGTAGACTCTTTAGGCGAGGGTAAG	1441 6211	Db Qy
1440 6212	TTTACTCAGACCGCGGGTTCCTCTGTTATTATGGATGCGGGCACAACGTTAAAAGCAAGT	1381 6271	D 09
1380 6272	GTAACTCTAACTGCAGGAAATTTAGTACTTAAACGTGGTGTCACTCTCGATACGAAAGGC	1321 6331	dd Vy
1320 6332	AAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAACCTCACTTCTACGCTGAAGCAGCCT	1261 6391	рь
1260 6392	. AATAAGGCTGATGCAGGTAATAGTACAGATTATAGTGGGTCGATTGTTTTTTCTGGTGAA 	1201 6451	Оy
1200 6452	TTTTTCTACGATCCGATTACTGCTAATACGGCTGCGGATTCTACAGATACTTTAAATCTC	1141 6511	Db Qy
1140 6512	1 ATTGACATAGGATCTACTGCAAAGATCACGAATTTACGTGCAATATCTGGGCATAGCATC	08 57	Оy
1080 6572	1 ATTACCTTCAATGGGAATGCCATTGTTGCAACTACACCACAAACTACAAAAAAAA	102 663	P Q
1020 6632	1 GGTGGAGCCATTTCTATACTGGCAGCTGGAGAGGTGTAGTCTTTCAGCAGAAGCAGGGGAC	96	рь
960 6692	1 GGGGGGGGGGGGTATCTCCTTTTCTAACAATATAGTCCAAGGTACCACTGCAGGTAAT	90 675	Db Qy
6751	0 GGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCTAAGAAGCTTACACTGGCTTCC	681	ДЬ

RGTCTCAGAAATTCTG 2815	GATCTTGGGGGTAAGTTCCAATTCTAGGAGCGTCTCTCATGTCTCAGAAATTCT	2761 4891	DP QA
CCTCACGGATTTATAATGTA 489	TTTGAAGTGCTCGGCCAGTTTGTCTTTGAAGTTCGTGGA		Ъ
CCTCACGGATTTATAATGTA 276	TTTGAAGTGCTCGGCCAGTTTGTCTTTGAAGTTCGTGGATCCTCACGGATTTATAATGTA	2701	Qy
PACTACGCCTTCTCTCTATG 495	AACTTAGCACGACAGGCCTTGCAAGTGCGTGCAGGCAGTCACTACGCCTTCTCTCTC	5011	В
CACTACGCCTTCTCTCTATG 2700	AACTTAGCACGACAGGCCTTGCAAGTGCGTGCAGGCAGTC	2641	ΩУ
CTTGGGAAACTTATGCCAAT 5012	GATCCCAAATGCACTACAGCACTTGTAATCAGCGGAGCCTCTTGGGAAACTTATGCCAAT	5071	Вδ
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FATGCTCCATACATCAAACTG 525	TCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATGCTCCATACATCAAACTG	5311	Ъ
FATGCTCCATACATCAAACTG 2400		2341	Qy
AACATGATGTTGGGAGCTTCT 5312	TATCCTGAGGTGAAAGGTTCTTGGGGGAATAATGCTTTTAACATGATGTTGGGAGCTTCT	5371	Дb
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TGAAGACAAAGTATACTGCG 537	TTAGAAGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTATACTGCG	5431	Db
TGAAGACAAAGTATACTGCG 2280	TTAGAAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATC	2221	Qy
RGGAGTCATAAACCCCTCGTT 543	GGGTTCATAGGTTGTCTCTTAGATAAACTTCCTGGCTCTTGGAGTCATAAACCCCCTCGTT	5491	рь
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ಕ -	AAAAATCATACTGATACCTATGCAGGAGCCTTCTATATCCAACACATTACAGAATGT	5551	Dδ
CAACACATTACAGAATGTAGT 2160	AAAAATCATACTGATACCTATGCAGGAGCCTTCTATATCC	2101	Qy
BATAAAGATTTCTTAGTCGCT 555	AACTTAATTAGCTTTTGCCTTTTGCCAACTCTTTGGTAGCGATAAAGATTTCTTAGTCGCT	5611	Db
SATAAAGATTTCTTAGTCGCT 2100	AACTTAATTAGCTTTTGCCTTTTGCCAACTCTTTTGGTAGCC	2041	ΩУ
CAGCGCAAACTTGTTCTGAA 5612	AAATACCGTCATAAATCTGGTGGATATGCTATCGGAGGTGCAGCGCAAACTTGTTCTGAA	5671	Db
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RESULT 6
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL unidentified.
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unclassified.
1 (bases 1 to 3000)
1 (bases 1 to 3000)
Madsen,A. and Birkelund,S.
NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
Patent: WO 9858953-A 25 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK) A81851 3000 bp DNA Sequence 25 from Patent WO9858953. A81851 A81851.1 GI:6731876

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                                                    GGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACCCCCTCAGGA
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                                                    AAAGTTGTAATTGCTGCTCTGCAGCAAGTAAAAATGTAGCCCTTAGTGGTCCGATTCTT
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Submitted (29-AUG-1997) Knudsen K., Department of Medical Microbiology and Immunology, University of Aahus, The Bar building, University of Aahus, DK-8000 Aarhus C, DENMARK 2 (bases 1 to 6030)
Knudsen K Madsen A S Mygrind D Christiansen G and Knudsen K Madsen A S
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Chlamydophila pneumoniae
Bacteria; Chlamydiales; Ch
(bases 1 to 6030)
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Birkelund,S.
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/db_xref="GI:325935"
/db_xref="GI:225935"
/dl_xref="GI:22593
/gene="omp5"
/note="putative"
complement(2777.
/gene="omp5"
                                                                                                             /product="outer membrane
complement(2698. .2742)
/gene="omp5"
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/gene="omp5"
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/gene="omp5"</pre>
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/gene="omp5"
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/clone="B8F3"
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/isolate="CDC/CWL-029/VR-1310"
/db_xref="taxon.83558"
                                                                                        complement (2747.
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                                                           GGAGATATAACTCTGCAAAACCTTGGGGATTCGGCAGCTTTAACGAAGGGTTGTTTTCT 2503
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FSQEAGSLLGMDSGTTLSTPAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGK
LNLIDIEGNIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEVGFQG
QWNVWTTDTATNTKEATAUWTKTGFVPSPERKSALVCNTLMGVFTDIRSLQQLVEIG
ATGMEHKQGFWVSSMTNFLHKTGDENRKGFRHTSGGVVIGGSAHTPKDDLFTFAFCHL
FARDKDGFIAHNSRTYGGTLFFKHSHTLQPQNYLLGFAKFSESALIKFPREIPLAL
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GAAASTTANKKLTESGFSLLSEDSSPSTTVTTGQGTLSSAGGVKLENIRKLVVAGNFS
TADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYRFLSNIAS
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VAETSGGAIHAKKLALSSGGFTEFLRNVSSATPKGGAISIDASGELSLSAETCNITF
VRNTLTTTGSTDTPKRNAINIGSNGKFTELRAAKNHTIFFYDPITSEGTSSDVLKINN
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/gene="omp4"
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KVEMVYVSQNSFFESSSDGRGFSTGRLLNLSTPVGAKFVQGDTGDSYTYDLSGFFVSD
VYRNNPQSTATLYMSPDSWKTRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
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2905. .2955
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/translation="MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                         97.4%; Score 2742;
100.0%; Pred. No. 0;
tive 0; Mismatches
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1440	TTTACTCAGACCGCGGGTTCCTCTGTTATTATGGATGCGGGCACAACGTTAAAAGCAAGT	1381	Qy
1380	GTAACTGTAACTGCAGGAAATTTAGTACTTAAACGTGGTGTCACTCTCGATACGAAAGGC	1321	Qy
1363		1422	Db
1320	AAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAACCTCACTTCTACGCTGAAGCAGCCT	1261 <sup>°</sup>	Qy
1423		1482	Db
1260	AATAAGGCTGATGCAGGTAATAGTACAGATTATAGTGGGTCGATTGTTTTTTTCTGGTGAA	1201	Qy
1483		1542	Db
1200	TTTTCTACGATCCGATTACTGCTAATACGGCTGCGGATTCTACAGATACTTTAAATCTC	1141	Qy
1543		1602	Db
1140	ATTGACATAGGATCTACTGCAAAGATCACGAATTTACGTGCAATATCTGGGCATAGCATC	1081	Qy
1603		1662	Db
1080	ATTACCTTCAATGGGAATGCCATTGTTGCAACTACACCACAAACTACAAAAAGAAATTCT	1021	Qy
1663		1722	Db
1020	GGTGGAGCCATTTCTATACTGGCAGCTGGAGAGTGTAGTCTTTCAGCAGAAGCAGGGGAC	961	Qy
1723		1782	Db
960	GGGGGGGGGGGGTATCTCCTTTTCTAACAATATAGTCCAAGGTACCACTGCAGGTAAT	901	Qy
1783		1842	Db
900	GGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCTAAGAAGCTTACACTGGCTTCC	841	Qy
		1902	Db
840 1903	GGACCTCTTTCTGGAGATGCCGATGTTACCATATCTGGGAATCAGAGTGTAACTTTCTCA	781 1962	Qy
780	ACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCGACCGCAGGAAATGGA	721	Qy
1963		2022	Db
720	TCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACAGGAAACTGTACAATT	661	Qy
2023		2082	Db
660	GGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACGGCTCCTACCCTCTTC	601	Qy
2083		2142	Db
600	AACAGCACGGGATCGATTTCTTTTGAAGGGAATAAATCGAGCGCAACAGGGAAAAAAGGT	541	Qy
2143		2202	Db
540	AAACAAGATTACTGTGAGGAAAATGGCGGAGCCATTTCTACCAAGAATCTTTCTT	481	Qy
2203		2262	Db
480	AAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATTTTATTT	421	Qy
2263		2322	Db
420	GGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACCCCCTCAGGA	361	Qy
2323		2382	Db
2383		2442	Db

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TCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATGCTCCATACATCAAACTG
                                                                                                                           AAAAATCATACTGATACCTATGCAGGAGCCTTCTATATCCAACACATTACAGAATGTAGT
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                                        TTAGAAGGGCAGCTCGCTTATAGGCCACGTCAGTAATGATCTGAAGAACAAAGTATACTGCG
                                                                                                                                                                                                                                                                                                                                                     AAATACCGTCATAAATCTGGTGGATATGCTATCGGAGGTGCAGCGCAAACTTGTTCTGAA
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ACCESSION
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Best Local Similarity 55.8%;
Matches 1570; Conservative
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GGGATTACGAAATTCTCAGGATTTTCAACTCTTCGGATGCTTGCAGCTCCTAGGA-----
                   TCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCCCATCATCGGTAATCACAACC
                                                       TTAAATATTAAGTCTAGTGCTGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTG
                                                                                      TGTTTTCTAACACTGCAGGAAATCTTACCTTCTTAGGGAACGGATTTTCTCTTCATTTT
                                                                                                 ACTCTGACAGGAGATATAACTCTGCAAAACCTTTGGGGATTCGGCAGCTTTAACGAAGGGT
                                                                                                                                                                            AGTGTTTCTGCAGATGCTGCCGATCTCACATTAGGGAGTCGTGACAGTTATAATGGTGAT
                                                                                                                                                                                                                                       TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTTGACGGAAGT
                                                                                                                                                                                                                                                                     ATGAGATCGTCTTTTCCTTGTTAATAATATCTTCATCTCTAGCCTTTCCTCTTAATG
                                                                                                                                                                                                                                                                                            ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT
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Sequence
A81837
A81837.1
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Madsen,A. and Birkelund,S.

NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA

PATENT: WO 9858953-A 11 30-DEC-1998;

MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)

LOCATION/QUALIFIERS

1. 2757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unidentified unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unclassified
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                                                                                                                                                                                                                                                                                                                                                                                    /organism="unidentified"
/db_xref="taxon:32644"
1 564 c 642 g 78
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from 1
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Patent
                                                                                                                                                                                                                                                                                                                 Score 670.6; DB 9;
Pred. No. 3.2e-150;
0; Mismatches 1159;
                                           GTTGCAGGTGTTGTTAGCAATACAGCAGCTTCT
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1536	GTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTTCTGCAGCAAGTAAAAAT	1477	Qy
1467		1408	Db
1476	TTTAACAGGTCTTTCCATTCCT	1417	Qy
1416 1407	GGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATTATGGAT	1357 1348	Дb
1356 1347	CTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTTAAACGT	NN	рь
28	GGCTACATCGTTTTCTCTGGAGAGAAACTCTCAGAAGAGGGAACTTAAGAAACCTGACAAT	22	Db &
1227	GGAGCTACTGATAAGCTCTCTTTGAATAAAGCTGACGCAGGATCTGGAAATACCTATGAA	1168	g B
1236	GATTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGTAATAGTACAGATTATAGT	17	Qy
1176 1167	CGTGCAATATCTGGGCATAGCATCTTTTCTACGATCCGATTACTGCTAATACGGCTGCG	1117	Db Qy
1116	CCTGCGAGTGTGACCAGAAATGCTATAGATCTTGCATCGAATGCAAAATTTTTAAATCTC	1057	밁
1116	CCACAAACTACAAAAAGAAATTCTATTGACATAGGATCTACTGCAAAGATCACGAATTTA	1057	Q
1056	ATTTCTGCAGATCTCGGCAATATCATTTTCGAGGGCAATACTACGAGCACTACAGGAAGT	997	Db
1056	CTTTCAGCAGAAGCAGGGGACATTACCTTCAATGGGAATGCCATTGTTGCAACTACA	1000	Qy
996	ATGCTACTCCTAAAGGAGGGGCAATTCCGATTCTAGATTCTGGAGAGATTAGC	943	рь
999	CAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATACTGGCAGCTGGAGAGTGTAGT	940	Qy
942	AAAAAATTGGTGTTATCCTCAGGACGAGGAGGAGTGTTATTTCTAACAACAAGCTGCG	883	Db
939	AAGAAGCTTACACTGGCTTCCGGGGGGGGGGGGGGGGTATCTCCTTTTCTAACAATATAGTC	880	Qy
882	ATGAGAGCCTGCATTTTCTGAATAACACAGCAGGAAATAGTGGAGGTGCGATTTATACC	823	В
879	AATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCT	820	Qy
822		763	рь
819	GGAAATGGAGGAGCTCTTTCTGGAGATGCCGATGTTACCATATCTGGG	772	Qy
762	CTTGTGATCTCCAATAACCAAAATATCTTTTTCGATAGCAAACGAACTACAAATGGC	703	B 5
702	TTGAGCTTCGGAAACAACAGTGCGACAACATCAGGAGGCGCGATCTCTGCTGAAGGGAAC	٠,	문
711		Ċ	Qy
642	CAACAAGGGGAGCGATCTATGCTTCTGGTGACTCTGTGATTTCTGAGAATGCAGGAATC	583	Дb
651	AAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACGGCTCCT	592	Qy
582		532	В
591	TCTTTGAAAAACAGCACGGGATCGATTTCTTTTGAAGGGAATAAATCGAGCGCAACAGGG	532	Qy
531	ALLITALITAMENHAMATIK/ISTSKASSKASKASISSKSCKATTICIAK/CAMSKASICTI 	472	B 2
4 / L	-CCACAGGIAAAGGAAGCCAITAAAAITACCGAIGGICTGGIGITTTGAGAGTAIAAGGAAAI	J F	2 5
471	CCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACT	ىر د	γ <sub>0</sub>

Qy 2554 TCCT 	Qy 2494 ATAGG         Db 2470 GTAGG	Qy 2434 GAGF       Db 2410 GAAF	Qy 2374 GATF       Db 2350 GATF	Qy 2317 TTT# 	Qy 2257 GATCTG         Db 2230 AACATG	Qy 2197 TCTT       Db 2170 AATT	QY 2137 ATCCAAC       Db 2122 TACCGAC	QY 2077 AGCGAT     Db 2062 TACGAC	Qy 2017 GGTC      Db 2002 GGAC	Qy 1957 AAAC       Db 1942 GAAC	Qy 1897 GCT7     Db 1882 ACAA	Qy 1837 AAT?        Db 1822 AAT?	Qy 1777 TTAC  +  Db 1762 TTAJ	Qy 1717 ACTT           Db 1708 ACTC	Qy 1657 ACTAC:        Db 1648 ACTAC	Qy 1597 GACT       Db 1588 AATC	Qy 1537 GTAC       1    1528 GTTC	   Db   1468 ATAC
ATGTTCCTGATCTTATCO	GGTGAAG        GATAAAA	AGAAAGGTACAGAAGGAAGATCTT 	CCTATGCTCCATACATC 	TTAACATGATGTTGGGAGCTTCTTCTCATTCTTATCCTGAATACCTG	CTGAAGACAAAGTATACTV               	GGAGTCATAAACCCCTC     	AACACATTACAGAATGTAG 	ATAAAGATTTCTTAGTCGCTAAA 	CAGCGCAAACTTGTTCTI 	ATAAGAAAGGGAAAAA                ATCAGAAAGGAAACCAA	TGACTCTTTGTTCAGAT	GCCTTTGGGGATCTTTT                 GCCTGTGGGGTTCTTTT	CTTGGACCAATACAGGC                  CTTGGACTAAAACAGGA	TTGGGGAATGACTTGGGTTGATGATAC 	CAGATGTTCCAGCGGTT     -          CAGATATCCCCGATACC	TAGGAAAAACTCAAGAC 	TAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATG 	 ATTCCTTAGATGGGACA
CGCAATGATCCCAAATG	TTTGAGAAGTTCTCTGATTGTAATGA 	TCTTTTGATGACAGCAA 	AAACTGAATCTGACCTA                         AACCTAGAGATGATCTA	TTGGGAGCTTCTTCTCATTCTTATCCT	aagacaaagtatactgcgtatcctgaggtgaaaggttcttgggg 	GTTTTAGAAGGGCAGCT 	AGTGGGTTCATAGGTTG     AAGAC	GCTAAAAATCATACTGA 	GAAAACTTAATTAGCTT               GAAAATTTCTTTAATTT	CGCAAATACCGTCATAA 	CGAGGCTTCTGGGCTGC              ACAAATTTGTGGGTATC	TCAGACATCCAAGCGAT 	TACCTTCCGAATCCTGA                TACAAGCCGAATCCAGA	GATGATACCGCAAGCAC 	CCTACAGTAGCAACTCC 	TTTTCATTTGTGCAGCT                TTTCCTTTAATAGAGCT	CTTCTTTTGGATAACCA 	 AATAAAGCTATCATTAA
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AGC 2613	TTA 2553    ATA 2523	CCT 2493      CCT 2469	TCTCG 2433 	TTTT 2373    GGTG 2349	GCT 2316 	AAT 2256     AAT 2229	GGC 2196    GGA 2169	TAT 2136   AGT 2121	GGT 2076    GGC 2061	GGA 2016      GGA 2001	GAT 1956    CAT 1941	AGT 1896    AGC 1881	CCT 1836  -  CCT 1821	ACA 1776    ACC 1761	GGT 1716     GGA 1707	ACA 1656     ACT 1647	CAC 1596    CAT 1587	 GAT 1527

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AE001587.1 GI:4376271
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Kalman,S., Mitchell,W., Marathe,R., Lammel,C.,
Grimwood,J., Davis,R.W. and Stephens,R.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydophila pneumoniae CWL029. Chlamydophila pneumoniae CWL029
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Best Local Similarity
Matches 1565; Conserv
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                                                                                                                        AAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATAATACGGCTCCT
                                                                                                                                                                                               TCTTTGAAAAACAGCACGGGATCGATTTCTTTTGAAGGGAATAAATCGAGCGCAACAGGG
                                                                                                                                                                                                                                                                ATTTTATATAACAAGATTACTGTGAGGAAAATGGCGGAGCCATTTCTACCAAGAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                           TCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACC
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                                TTGAGCTTCGGAAACAACAGTGCGACAACATCAGGAGGCGCGATCTCTGCTGAAGGGAAC
                                                                 ACCCTCTTCTCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACAGGAAAC
                                                                                                     CAACAAGGGGGAGCGATCTATGCTTCTGGTGACTCTGTGATTTCTGAGAATGCAGGAATC
                                                                                                                                                                           TCTTTGACTGGGAGTACGCGGTTTGTAGCGTTCCTTGGCAATAGCTCGTC-----
                                                                                                                                                                                                                                              CTTGATCTTAATGAAAATGCCTCTAGTGAAAATGGGGGAGCCATCAATACGAAGACTTTG
                                                                                                                                                                                                                                                                                                                                                    CCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACT
                                                                                                                                                                                                                                                                                                                                                                                         GGGATTACGAAATTCTCAGGATTTTCAACTCTTCGGATGCTTGCAGCTCCTAGGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACAATATTATTTCGTCTACT---GTTGCAGGTGTTGTTAGCAATACAGCAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAAATATTAAGTCTAGTGCTGAAGGCGCGCAGCACTTTCTGTTACAACTGATAAAAATCTG
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TGTACAATTACAGGGAATACGTCTTGTATTTTCTGAAAATAGTGTGACAGCGACCGCA
                                                                                                                                                                                                                                                                                                                 -CCACAGGTAAAGGAGCCATTAAAATTACCGATGGTCTGGTGTTTGAGAGTATAGGGAAT
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SGLRISEIVAVNKQDFDLSTHLIRIRGKKERILPTVSNAIQMIQIYLNHDDKKRLE
KDPQAIFLNRFGRAIGFRSIDKSFGEYYLRRSGLSGHTPHTIKHTIATHWLESGMDLK
TIOALLGHSSLETTTVTTQVSVKLKKQTHQEAHPHA"
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Pred. No. 2.3e-148;
0; Mismatches 1165;
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δõ 밁 Ş 밁 Š 밁 Ş 밁 Qy 밁 δÃ 밁 ρ 밁 Š 밁 Qy 밁 Qy 밁 δÃ 밁 Qy В δÃ 밁 δÃ Ър δÃ Ωy 밁 Qy Вb δÃ 밁 밁 1177 1777 4783 4723 1477 4603 4543 4423 4312 4843 1657 1597 1537 4663 1417 4483 1297 1237 4363 1117 4252 1057 4192 1000 4138 4078 4018 3898 TTAGCTTGGACCAATACAGGCTACCTTCCGAATCCTGAGCGTCAAGGACCTTTAGTTCCT AACTGGAATAATTGTTTGGGTCG-----ACGATGCAACTGCAAAAAACAAAAATGCTACC ACTTGGGGAATGACTTGGGTTGATGATACCGCAAGCACTCCAAAGACTAAGACAGCGACAC ACTACAGATATCCCCGATACCCCAATTCTAAATACTACGAATCACTATGGGTATCAAGGG ACTACAGATGTTCCAGCGGTTCCTACAGTAGCAACTCCTACGCACTATGGGTATCAAGGT AATCTCAGTCAACAGCAGGTCTTTCCTTTAATAGAGCTTTCTGCACAAGGAACGATGACT GACTTAGGAAAAACTCAAGACTTTTCATTTGTGCAGCTCTCTGCTCTGGGTACTGCAACA GTTGCCTTATCAGGGCCTATCATGCTTGTAGATGCTCAGGGGAACTATTATGAGCATCAT GTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATGAAAATCAC ATAGATTCCTTAGATGGGACAAATAAAGCTATCATTAAGGCGACGGCAGCAAGTAAGGAT GTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTGCTTCTGCAGCAAGTAAAAAT GGAGGGACTACTTTTGAGGCAAGCGCTGAGGGGGTCACTCTCAATGGCCTAGCCATTAAT GCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGGCGCTTTAACAGGGCTCTTTCCATTCCT GGAGTGACTGTAGTTGCAAATACTATAACGCAGGTCGAGGGATCGAAAGTCGTTATGGAT GGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATTATGGAT CTGAAGTCTACATTTACACAGGCTGTAGAGCTTGCTGCAGGTGCCTTAGTATTGAAAGAT CTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTTAAACGT GGCTACATCGTTTTCTCTGGAGAGAAACTCTCAGAAGAGGAACTTAAGAAACCTGACAAT GGGTCGATTGTTTTTTCTGGTGAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAAC GGAGCTACTGATAAGCTCTCTTTGAATAAAGCTGACGCAGGATCTGGAAATACCTATGAA GATTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGTAATAGTACAGATTATAGT CGAGCGACTCGGGGAAATAAAGTTATTTTCTATGATC-----CTATCACGAGCTCA CGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATTACTGCTAATACGGCTGCG CCTGCGAGTGTGACCAGAAATGCTATAGATCTTGCATCGAATGCAAAATTTTTAAATCTC CCACAAACTACAAAAAGAAATTCTATTGACATAGGATCTACTGCAAAGATCACGAATTTA 1116 ATTTCTGCAGATCTCGGCAATATCATTTTCGAGGGCAATACTACGAGCACTACAGGAAGT CTTTCAGCAGAAGCAGGGGACATTACCTTCAATGGGAATGCCATTGTTGCAACT---ACA ATGCTACTCC-----TAAAGGAGGGCAATTGCGATTCTAGATTCTGGAGAGATTAGC CAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATACTGGCAGCTGGAGAGTGTAGT AAAAAATTGGTGTTATCCTCAGGACGAGGAGGAGTGTTATTTTCTAACAACAAAGCTGCG AAGAAGCTTACACTGGCTTCCGGGGGGGGGGGGGGGGTATCTCCTTTTCTAACAATATATAGTC AATGAGAGCCTGCATTTTCTGAATAACACAGCAGGAAATAGTGGAGGTGCGATTTATACC AATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCT GGAGCTATTGATTGTAACAAAGCAGGGGCGAACCCAGACCCTATCTTGACTCTTTCAGGA CTTGTGATCTCCAATAACCAAAATATCTTTTTCGATGGCTGCAAAGCAACTACAAATGGC **AATGGAGGAGCTCTTTCTGGAGATGCCGATGTTACCATATCTGGG** 1776 1656 1296 4251 1836 4957 4782 4722 4662 1476 4602 1416 4422 4362 4311 1056 4191 4017 4902 4842 1596 4542 1356 1236 4077 4482 4137 939 879 3957 999 819

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Christiansen, G.

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RESULT 10
CPN133035
LOCUS
                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                          GGCAGTCACTACGCCTTCTCTCCCTATGTTTGAAGTGCTCGGCCAGTTTGTCTTTGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAGGGGTGAAGTTTGAGAAGTTCTCTGATTGTAATGACTTTTCTTATGATCTGACTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGAAAGGTACAGAAGGAAGATCTTTTGATGACAGCAACCTCTTCAATTTATCTTTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATACCTATGCTCCATACATCAAACTGAATCTGACCTATATACGTCAGGACAGCTTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATCTGAAGACAAAGTATACTGCGTATCCTGAGGTGAAAGGTTCTTGGGGGGAATAATGCT
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                                                                                                                                                                                                                                                                                                                                                           GGGGATTCTTGGTCGACATGTGGTACAAGCTTGTCTAGACAAGCTCTTCTTGTACGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTTACGTTCCCGATGTGATTCGTAATGATCCAGGCTGCACGACAACTCTTATGGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAGGGATAAAATTTGAGAAATTCTCCGATA----AGTCTACGTATGATCTCTCCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAAACGGCACAGAAGGCCGTTCTTTCCAAAGTGAAGACCTCTTCAATCTAGCGGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATACCCACACGCCATTTCTAAACCTAGAGATGATCTATGCACATCAGAATGACTTTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACATGACCACAAAGTACACTGGCTATTCTCCTGTTAAGGGAAGCTGGGGAAATGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTCTGACTCCCTACCTTTTGTCTTCAATGCTCGGTTTGCTTATGGCCATACCGACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACCGACACCTCGGAGAGTCTA-------AGACCCTCGCTAAGATTTTGTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCCAACACATTACAGAATGTAGTGGGTTCATAGGTTGTCTTAGATAAACTTCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGACAAGGACCATCTTGTGGCTAAGAACCATACCCATGTATATGCAGGGGCAATGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGGATTCTTCACGGCTTCTGAAAATTTCTTTAATTTTGCTTTTTGTCAGCTTTTTGGC
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                            CPN133035
Chlamydia
hb1, hb2,
omp15,
   strain VR1310
                     26920 bp DNA 27-FEB-2 pneumoniae GGAI-protein family cluster B, genes hb3, hb4, hb5, hb6, hb7, omp7, pseudogenes omp8
                                                                                       27-FEB-2001
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AJ133035.1 GI:4455890
AJ133035.1 GI:4455890
HB1 gene; HB2 gene; hb3 gene; hb4 gene; hb5 gene; hb6 gene; gene; omp15 gene; omp6 gene; omp7 gene; omp8 gene; omp9 gene membrane protein 6; outer membrane protein 7; pseudogene. Chlamydophila pneumoniae. Chlamydophila pneumoniae
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Building, DK-8000 Aarhus, DENMARK
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="HB3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="hypothetical"
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Query Match
Best Local (
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ACTCTGACAGGAGATATAACTCTGCAAAACCTTGGGGATTCGGCAGCTTTAACGAAGGGT 231
                                                                                                                                                                                                                  ACTAACACAGGCACCTATACTCCTAAAAATACGACTAC-----TGGAATAGACTAT 171
                                                                                                                                                                                                                                                                              AGTGTTTCTGCAGATGCTGCCGATCTCACATTAGGGAGTCGTGACAGTTATAATGGTGAT
                                                                                                                                                                                                                                                                                                                           TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGAAGT 120
                                                                                                                                                                                                                                                                                                                                                                                    ATGAGATCGTCTTTTTTCCTTGTTATTAATATCTTCATCTTCTAGCCTTTCCTCTTAATG 20845
                                                                                                                                                                  ACAAGCACCACAGAATTTACTCCTAAAGCGGCAACTTCTGATGCTAGTGGCACGACCTAT
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14954. .17479

/gene="omp7"

/note="putative"

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/note="
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13014. .14585
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RELPDEEKIELLSGBBLLEFTAANLFKQGRDVYLNLGNLADIRAYMGPNNYKVAMVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKEKCAEAEKAFLEQQKILLDYGKSIFWLNENDEINLNDPWSWGLNTVRTRKVFQEVD
DSERWHKVLLQKLEDNYEKLLEESSKESTEANKKLLSDLVDRLEDAKTKFFLKKQEE
VETRVKDLRARYGGTVDPKQDTEAKKKVELEASLETFLDSIESELVQCLEDQDIYWKE
QDVKDLARTQELEEQDIEAKREEAAEDLRSLNERLKKSKTMLDEAKWHIENAEDSIYWK
WTSQIEMKDMKARLKILKEDITSVLPEIDEIETCLSLEELPLLTTRELLTKSYLKFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSETLLKMTSVFENNIYVQEYEVQLQNLGFKLQGISQRFGKKQDDFANLEEQVALQKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANARRLYYVRDWYDÓEFORAGERLEKLHALY PEVSVSIRENKI DETRSNILEKAYEAIE
ENYROCVREOEDYWK SEEKREAEF RERGNK ILS PEELESELEOFDHGLKNF SEKLMEL
EGHILKLOKEATABVENK ILSDAESRILEIVFEDVK EMPCRIEEIEKTLHAMAELPLLPT
KKAFEKACSOYNSCAEMLEKYK PYCKESLAY VTSKERLVSLDEDLRRAY TECOKRFOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRIAEELALELKKKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAKAVVHEFIVLTTMARELEFFF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSGLESEVRACREQLRERIQEFETQGLDLVEKELLCVSSRLRNTECDCVSGVKKEAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLELMYNCADSYRDAKKKLCSLRLDEKELLQKEIKKEEFYQKKQQRHADRSRHTTYQK
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Pred. No. 2.3e-148;
0; Mismatches 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 26920;
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1356 22132	1297 CTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTTAAACGT :	Оy
1296 22072	1237 GGGTCGATTGTTTTTTCTGGTGAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAAC	д <sub>0</sub>
1236 22012	1177 GATTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGTAATAGTACAGATTATAGT :	D Q
1176 21952	1117 CGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATTACTGCTAATACGGCTGCG	β Q
1116 21901		d Qy
1056 21841	000 CTTTCAGCAGAAGCAGGGGACATTACCTTCAATGGGAATGCCATTGTTGCAACTACA	Db 24
999 21781	940 CAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATACTGGCAGCTGGAGAGTGTAGT	D Qy
939 21727	880 AAGAAGCTTACACTGGCTTCCGGGGGGGGGGGGGGGGGTATCTCCTTTTCTAACAATATAGTC	Дb
879 21667	820 AATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCT	Дb
819 21607	772 GGAAATGGAGGAGCTCTTTCTGGAGATGCCGATGTTACCATATCTGGG	Db Qy
771 21547	TTACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCGACCGCA	Дb
711 21487	652 ACCCTCTTCTCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACAGGAAAC	Db Qy
651 21427	2 AAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACGCTCCT	Db Qq
591 21367	532 TCTTTGAAAAACAGCACGGGATCGATTTCTTTTGAAGGGAATAAATCGAGCGCAACAGGG	Db
531 21316	472 ATTTTATTTAAACAAGATTACTGTGAGGAAAATGGCGGAGCCATTTCTACCAAGAATCTT	Qу Дъ
471 21256	412 CCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACT	. Qy
411 21197	352 TCGCTAACAGGATTTTCGAGTCTTACTTTAGCGGCCCCATCATCGGTAATCACAACC	B 8
351 21142	292 TTAAATATTAAGTCTAGTGCTGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTG	Фу
21085	TTT	В

CAGGACAGCTTCTCG 2433             CAGAATGACTTTAAG 2319	GATACCTATGCTCCATACATCAAACTGAATCTGACCTATATACGTCAGGACAGCTTCTCG	2374 23136	Qу
GAATACCTGCATTGTTTT 237	TITAACATGATGTTGGGAGCTTCTTCTTCTTATCCTGAATACCTGCATTG	2317 23076	Фр
TGGGGGAATAATGCT 2316                TGGGGAAATGATGCC 2307	GATCTGAAGACAAAGTATACTGCGTATCCTGAGGTGAAAGGTTCTTGGGGGAATAATGCT	2257 23016	Qy Db
AGCCACGTCAGTAAT 2256            GGCCATACCGACAAT 2301	TCTTGGAGTCATAAACCCCTCGTTTTAGAAGGGCAGCTCGCTTATAGGCACGTCAGTAAT	2197 22956	Qy Db
SATAAACTTCCTGGC 219 	ATCCAACACTTACAGAATGTAGTGGGTTCATAGGTTGTCTCTTAGATAAACTTCCTGGC	2137 22908	ОУ
GCAGGAGCCTTCTAT 2136                GCAGGGGCAATGAGT 22907	AGCGATAAAGATTTCTTAGTCGCTAAAAATCATACTGATACCTATGCAGGAGCCTTCTAT	2077 22848	Qy Db
TGCCAACTCTTTGGT 2076                   TGTCAGCTTTTTGGC 22847	GGTGCAGCGCAAACTTGTTCTGAAAACTTAATTAGCTTTGCCTTTTGCCAACTCTTTGGT 	2017 22788	dq Vo
GGATATGCTATCGGA 2016                GGTTATGCATTAGGA 2278	AJAGATAJGAAAGGGGAAJAACGCAAATACCGTCATAJATCTGGTGGATATGCTATCGGA	1957 22728	Db Qy
GCCAATTTCTTAGAT 1956                 CGGACTTTTTGCAT 2272	GCTTTGACTCTTTGTTCAGATCGAGGCTTCTGGGCTGCGGAGTCGCCAATTTCTTAGAT	1897 22668	ОУ
GTCATAGAGAGAAGT 1896               CTCATGGACCGGAGC 22667	AATAGCCTTTGGGGATCTTTTTCAGACATCCAAGCGATTCAAGGTGTCATAGAGAGAAGT	1837 22608	Qy Db
GGACCTTTAGTTCCT 1836           GACCTTTGGTTCCT 22607	TTAGCTTGGACCAATACAGGCTACCTTCCGAATCCTGAGCGTCAAGGACCTTTAGTTCCT	1777 22548	Оy
ACTCCAAAGACTAAGACAGCGACA 1776                     ACTGCAAAAACAAAAAATGCTACC 22547	ACTTGGGGAATGACTTGGGTTGATGATACCGCAAGCACTCCAAAGACTAAGACAGCGACA	1717 22493	Qy Db
TATGGGTATCAAGGT 1716                  TATGGGTATCAAGGG 2249	ACTACAGATGTICCAGCGGTTCCTACAGTAGCAACTCCTACGCACTATGGGTATCAAGGT	1657 22433	Oy Db
CTGGGTACTGCAACA 1656             CAAGGAACGATGACT 2243	GACTTAGGAAAAACTCAAGACTTTTCATTTGTGCAGCTCTCTGCTCTGGGTACTGCAACA	1597 22373	, DP
GCTTATGAAAATCAC 1596            TATTATGAGCATCAT 22372	GTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATGAAAATC	1537 22313	Qy Db
GCAGCAAGTAAAAAT 1536              GCAGCAAGTAAGGAT 22312	GTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTTCTGCAGCAAGTAAAAAT	1477 22253	Qy Db
GGTCTTTCCATTCCT 1476                 	GCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTTCCATTCCT	1417 22193	Qy Db
TCTGTTATTATGGAT 1416             AAAGTCGTTATGGAT 2219	GGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATTATGGAT 	1357 22133	Qy Db

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REFERENCE
AUTHORS
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SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23490 CGAGGTTCTTCTCGTAGCTATGCTATCGATCTTGGAGGAAGATTCGGATTTTA 23542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2734 CGTGGATCCTCACGGATTTTATAATGTAGATCTTGGGGGTAAGTTCCAATTCTA 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2434 GAGAAAGGTACAGAAGGAAGGATCTTTTGATGACAGCAACCTCTTCAATTTATCTTTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAGTCACTACGCCTTCTCTCCTATGTTTGAAGTGCTCGGCCAGTTTGTCTTTTGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAGGGATAAATTTGAGAAATTCTCCGATA-----AGTCTACGTATGATCTCTCCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAGGGGTGAAGTTTGAGAAGTTCTCTGATTGTAATGACTTTTCTTATGATCTGACTTTA 2553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTACGTTCCCGATGTGATTCGTAATGATCCAGGCTGCACGACAACTCTTATGGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGATTCTTGGTCGACATGTGGTACAAGCTTGTCTAGACAAGCTCTTCTTGTACGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTATGTTCCTGATCTTATCCGCAATGATCCCAAATGCACTACAGCACTTGTAATCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydophila pneumoniae AR39.
Chlamydophila pneumoniae AR39
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 10026)
Read, T.D., Brunham, R.C., Shen, G., Gill, S.R., Heidelberg, J.F., White, O., Hickey, F.E.K., Peterson, J., Umayam, L.A., Utterback, T., White, O., Hickey, E.K., Peterson, J., Khouri, H., Craven, B., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Berman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
Genome Sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE002193 10
Chlamydophila
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                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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AE002193.2 GI:8163406
                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-MAR-2000) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 McClarty, G., Salzberg, S.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                             Submission
                                      similarity; putative"
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                                                                                                                                                                                                                                                           /strain="AR39"
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    membrane
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                                                                                                                                                                                                                                                                             pneumoniae AR39"
                                                                                                                                                                                                                pneumoniae
                                                                                                     identified by sequence
                    protein G family"
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complement(6013.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFTQNFSSDNGGVINTKNFLLSGTSQFASFSRNQAFTGKQGGVVYATGTITIENSPGI
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gene

/note="similar to GP:4376727; identified by sequence similarity; putative" complement(6013. .9843) /gene="CP0309" /gene="CP0309"

CDS gene

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ORIGIN

COUNT

Query Match Best Local S Matches 1548 1 ATGAAATCGCAATTTTCCTGGTTAGTGCTCTTCGACATTGGCATGTTTTACTAGTTGT AATCTTTCTTTGAAAAACAGCACGGGATCGATTTCTTTTGAAGGGAATAAATCGAGCGCA CTAACAGGATTTTCGAGTCTTACTTTAGCGGCCCCATCATCGGTAATCACAACCCCC 1548; GGAAACTGTACAATTACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCG CTCTTTAGCCAAAACGTCTCCAATGAAGCTAATAACAATGGCGGAGCGATCACCGCAAAA TCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATT TTCACAGGATTTTCTAACCTTTCCTTCATTGCAGCTC----CTGGAACTACAGTTGCT GTAGATGCGGGTTCGAATGCAGGAGCTGCGGCAAGCACAACTGCTGATAAAGCCCCTAACA TCAGGAAATGTCTATATAAACGATGCTGGGAAAGGCACAGCATTAACAGGCTGCTTT ACAGGAGATATAACTCTGCAAAACCTTGGGGATTCGGCAGCTTTAACGAAGGGTTGTTTT AGTACTAACACAGGCACCTATACTCCTAAAAATACGACTACTGGAATAGACTATACTCTG AGCATTGCAACTTACGGAGCAGATGCTTCTTTATCCCCTACAGATAGCTTTGATGGAGCG TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGA---ATGAAAATACCCTTGCACAAACTCCTGATCTCTTCGACTCTTGTCACTCCCATTCTATTG ACCGCAGGAAATGGAGGAGCTCTTTCTGGAGA-----GCCAGCTCCTCGATTACTCAAAATAGCTCCCTTTTCTTCTCTGGAAACACTGCAACAGAT GCTCCTACCCTCTTCTCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACA ACAGGGAAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACG ACTCTTTCTATTTCTGGGAATACCTCTTCTATAACCTTCACTAGTAATAGCGCAAAA---TTATTTAAACAAGATTACTGTGAGGAA-----AATGGCGGAGCCATTTCTACCAAG TCAGGAAAAAGTACTTTAAGTTCTGCAGGAGCCTTAAATCTTACCGATAATGGAACGATT GCTGCAGGCAAGGGCGGGGCCATTTATTGTGAAAAAACAGGAGAGACTCCTACTCTTACT ATTAAGTCTAGTGC---TGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTGTCG Similarity 54.! 48; Conservative 2726 þ PDYGYQGSWTLVPKVGAGGKYTLVAEWQALGYTPKPELRATLVPNSLWNAYVNIHSIQ QEIATAMSDAPSHPGIWIGGIGNAFHODKQKENAGFRLISRGYLVGGSWTTPOEWYTFA VAFSQLFGKSKDYVVSDIKSQVYAGSLCAQSSYVIPLHSSLIRHVLSKVLPELPGETP LVLHGQVSYCRNHHMYTKLANNTQGSLCAQSSYVIPLHSSLRHVDLMYRYLTSYSPSY VKLQVVSVNQKGFQEVAADPRIFDASHLVNVSIPMGLTFKHESAKPPSALLLTLGYAV VKLQVVSVNQKGFQEVAADPRIFDASHLVNVSIPMGLTFKHESAKPPSALLLTLGYAV SRSYNANCGTRYSF" 2051 c 236 23.1%; 54.5%; 0; 2367 g Score 649.4; DB 1; Pred. No. 4.1e-145; 0; Mismatches 1231; 2882 + Indels Length TGCCGATGTTACC 10026 60; 2073 2424 2484 414 2598 2718 2838 525 297 10;

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ATATCTGGGAATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCC

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Chlamydophila pneumoniae CWL029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSTKKGLWIEDNENVSLSGNTATVSGGAIYATKCALHGNTTLTFDGNTAETAGGAIYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNSSLTGNTNLLFSGNKATGPSNSSANQEGCGGAILAFIDSGSVSDKTGLSIANNQEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEHEASQRQDARHRRIGREAQGSFFYSSRNPEHRRSFGSLSRFKTKPSDAASTRPASI
SPPFKDDFQPYHFKDLRSSSFGSGASSAFTPIMPASSRSPNFSTGTVLHPEPVYPKGG
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/transl_table=11
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475 TTATTTAAACAAGATTACTGTGAGGAA------
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gene

CDS

-AATGGCGGAGCCATTTCTACCAAG

525

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Query Match
Best Local Similarity
Matches 1548; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12532 TTCACAGGATTTTCTAACCTTTCCTTCATTGCAGCTC-----CTGGAACTACAGTTGCT 12585
                                                                                                                                   355 CTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACCCCC
                                                                                                                                                                                                                                                                                                                                                                 178 ACAGGAGATATAACTCTGCAAAAACCTTGGGGATTCGGCAGCTTTAACGAAGGGTTGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT
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TCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATT
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GSAHIYNVDCGLRYSF"
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LKEVEPFVKVQYIYAHQQDFYERHAEGRAFNKSELINVEIPIGVTFERDSKSEKGTYD
LTLMYILDAYRRNPKCQTSLIASDANWMAYGTNLARQGFSVRAANHFQVNPHMEIFGQ
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Pred. No. 4.2e-145;
0; Mismatches 1231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 15068;
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1590 13767	1531 AAAAATGTAGCCCTTAGTGGTCCGATTCTTTTGGATAACCAAGGGAATGCTTATGAA ; 	7 70 70	
13707	648 GTTGATCTTCTGCCTTAGAGGGAAATAAGAGTGTGTCCATTGAAACAGCAGGAGCCAAC	Db 1	
1530	CAAGT	Qy	_
1470 13647	1411 ATGGATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCCACTTTAACAGGTCTTTCC:	Db 1	
13587	528 AAAGGAAATGTCGAGTTAGATGTCAATGGTTTCACACAGACTGAAGGCTCTACACTCCTC	Db 1	
1410	1351 AAACGTGGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATT :	Qy	
ω i		Db 1	
w	291 GACAACCTTCACTTCTACGCTGAAGCAGCCTCTAACTCTAACTTCCAGGAAATTTAGTACTT		
1290 13467	1231 TATAGTGGGTCGAITGTTTTTTCTGGTGAAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCA :	ΟΥ 1	
13407		Db 1	
1230	VTTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGTAATAGTACAGAT	Qy	
1170	1111 AATTTACGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATTACTGCTAATACG	рь 1	
32	ACCTCCGCGCCAACATCGACACGGAATGCTATCTACCTGGGATCGTCAGCAAAAATTACG	рь 1	
$\mu$	051 ACTACACCACAAACTACAAAAAAGAAATTCTATTGACATAGGATCTACTGCAAAGATCACG		
13230	3171 TCTTTAAGTCTCTGCAAATCAAGGAGACATCACGTTCCTTGGCAACACTCTAACCTCA	Db 1	
1050	CCATTGTTGCA	Qy	
990 13170	931 AATATAGTCCAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATACTGGCAGCTGGA 9	Оу рь 1	
13110	ATCTGTGCCCATGGTCTAGATCTTTCCGCTGCTGCCCTACCCTATTTTCAAAT	Db 1	
930	871 ATTTATGCTAAGAAGCTTACACTGGCTTCCGGGGGGGGGG	Qy	
870 13056	811 ATATICTGGGAATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCC:	ρ <sub>γ</sub>	
12996	GCTGCAGGCAAGGGCCGTTTATTGTGAAAAAACAGGAGAGACTCCTACTCTTACT	Db 1	
810		Qγ	
765 12936	706 GGAAACTGTACAATTACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCG (	Qу рь 1	
705 12876	646 GCTCCTACCCTCTTCTCGAACAAATATTGCTGAAGCTGCAGCTGGAGCTATAAATAGCACA	Qу 1	
	03	, 5	
45	586 ACAGGGAAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGATATACAAATAATACG		
12762	2706 ACTCTTTCTATTTCTGGGAATACCTCTTCTATAACCTTCACTAGTAATAGCGCAAAA:	Db 1	
585	GAAGGGAATAAATCGAGCGCA	Qy	
12705	.2646 CTCTTTAGCCAAAACGTCTCCAATGAAGCTAATAACAATGGCGGAGCGATCACCACAAAA	Db .	

14844	GTCAGTGGAGCCTCTTGGACTTCGCTATGTAAAAACCTCGCACGACAAGCCTTCTTAGCA	14785	Db
2667	AGCGGAGCCTCTTGGGAAACTTATGCCAATAACTTAGCACGACAGGCCTTGCAAGTG	2608	Qy
2607 14784	ACTITATCCTATGTTCCTGATCTTATCCGCAATGATCCCAAATGCACTACAGCACTTGTA	2548 14725	Db Qy
14724		14665	Db
2547	GGGTGAAGTTTGAGAAGTTCTCTGATTGTAATGACTTTTCTTATGATCTG	2488	Qy
14664	TTTAAAGAGAGTGGCGCTGAAGCCCGTGCTTTTGATGAGTGAG	14605	Дb
2487		2428	Qy
14604	TITOCAGGGATATTTCCCCTTCTTAAAGTTCCAGGCAGTCTACAGCCGCCAACAAAAC	5	망
2427		2368	Q V
14544		14485	Db
2367	TCTCATTCTTATCCTGAATACCTGCAT	2311	Qy
14484	AGTAANIGATCICIAAGACAAAGTIATTACTICGITATICGAAGACATAATGATCATTGAAGTTCTTGAAGCACAAGTTCTTCAAGCACAAGTTCTTCAAGCACAAGATCATCATTCTTCAAGCACAAGATCATCAAGACACAAGATCATCAAGACACAAGATCATCAAGACACAAGATCAAGACACAAGATCAAGACACAAGACAAGAAGATCAAGACAAGACAAGACAAGAAGATCAAGACAAGACAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	14425	F &
	CANCHIACIAMMANINIIICCICICIIIIIIAMIIACCCMACIIMAACIACAACIACAACI	1 0	, 5
(4	TCTTGGAGTCATAAACCCCTCGTTTTAGAAGGGCAGCTCGCTTATAGCCACGTC	• N	, Q
14364	CTATACCTGCAACATCGAGCATTCCTAGGAGGACTTCCCATGCCCTCATTTGGAAGTATC	14305	Дb
2190	ACATTACAGAATGTAGTGGGTTCATAGGTTGTCTCTTAGATAAACTT	2131	Qy
14304	TTCGGTAAAGATAAAGACCTGTTTATAGTTGAAAATACCTCTCATAACTATTTAGCGTCG	14245	ДĎ
2130		2071	γQ
14244	ATCGGAGGTGCAGCCAAACTTGTTCTCAAAACTTAATTAGCTTTTCCCTTTTGCCAACTC	2011	Ωу
41		14125	DЬ
0	AAAGATAAGAAAGGGGAAAAACGCAAATACCGTCATAAATCTGGTGGATATGCT	195	Qy
14124		14065	Дb
1950	TGGGCTGCGGGAGTCGCCAATTTC	1891	Qy
14064		14005	Db
1890	TTCCTAATAGCCTTTGGGGATCTTTTTCAGACATCCAAGCGATTCAAGGTGTCATAGAG	1831	Qy
14004	GGAACTATGACTTGGGTAACTACGGGCTACAACCCTAATCCTGAGCGTAGAGCTTCCGTA	13945	рь
1830		1771	Qy
13944	TACGGGTATCAGGGACATTGGGAAGCCACTTGGGCAGACACCATCAACTGCAAAATCA	13888	Db
1770		1711	Qy
13887	GCTAGCGATATTTATATCGATGCGCTTCTCACCTTCTCCAGTACAAACTCCAGAACCTCAT	13828	Db 43
1710		166	? {
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Department of Microbiology, 1-1-1 Minamikogushi, Ube, Yamaguchi
755-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-227, Fax:81-836-22-2415)
On Sep 15, 2000 this sequence version replaced gi:6172290
gi:6172292 gi:6172294 gi:6172296 gi:6172326 gi:6172328 gi:6172382
gi:6172332 gi:6172334 gi:6172336 gi:6172338 gi:6172382
gi:6172332 gi:6172334 gi:6172336 gi:6172339 gi:6172384
gi:6172386 gi:61572389 gi:6172390 gi:6172392 gi:6172384
gi:6174668 gi:6635174 gi:6635176 gi:6635178 gi:6635180 gi:8547433
gi:8547438 gi:8978640.
AB033782-AB033785, AB033800-AB033815: Submitted (14-Feb-2000).
AB036079-AB036082: Submitted (18-Dec-2000).
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144..9
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3656. .4387
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complement(5246.
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/gene="dnax_2"
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DELFDVDLETPKEALEELILNLNRPYNEIIIGGFSQGAILATHLVLTSQNPYAGALIF
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/gene="ywlC"
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                                                                                                                                                                                                            :LCSKETFSYLFRYAQCEIPVTEVSQIIKESSETDKQVLRDKVQRFMEVLLELYRDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11/
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="CPj0269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3347)
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                                                                                                         .5866)
                                                                                                                                                                                                                                                                                                                                                                                                                     III gamma
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Query Match
Best Local Sin
Matches 1548;
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SKFPNLLCNGSSGIAVCHATNIPPHNLGELIBATLLLANPQASVDEILQVMGGDFF
FGGIIGSEGIRSTYTTGRGKIKVRARLHVEENEDKHRESIIITEMPYNVNKSRLIEQ
IANLVNEKTLAGISDVRDESDKDGIRVVLEIKKGESSEIIIRRLYKFTDVQVTFGANM
IALDKNLPRTMSIHRMISAWIRHRKEVIRRRTRYELNKAETRAHVLEGYLKALSCLDA
LVKTIRRSGNKEHAKERIIESFGFTEPQALAILERLYGTTGLAEKIQKEVEELLNK
IAYYKQVLSDEGLVKDIINRLGDLLKHKVARRTIIEFDGLRDIEDIITNESVII
TISGDDVVKRMPVVFKEQORGGHGVTGFDMKKGAGFLKAVSAFTKOVLLFTNEGO
CYWLKVQCPEEERRAKGKFIINFLEGIRPGEELAAILNIKNEDNAGFLFLATKRGVV
                                                                                                                                                                                                                                                                                                                                                                                                                      complement(10812. .11159)
/gene="CPj,0276"
complement(10812. .11159)
/gene="CPj0276"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFDKVTFFYEGGIQSFVSYLNONKESLESEPIYICGTRVGDDGEIEFEAALQWNSGYS
ELYYSYANNIPTRQGGTHLTGFSTALTRVINTYIKAHNLAKNNKLALTGEDIREGLTA
VISVKYPNPOPEGQTKOKLGNSDVSSYAQQVVGEALTIFFEENPOIAKNIVDKYFVAA
QAREAAKKARELTLKKSALDSARLPGKLIDCLEKDPEKCEMYIVEGDSAGGSAKQGRD
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MTDADVDGSHIRTLLLTFFYRHMTALIENECVYIAQPPLYKVSKKKDFRYILSEKEMD
SYLLMLGTNESSILFKSTERELRGEALESFINVILDVESFINTLEKKAIPFSEFLEMY
                                                                                                                                           SHVQIREIQFLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-*DNA gyrase subunit B*
/protein_id-*BAA98485.1*
/protein_id-*BAA98485.1*
/db_xref-*G1:8978649*
/translation-*MDPKEKNYDASAITVLEGLQAVRERPGMYIGDTGITGLHHLVYE
/translation-*MDPKEKNYDASAITVLEGLQAVRERPGMYIGDTGITGLHHLVYE
/TVDNSIDEAMAGYCSRIDVRILEDGGIVIVDNGGGIF IF EVPHERSAKQGREVSALEVV
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LTVLHAGGKEPKDSYKVSGCHGVFSTCTFDRSILMKRLRELAFLNRGITIVFEDDRDV
PLQYVSVSDRQGTEIVFYPDPKIFSTCTFDRSILMKRLRELAFLNRGITIVFEDDRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKVSLDAFSNPRKKGIRALEIDEGDELIAACHIVSDEEKVMLFTHLGMAVRFPHEKVR
PMGRTARGVRGVSLKNEEDKVVSCQIVTENQSVLIVCDQGFGKRSLVEDFRETNRGGV
GVRSILINERNGNVLGAIPVTDHDSILLMSSQGQAIRINMQDVRVMGRSTQGVRLVHL
                                                                                                                                                                            /translation="mflkrkkrggsqvqnkrtaspikhakhylhnylqelqkimaarp
HDaidawnqvfrdkykgmsqaigfrdhillvkvynsslyallkqtpqndlimslyqva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(8391. .10808)
                                                                                                                                                                                                                                             /product="CT191 hypothetical protein"
/protein_id="BAA98486.1"
/db_xref="GI:8978650"
                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RINNLDI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEGTGYPLYYLAPATGMQGGRYLYSDEEKEEALAQEETHKFKIIELYKVAVFVDIQNQ
LKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCYTLEEVINYLKNLGRKGIEIQRYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8391. .10808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEGDALVSMEKLSSNENDDEVLSGSEEECSDTVSLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5871.
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YHNRIREGFLSLASADPSRYLVLDARESLASLIDKVMLHTQLGLCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MFIVIEGGEGSGKSSLAKALGDQLVAQDRKVLLTREPGGCLIGE
RLRDLILEPPHLELSRCCELFLFLGSRAQHIQEVIIPALRDGYIVICERFHDSTIVYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="thymidylate kinase"
/protein_id="BAA98483.1"
/db_xref="GI:8978647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGEMNADQLWDTTMNPEQRTLIHVSLKDAVEADHIFTMLMGEEVPPRREFIESHALSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="gyrB_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="gyrB
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/protein_id="BAA98484.1"
/db_xref="GI:8978648"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="gyrA_1"
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                             23.1%;
Score 649.4; DB 2;
Pred. No. 4.7e-145;
0; Mismatches 1231;
                                                                 Length 300650;
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Similarity

Conservative

0;

Indels

60;

Gaps

10;

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198342 TCTTTAAGTCTCTCTGCAAATCAAGGAGACATCACGTTCCTTGGCAATACTCTAACCTCA 198401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197643
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                                                                                                                                                                                                                                    ATCTCTGGAAATAAAAGTCTGACCTTCGCCGAGAACTCTTCAGTAACTCAAGGCGGAGCA 198227
                                                                                                                                                                              GCTGCAGGCAAGGGCGGGGCCATTTATTGTGAAAAAAACAGGAGAGACTCCTACTCTTACT 198167
                                                                                                                                                                                                                                                                                                                                                                                                TCAGGAAAAGTACTTTAAGTTCTGCAGGAGCCTTAAATCTTACCGATAATGGAACGATT 197816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAAAATACCCTTGCACAAACTCCTGATCTTTTCGACTCTTGTCACTCCCATTCTATTG
                                                                              AATAGATGCGGGAACAGCTGCAGGCAAGGGCGCGCTATTGCAATTGCCGACTCTGGA
                                                                                                                 AATATAGTCCAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATACTGGCAGCTGGA 990
                                                                                                                                                     ATCTGTGCCCATGGTCTAGATCTTTCCGCTGCTGGCCC----TACCCTATTTTCAAAT 198281
                                                                                                                                                                                                                                                                           ATATCTGGGAATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCC
                                                                                                                                                                                                                                                                                                                                                       ACCGCAGGAAATGGAGGAGCTCTTTCTGGAGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAACTGTACAATTACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCAGTTAGTCTTTATGAATAATAAAGGAGAAACTGGGGGTGGGGCTCTGGGCTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCCTACCCTCTTCTCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACA 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGGGAAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTCTTTCTATTTCTGGGAATACCTCTTCTATAACCTTCACTAGTAATAGCGCAAAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTTTAGCCAAAACGTCTCCAATGAAGCTAATAACAATGGCGGAGCGATCACCGCAAAA 197876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTATTTAAACAAGATTACTGTGAGGAA-----AATGGCGGAGCCATTTCTACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCCCATCATCGGTAATCACAACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAGATGCGGGTTCGAATGCAGGAGCTGCGGCAAGCACAACTGCTGATAAAGCCCTAACA 197702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGGAAATGTCTATATAAACGATGCTGGGAAAGGCACAGCATTAACAGGCTGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AAATTAGGTGGAGCGATCTATAGCTCTGCGGCTGCAAGTATTTCAGGAAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATCTTTCTTTGAAAAACAGCACGGGATCGATTTCTTTTGAAGGGAATAAATCGAGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTAAGTCTAGTGC---TGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTACTAACACAGGCACCTATACTCCTAAAAATACGACTACTGGAATAGACTATACTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCATTGCAACTTACGGAGCAGATGCTTCTTTATCCCCTACAGATAGCTTTGATGGAGCG 197462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT
                                                                                                                                                                                                                                                                                                                                                       TGCCGATGTTACC
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2190	TTCTATATCCAACACATTACAGAATGTAGTGGGTTCATAGGTTGTCTCTTAGATAAACTT	2131	Ωy
99	TTCGGTAAAGATAAAGACCTGTTATAGTTGAAAAATACCTCTCATAACTATTAGCGTCG	41	Db 45
100	TTGGTAG	207	Q Q
2070 199 <b>4</b> 15	ATCGGAGGTGCAGCGCAAACTTGTTCTGAAAACTTAATTAGCTTTGCCTTTTGCCAACTC	2011	B 5
2010 199355	TTAGATAAAGATAAGAAAGGGGAAAAACGCAAATACCGTCATAAATCTGGTGGATATGCT	1951 199296	B 6
1950 199295	AGAAGTGCTTTGACTCTTTGTTCAGATCGAGGCTTCTGGGCTGCGGGAGTCGCCAATTTC	1891 199236	Db Qq
1890 199235	GTTCCTAATAGCCTTTGGGGATCTTTTTCAGACATCCAAGCGATTCAAGGTGTCATAGAG	1831 199176	д Q
1830 199175	GCGACATTAGCTTGGACCAATACAGGCTACCTTCCGAATCCTGAGCGTCAAGGACCTTTA	1771 199116	₽ Q
1770 199115	CAAGGTACTTGGGGAATGACTTAGGGTTGATGACGCAAGCACTCCAAAGACTAAGACA	1711 199059	дь Qy
1710 199058	GCAACAACTACAGATGTTCCAGCGGTTCCTACAGTAGCAACTCCTACGCACTATGGGTAT	1651 198999	Db Qq
1650 198998	AATCACGACTTAGGAAAAACTCAAGACTTTTCATTTGTGCAGCTCTGCTCTGGGTACT	1591 198939	β Q
1590 198938	AAAAATGTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATGAA	1531 198879	B 성
1530 198878	ATTCCTGTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTTCTGCAGCAAGT	1471 198819	ρb
1470 198818	ATGGATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTTCC	1411 198759	당 성
1410 198758	AAACGTGGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATT	1351 198699	B 8
1350 198698	GACAACCTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTT	1291 198639	ρ δ
1290 198638	TATAGTGGGTCGATTGTTTTTTCTGGTGAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCA	1231 198579	Db Qy
1230 198578	GCTGCGGATTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGTAATAGTACAGAT	1171 198522	D 02
1170 198521	AATTTACGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATTACTGCTAATACG	1111 198462	DP 64
1110 198461	ACTACACCACAAACTACAAAAAGAAATTCTATTGACATAGGATCTACTGCAAAGATCACG	. 1051 198402	dd Vo

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RESULT 14
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                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGCTTTTAACATGATGTTGGGAGCTTCT---TCTCATTCTTATCCTGAATACCTGCAT 2367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGCTTCGTGGCTCAGCACACATCTACAATGTAGATTGTGGGGCTAAGATACTCATTCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                             CPN133034 17280 bp DNA BCT 27-FEB-2001 Chlamydia pneumoniae GGAI-protein family cluster A, genes omp12 (partial), omp11, omp10, omp5, omp4, omp13 and omp14 (partial) and ORF1, strain VR1310.
Direct Submission
Submitted (21-JAN-1999) Boesen T., Department of Medical
Microbiology and Immunology, University of Aarhus, The Bartholin
                                                                                                                                                                                                              protein 5.
Chlamydophila pneumoniae.
Chlamydophila pneumoniae.
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AJ133034.1 GI:4455881
AJ133034.1 GI:4455881
hypothetical protein; omp10 gene; omp11 gene; omp12 gene; omp13 gene; omp14 gene; omp5 gene; ORF1; outer membrane protein protein; outer membrane protein 11; outer membrane protein 12; outer membrane protein 14; outer membrane protein 4; outer membrane
                                                                                           Unpublished
2 (bases 1
                                                                                                                                   Daugaard, L., Hjerno, K., and Birkelund, S.
                                                                    Boesen, T
                                                                                                                                                                          Bacteria; Chlamydiales;
1 (bases 1 to 17280)
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                                                                                                                                                      Knudsen, K., Madsen, A.S., Christiansen, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQNVSNEANNNGGAITTKTLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQL
VFMNNKGETGGGALGFEASSSITQNSSLFEGYTATDAAGKGGAICCEKTGETFTLTI
SGNKSLTFAENSSVTOGGAICAHGLDLSAAGFFTKFSNNFGGYTAAGKGGAIAIADSS
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                                                                                                                                                                                                                                            /product="outer membrane
/protein_id="CAB37069.1"
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3827. .6613
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GDVYRKNPRSRTSLMVSGASWTSLCKNLARQAFLASAGSHLTLSPHVELSGEAAYELR
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IFSVAFCQLFGKDKDLFIVENTSHNYLASLYLQHRAFLGGLPMPSFGSITDMLKDIPL
ILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNNSGALELGGSLALYLPKEAPFFQGYFP
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ALKGNVELDVNGFOJEGSTLLMOPGTKLKADTEA I SLTKLVVDLSALEGNKSU IET
AGANKTITLISPLY FODSSGONEYESHTI NOAETOPLVFTAATAASDIT IDALLTSPV
OTPEPHYGYOGHWEATWADTSTAKSGTMTWVTTGYNPNPERRASVVPDSLWASFTDIR
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AGSNAGAAASTTADKALIFFTGFSNLSFIAAPGTTVASGKSTLSSAGALNLIDNGTILF
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                                                                                                                                                                                                                                                                                                                                                                                                           'note="putative"
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/strain="VR1310"
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LEGGLAYSHYSNDLKTKYTAYPEXKGSWGNNAFNMLGASSHYPEYLIGFDTYAPPI
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PIHWCYOGNWALSWOEDTATKSKAATLTWTKTGYNWAPERROTLVANTLWGSSTVDVRS
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AQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIK
VEASYIHQDSFKERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDAAIRNLIKKQTEAGLIFFTDGEFRRYSWDFDFMWGFHGVDRRRDSNDPEIGVYLKD
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LIDDIVFYYRQVIQDLYAAGCRNLQLDDCAWCRLLDIRAPSWYGVDSHDRLQEILEQF
                                    {	t KLNLTYIRQDSFSEKGTEGRSFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPD}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8586. .11372)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDKYSGGAEPLAYVSGEKHVCLGLISSNHSCIEDRDAVVSRIYEAASYIPLERLSLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="SPTREMBL:
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VAETSGGAIFTFKNAINIGSNGKFTELRAAKNHTIFFYDPITSEGTSSDVLKINN

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1547; Conserv
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                                                                                                                                                                                                                                                                TTCACAGGATTTTCTAACCTTTCCTTCATTGCAGCTC
                                                                                                                                                                                                                                                                                                               CTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACCCCC
                                                                                                                                                                                                                                                                                                                                                                   GTAGATGCGGGTTCGAATGCAGGAGCTGCGGCAAGCACAACTGCTGATAAAGCCCTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGGAAATGTCTATATAAACGATGCTGGGAAAGGCACAGCATTAACAGGCTGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCATTGCAACTTACGGAGCAGATGCTTCTTTATCCCCTACAGATAGCTTTGATGGAGCG
                                                 CTCTTTAGCCAAAACGTCTCCAATGAAGCTAATAACAATGGCGGAGCGATCACCACAAAA 1418
                                                                             TTATTTAAACAAGATTACTGTGAGGAA------AATGGCGGAGCCATTTCTACCAAG
                                                                                                                                                    TCAGGAAAAAGTACTTTAAGTTCTGCAGGAGCCTTAAATCTTACCGATAATGGAACGATT
                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt ATTAAGTCTAGTGC---TGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTGTCG}
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SGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYCGAIGTHNLTLTTRGPSCFE
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SFDSLLLGETTLERTQVTTENDAVRGFWSLSWEEXPPSLDKDRRITPTKKTVFLTWNP
EITSTP"
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FSQEAGSLLGNDSGTTLSTTAGSITTINLGINVDSLGLKQPVSLTAKGASNKVIVSGK
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VYRNNPQSTATLYMSPDSMKIRGGNLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGS
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14579. .16123
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|4579. .16123
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Pred. No. 1e-144;
0; Mismatches 1232;
                                                                                                                                                                                                                                                             -CTGGAACTACAGTTGCT
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                                                                                                                                                ATTCCTGTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTTCTGCAGCAAGT
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                                                                                         AAAAATGTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATGAA
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                     TTATTTAAACAAGATTACTGTGAGGAA-----AATGGCGGAGCCATTTCTACCAAG
                                                        TCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATT
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                                                                                                      CTAACAGGATTTTCGAGTCTTACTTTAGCGGCCCCATCATCGGTAATCACAACCCCC
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NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
Patent: WO 9858953-A 15 30-DEC-1998;
MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
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Pred. No. 2e-144;
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ATTTGTGCAGCTCTCTGCTCTGGGTACT 1650	1591 AATCACGACTTAGGAAAAACTCAAGACTTTTCA
TTTGGATAACCAAGGGAATGCTTATGAA 1590 	1531 AAAAATGTAGCCCTTAGTGGTCCGATTCTTTTGGATAACCAAGGGAATGCTTATGAA
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AGAGGAGGTCACTTTAACAGGTCTTTCC 1470	1411 ATGGATGCGGGCACAACGTTAAAAGCAAGTACAC
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AACTCTAACTGCAGGAAATTTAGTACTT 1350	1291 GACAACCTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTT
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CCAACCGGATAGCAACTCGCCTTTAGAT 1236	
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CAGACTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCC 870 	811 ATATCTGGGAATCAGAGTGTAACTTTCTCAGGAI 
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AACACTGCAACAGAT	90
TGTATTTTCTGAAAATAGTGTGACAGCG 765	706 GGAAACTGTACAAGTTACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCG
AGCTGCAGGTGGAGCTATAAATAGCACA 705	646 GCTCCTACCCTCTTCTCGAACATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACA 
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AACCTTCACTAGTAATAGCGCAAAA 591	35 AC
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2727	8 CGTGCAGGCAGTCACTACGCCTTCTCTCTATGTTTGAAGTGCTCGGCCAGTTTGTCTTT	у 266	Qy
2673	4 GTCAGTGGAGCCTCTTGGACTTCGCTATGTAAAAACCTCGCACGACAAGC	b 261	В
2667	8 ATCAGCGGAGCCTCTTGGGAAACTTATGCCAATAACTTAGCACG	у 260	γ
2607 2613	8 ACTITATCCTATGTTCCTGATCTTATCCGCAATGATCCCAAATGCACTACAGCACTTGTA	y 254 b 255	Db Oy
2547 2553	18 TTGCCTATAGGGGTGAAGTTTGAGAAGTTCTCTGATTGTAATGACTTTTCTTATGATCTG	y 248 b 249	P 44
2487 2493	8 TTCTCGGAGAAAGGTACAGAAGGAAGATCTTTTGATGACAGCAACCTCTTCAATTTATCT	y 242 b 243	Db Qy
2427	4 8	у 236	Db
2433		b 237	Qy
2367 2373	1 AATGCTTTTAACATGATGTTGGGAGCTTCTTCTCATTCTTATCCTGAATACCTGCAT	y 231 b 231	P 40
2310	I AGTAATGATCTGAAGACAAAGTATACTGCGTATCCTGAGGTGAAAGGTTCTTGGGGGAAT	y 225	Qy
2313		b 225	db
2250	11 CCTGGCTCTTGGAGTCATAAACCCCTCGTTTTAGAAGGGCAGCTCGCTTATAGCCACGTC	y 219	40
2253		b 219	VQ
2190	11 TTCTATATCCAACACATTACAGAATGTAGTGGGTTCATAGGTTGTCTCTTAGATAAACTT	y 213	
2193		b 213	04
2130	1 TITGGTAGCGATAAAGATITCTTAGTCGCTAAAAATCATACTGATACCTATGCAGGAGCC	y 207	Qy
2133		b 207	Db
2070	1. ATCGGAGGTGCAGCGCAAACTTGTTCTGAAAACTTAATTAGCTTTTGCCTTTTGCCAACTC	y 201	dq
2073		b 201	VQ
2010	I TTAGATAAAGATAAGAAAGGGGAAAAACGCAAATACCGTCATAAATCTGGTGGATATGCT	y 195	Qy
2013		b 195	Db
1950	11 AGAAGTGCTTTGACTCTTTGTTCAGATCGAGGCTTCTGGGCTGCGGGAGTCGCCAAFTTC	y 189	Db
1953		b 189	dd
1890	GTTCCTAATAGCCTTTGGGGATCTTTTTCAGACATCCAAGCGATTCAAGGTGTCATAGAG	y 183	Db
1893		b 183	VQ
1830	1 GCGACATTAGCTTGGACCAATACAGGCTACCTTCCGAATCCTGAGCGTCAAGGACCTTTA	y 177	dd
1833		b 177	VQ
1770 1773	1 CAAGGTACTTGGGGAATGACTTGGGTTGATACCGCAAGCACTCCAAAGACTAAGACA	y 171 b 171	Db Qy
1710	1 GCAACAACTACAGATGTTCCAGCGGTTCCTACAGTAGCAACTCCTACGCACTATGGGTAT	y 165	Qy
1716		b 165	Db
1656		b 159	Дb

- Ъ 2674 AGTGCTGGAAGCCATCTGACTCTCCCCCTCATGTAGAACTCTCTGGGGAAGCTGCTTAT 2733
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Mygind P;
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                                                                (BIRK/) BIRKELUND S.
(CHRI/) CHRISTIANSEN G.
                                        Christiansen
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	Oligonucleotide Di	Oligonucleotide D1	Oligonucleotide D1		Sed ID No. 23 of W		. trachomatis	. trachom					Chlamydia pneumoni	A encoding (	5	Chlamydia pneumoni	C. pneumoniae CPN1	Chlamydia pneumoni	Chlamydia antigen	pneumon					'n.	ing the	pneumon			Chlamydia antigen

## Chlamydia pneumoniae. Omp5; outer membrane protein 5; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma; ss. Chlamydia pneumoniae surface exposed protein Omp5 DNA. 26-APR-1999 (first entry) AAX06817 standard; DNA; 2815 BP Location/Qualifiers /\*tag= a ..2787

98WO-DK00266

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Knudsen K,

Madsen Α,

P-PSDB; AAW88418

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This DNA sequence codes for the novel 97.2 kDa surface exposed protein Omp5 (see AAW88418) of the human respiratory pathogen chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) cwas obtained which reacted with outer membrane proteins. The cantibody was used to identify the genes (see AAX06816-27) encoding CC Omp4-Omp15 proteins (see AAX88417-28) in an expression library of CC. pneumoniae DNA. The genes are situated in 2 gene clusters: CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89.6-100.3 kDa and cc the other, and encode polypeptides of about 89.6-100.3 kDa and 20 cmp4-Omp15 or detecting including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific test comparates considered with Chlamydia comp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnostis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals. The nucleic acids and proteins can also be used in the immunization of mammals. The proteins for effecting in vivo expression of antigens. The caccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 2815; Best Local Similarity 100.0%; Pred. No. 0; Matches 2815; Conservative 0; Mismatches
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1500 1500	ACAGAGGAGGTCACTTTAACAGGTCTTTCCATTCCTGTAGACTCTTTAGGCGAGGGTAAG	4 4	Qy Db
		1381 1381	Qу
1380 1380	GTAACTCTAACTGCAGGAAATTTAGTACTTAAACGTGGTGTCACTCTCGATACGAAAGGC	1321 1321	Qу Db
1320 1320	AACCTCACTTCTACGCTGAAGCAGCCT 		Qy
	AATAAGGCTGATGCAGGTAATAGTACAGATTATAGTGGGTCGATTGTTTTTTTCTGGTGAA	1201 1201	Оy
1200 1200	TTTTTCTACGATCCGATTACTGCTAATACGGCTGCGGATTCTACAGATACTTTAAATCTC	1141 1141	Оy
1140 1140	ATTGACATAGGATCTACTGCAAAGATCACGAATTTACGTGCAATATCTGGGCATAGCATC	1081	Qy Db
1080 1080	ATTACCTTCAATGGGAATGCCATTGTTGCAACTACACCACAAACTACAAAAAAAA	1021 1021	Qy Db
1020 1020	GGTGGAGCCATTTCTATACTGGCAGCTGGAGAGTGTAGTCTTTCAGCAGAAGCAGGGGAC 		Qу
960	GGGGGGGGGGGGTATCTCCTTTTCTAACAATATAGTCCAAGGTACCACTGCAGGTAAT	901 901	ОУ
900	GGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCTAAGAAGČTTACACTGGCTTCC	841 841	Фф
840 840	AGTGTAACTTTCTCA                 agtgtaactttctca	781 781	Qy Db
780 780	ACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCGACGGCAGGAAATGGA	721 721	Оу
720 720	H — H	661 661	Qу Db
660	GGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACGGCTCCTACCCTCTTC	601	Qу
600	AACAGCACGGGATCGATTTCTTTGAAGGGAATAAATCGAGCGCAACAGGGAAAAAAGGT 	541 541	Qy

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                                                be used for diagnostic purposes, for their enzymatic or structural cativity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizing fragment of N1; (2) an isolated nucleic acid (N2) that hybridizes under stringent conditions to N1; (3) an expression cassette comprising N1 under the transcriptional regulation of a transcriptional initiation region functional in an expression host, and a transcriptional termination region; (4) a cell comprising an expression cassette of (3) as part of an extrachromosomal element or integrated into the genome of a host cell as a result of induction of the expression cassette into the host cell as a result of induction of the host cell; (5) a method for producing a P1 comprising growing a cell of (4) where the protein is expressed and isolating the protein free of other producings; (6) a purified polypeptide composition comprising at least 50 weight % of P1; and (7) a monoclonal antibody binding specifically to the peptide of (6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae protein (P1), given in the specification. The isola
acid is useful for diagnostic and analytical methods, such as,
hybridization based assays or amplification based assays. The
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960 99152	1 GGGGGGGGGGGGTATCTCCCTTTTCTAACAATATAGTCCAAGGTACCACTGCAGGTAAT	9909	рy
900 99093	1 GGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCTAAGAAGCTTACACTGGCTTCC	9903	д У
840	1 GGAGCTCTTTCTGGAGATGCCGATGTTACCATATCTGGGAATCAGAGTGTAACTTTCTCA	9897	DP
99033			QA
780	11 ACAGGGAATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCGACCGCAGGAAATGGA	9891	д
98973			Уо
720	1 TCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACAGGAAACTGTACAATT	9885	g
98913			VQ
660	1 GGGGCTATTTGTGCTACTGGTACTGTÄGATATTACAAATAATACGGCTCCTACCCTCTTC	9879	Qy
98853			Db
600 98793	AACAGCACGGGATCGATTTCTTTTGAAGGGAATAAATCGAGCGCAACAGGGAAAAAAGGT 	9873	P S
540 98733	31 AAACAAGATTACTGTGAGGAAAATGGCGGAGCCATTTCTACCAAGAATCTTTCTT	9867	유 양
480	21 AAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATTTTATTT	9861	gg
98673			VQ
<b>4</b> 20	51 GGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACCCCCTCAGGA	9855	Qy
98613			Db
360	)1 AAGTCTAGTGCTGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTGTCGGTAACA	9849	g
98553			79
300 98493	GACACTACGGAATCTTTAAGCTTTGCCGGTAAGGGGTACTCACTTTCTTT	9843	ρ 2
240	31 GGAGATATAACTCTGGAAAACCTTGGGGATTCGGCAGCTTTAACGAAGGGTTGTTTTTCT	9837	B
98433			S
180	21 ACTAACACAGGCACCTATACTCCTAAAAATACGACTACTGGAATAGACTATACTCTGACA	, 12	ρ
98373		, 9831	γ
120	51 TCCACTGTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGAAGT	9825	g
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TTAGAAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTATACTGCG 2280	GGGTTCATAGGTTGTCTTAGATAAACTTCCTGGCTCTTGGAGTCATAAACCCCTCGTT 2220 	AAAAATCATACTGATACCTATGCAGGAGCCTTCTATATCCAACACACATTACAGAATGTAGT 2160 	AACITAAITAGCTITGCCTITTGCCAACTCTITGGTAGCGATAAAGATITCTTAGTCGCT 2100 	AAATACCGTCATAAATCTGGTGGATATGCTATCGGAGGTGCAGCGCAAACTTGTTCTGAA 2040 	g – g	GACÀTCCAAGCGATTCAAGGTGTCATAGAGAGAAGTGCTTTGACTCTTTGTTCAGATCGA 1920 	CTTCCGAATCCTGAGCGTCAACGACCTTTAGTTCCTAATAGCCTTTTGGGGATCTTTTTCA 1860	GATACCGCAAGCACTCCAAAGACTAAGACAGCGACATTAGCTTGGACCAATACAGGCTAC 1800 	ACAGTAGCAACTCCTACGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGTTGAT 1740 	TCATTTGTGCAGCTCTCTGCTCTGGGTACTGCAACAACTACAGATGTTCCAGCGGTTCCT 1680	CTTTTGGATAACCAAGGGAATGCTTATGAAAATCACGACTTAGGAAAAACTCAAGACTTT 1620 	AAAGTTGTAATTGCTGCTTCTGCAGCAAGTAAAAATGTAGCCCTTAGTGGTCCGATTCTT 1560 	ACAGAGGAGGTCACTTTAACAGGTCTTTCCATTCCTGTAGACTCTTTAGGCGAGGGTAAG 1500 	TTTACTCAGACCGCGGGTTCCTCTGTTATTATGGATGCGGGCACAACGTTAAAAGCAAGT 1440 	CGATACGAA/            cgatacgaaa	AAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAACCTCACTTCTACGCTGAAGCAGCCT 1320 	CAGGTA        caggta	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia antigen; diagnosis; infection; therapy; upper respiratory tract disease; asthmatic bronchitis; adult-onset asthma;
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01-DEC-1998;
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01-DEC-1998;
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                                                                                             (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes a Chlamydia antigen of the invention, designated CPN100635. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they represent the presence of the
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                       adult-onset asthma and acute exacerbations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumonia,
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DB; AAY90237, AAY90238.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids encoding polypeptide antigens from Chlamydia useful for ing, diagnosing and treating diseases such as community acquired ia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
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2950
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BP; 836 A;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       1 ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT
 AAAGGTGCAGTTAAATGTGGAGGGGATCTTACATTTGATAACAATGGAACTATTTTATTT
                         ggattttcgagtcttactttcttagcggccccatcatcggtaatcacaaccccctcagga
                                       GGATTTTCGAGTCTTACTTTCTTAGCGGCCCCATCATCGGTAATCACAACCCCCTCAGGA
                                                                               aagtctagtgctgaaggcgcagccctttctgttacaactgataaaaatctgtcgctaaca
                                                                                            AAGTCTAGTGCTGAAGGCGCAGCACTTTCTGTTACAACTGATAAAAATCTGTCGCTAACA
                                                                                                                                   GGAGATATAACTCTGCAAAACCTTGGGGATTCGGCAGCTTTAACGAAGGGTTGTTTTCT
                                                                                                                                                                                                                                              actaacacaggcacctatactcctaaaaaatacgactactggaatagactatactctgaca
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Pred. No. 0;
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 	Db 2	1560	1501 AAAGTTGTAATTGCTGCTCTGCAGCAAGTAAAAATGTAGCCCTTAGTGGTCCGATTCTT	Qy
581 GATCCC	0у 2	1600	1541 acagaggaggtcactttaacaggtctttccattcctgtagactctttaggcgagggtaag	DØ
	Db 2	1500	1441 ACAGAGGAGGTCACTTTAACAGGTCTTTCCCATTCCTGTAGACTCTTTAGGCGAGGGTAAG	ı Qy
2561 gatgaca 2561 gatgaca	J NJ	1540	1301 TITACTCAGACCCCGGGTTCCTCTGTTATTGATGCGGGCACAACGTTAAAAGCAAGT 	B &
501	рь 2 Qy 2	1480		Db -
2401 AATCTG!	0у 2	1380	1321 GTAACTCTAACTGCAGGAAATTTAGTACTTAAACGTGGTGTCACTCTCGATACGAAAGGC	Qy
	Db 2	1320 1420	1261 AAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAACCTCACTTCTACGCTGAAGCAGCCT	Дy
		1360	1201 AATAAGGCTGATGCAGGTAATAGTACAGATTATAGTGGGTCGATTGTTTTTTTCTGGTGAA 	Оу
 2321 ttagaa 2381 mamccmo		1300	1141 TTTTTCTACGATCCGATTACTGCTAATACGGCTGCGGATTCTACAGATACTTTAAATCTC	Оу
2261 gggttca	рь 2 Qy 2	1240		В .
		1180	1121 cattaccttaatgggaatgccattgttgcaactacaccacaaactacaaaagaaattct 1081 ATTGACATAGGATCTACTGCAAAGATCACGAATTTAGGGAATATCTGGGCATAGCATC	OV Db
2101 AAAAAT          2201 aaaaat	рь 2 2	1080	1021 AFTACCTTCAATGGGAATGCCATTGTTGCAACTACACCACAAACTACAAAAAGAAATTCT	Qγ
		1020	961 GGTGGAGCCATTTCTATACTGGCAGCTGGAGAGTGTAGTCTTTCAGCAGAAGCAGGGGAC	Qy Db
2081 aaataco	Db 2	1060	1001 gggggggggggggaatcccttttctaacaatatagtccaaggtaccactgcaggtaat	₽ . £
		1000	941 ggaaaccaagctgtagctaatggcggagccatttatgctaagaagcttacactggcttcc	용
1921 GGCTTC:        2021 qqcttc1	ОУ 1 2	900	841 GGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCTAAGAAGCTTACACTGGCTTCC	Qy
		940	781 GGAGCTCTTTCTGGAGATGCCGATGTTACCATATCTGGGAATCAGAGTGTAACTTTCTCA	Db Qy
1901 cttccga	Db 1 Оv 1	880		B .
101 CTTCCG	Qy 1	820	761 togaacaatattgotgaagotgoaggtggagotataaatagoacaggaaactgtacaatt 701 aCaGGGAATACGTCTCTTGTATTTTTTGAAAATTAGTGTGACAGGGACGCGACGGAAATGGA	<b>8</b> B
1/41 GATACCO	Db 1	720	661 TCGAACAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACAGGAAACTGTACAATT	Qy
781		760	601 GGGGCTATTTGTGCTACTGGTACTGTAGATATTACAAATAATACGGCTCCTACCCTCTTC	Qy Db
1721 tcattt	Db 1	700		Db
111111 	Ωу 1	600	501 aaacaayartartytyayyaaaaaryyyyyaytearttteattaayaateettettetteyaaa 541 AACAGCACGGGATCGATTTCTTTTGAAGGGAATAAATCGAGCGAAACAGGGAAAAAAGGT	Q 5
	ш,	540	481 AAACAAGATTACTGTGAGGAAAATGGCGGAGCCATTTCTACCAAGAATCTTTCTT	p oy
1601 aaagtts	Db 1	580		Дb

2640	GATCCCAAATGCACTACAGCACTTGTAATCAGCGGAGCCTCTTGGGAAACTTATGCCAAT	2581	Qy
2740		2681	Db
2580	GATTGTAATGACTTTTCTTATGATCTGACTTTATCCTATGTTCCTGATCTTATCCGCAAT	2521	Qy
2680		2621	Db
2520	GATGACAGCAACCTCTTCAATTTATCTTTTGCCTATAGGGGTGAAGTTTGAGAAGTTCTCTT	2461	Qy
2620		2561	Db
2460 2560	AATCTGACCTATATACGTCAGGACAGCTTCTCGGAGAAAAGGTACAGAAGGAAG		Оy
2400	TCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATGCTCCATACATCAAACTG	2341	Qy
2500		2441	Db
2340 2440	TATCCTGAGGTGAAAGGTTCTTGGGGGAATAATGCTTTTAACATGATGTTTGGGAGCTTCT		Qy Db
2280	TTAGAAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTATACTGCG	2221	Qу
2380		2321	Дъ
2220	GGGTTCATAGGTTGTCTTAGATAAACTTCCTGGCTCTTGGAGTCATAAACCCCTCGTT	2161	Qу
2320		2261	
2160 2260	AAAAATCATACTGATACCTATGCAGGAGCCTTCTATATCCAACACATTACAGAATGTAGT	2 2	Qy dd
2100	AACTTAATTAGCTTTTGCCTTTTGCCAACTCTTTGGTAGCGATAAAGATTTCTTAGTCGCT	2041	Qу
2200		2141	Дъ
2040	AAATACCGTCATAAATCTGGTGGATATGCTATCGGAGGTGCAGCGCAAACTTGTTCTGAA	1981	Qy
		2081	Db
1980	GGCTTCTGGGCTGCGGGAGTCGCCAATTTCTTAGATAAAGATAAGAAAGGGGAAAAACGC	1921	Qy
2080		2021	Db
1920	GACATCCAAGCGATTCAAGGTGTCATAGAGAGAAGTGCTTTGACTCTTTGTTCAGATCGA	9 8	Qy
2020			Db
1860	CTTCCGAATCCTGAGCGTCAAGGACCTTTAGTTCCTAATAGCCTTTGGGGATCTTTTTCA	1801	Qу
1960		1901	Db
1900	GATACCGCAAGCACTCCAAAGACTAAGACAGCGACATTAGCTTGGACCAATACAGGCTAC	1741 1841	Qy Db
1740 1840	ACAGTAGCAACTCCTACGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGTTGAT	7 6	Qy dd
1680	TCATTTGTGCAGCTCTCTGCTCTGGGTACTGCAACAACTACAGATGTTCCAGCGGTTCCT	1621	Qу
1780		1721	Дъ
1620 1720	CTTTTGGATAACCAAGGGAATGCTTATGAAAATCACGACTTAGGAAAAACTCAAGACTTT	ο U	Qy Db
	$a {\tt aagttgtaattgctgcttctgcagcaagtaaaaatgtagcccttagtggtccgattctt}$	1601	Db

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                                                                    This DNA sequence encodes the novel surface exposed protein Omp5 (see AAW88429) of Chlamydia pneumoniae, a human respiratory pathogen. It is described as a subsequence of a claimed nucleic acid fragment (see AAX06817) encoding Omp5 (see AAW88418). The invention provides a new species specific test for identifying mammals (including humans) infected with C. pneumoniae. The test comprises detecting antibodies specific for surface exposed proteins Omp4-Omp15 (see AAX088417-28) or detecting nucleic acid fragments encoding them (see AAX06816-27), especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines may also reflecting in vivo expression of antigens. The vaccines may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
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                             associated
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 73-77;
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CHRISTIANSEN
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Local Similarity 100.0%;
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ggagatataactctgcaaaaccttggggattcggcagctttaacgaagggttgtttttct
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                 Novel antigens and corresponding DNA molecules that can prevent, treat and diagnose disease caused by Chlamydia mammals, especially humans -
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1777 TTAGCTTGGACCAATACAGGCTACCTTCCGAATCCTGAGCGTCAAGGACCTTTAGTTCCT 183 	Db dg
1717 ACTTGGGGAATGACTTGGGTTGATGATGACAGCCAAGGCACTCCAAAGACTAAGACAGCGACA 17	Ф
1657 ACTACAGATGTTCCAGCGGTTCCTACAGTAGCAACTCCTACGCACTATGGGTATCAAGGT 171	Qy dd
1597 GACTTAGGAAAACTCAAGACTTTTCATTTGTGCAGCTCTCTGCTCTGGGTACTGCAACA 165 	Qу
1537 GTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATGAAAATCAC 159 	Оу
1477 GTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTTCTGCAGCAAGTAAAAAT 153 	ДQ
1417 GCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTTCCATTCCT 147 	Qy Db
1357 GGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATTATGGAT 141	Qy da
1297 CTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTTAAACGT 135 	B 8
1237 GGGTCGATTGTTTTTCTGGTGAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAAC 129 	P 64
1177 GATTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGTAATAGTACAGATTATAGT 123 	Ωу
1117 CGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATTACTGCTAATACGGCTGCG 117	DP QA
1057 CCACAAACTACAAAAAGAAATTCTATTGACATAGGATCTACTGCAAAGATCACGAATTTA 111 	Оу
1000 CTTTCAGCAGAAGCAGGGACATTACCTTCAATGGGAATGCCATTGTTGCAACTACA 105	рь
940 CAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATACTGGCAGCTGGAGAGTGTAGT 999	DP QA
80 AAGAAGCTTACACTGGCTTCCGGGGGGGGGGGGGGTATCTCC	Db 04
20 AATCAGAGTTACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCT 8	Db Qy
63 ggagctattgattgtaacaaagcagggcgaacccagaccctatcttgactctttcagga 9	B 7
772 GGAAATGGAGGAGCTCTTTCTGGAGATGCCGATGTTACCATATCTGGG 819	0

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Matches 1570; Conserv
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Best Local
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(CHRI/) CHRISTIANSEN G.
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     ACTCTGACAGGAGATATAACTCTGCAAAACCTTGGGGATTCGGCAGCTTTAACGAAGGGT
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TCTTGGAGTCATAAACCCCTCGTTTTAGAAGGGCAGCTCGCTTATAGCCACGTCAGTAAT 2256	gggggattcttcacggcttctgaaaatttctttaattttgcttttttgtcagctttttggc 2061 AGCGATAAAGATTTCTTAGTCGCTAAAAATCATACTGATACCTATGCAGGAGCCTTCTAT 2136	GCTTTGACTCTTTGTTCAGATCGAGGCTTCTGGGGCTGCGGGAGTCGCCAATTTCTTAGAT 1956	TTAGCCTTGGACCAATACAGGCTACCTTCCGAATCCTGAGGCGTCAAGGACCTTTAGTTCCT 1836	ACTACAGATGTTCCAGCGGGTTCCTACAGTAGCAACTCCTACGGCACTATGGGTATCAAGGT 1716	GTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATGAAAATCAC 1596	GCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTTCCATTCCT 1476	1228 ggctacatcgttttctctggagagaaactctcagaagaggaacttaagaaacctgacaat 1287 1297 CTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTTAAACGT 1356

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               This invention describes a novel nucleic acid (N1) encoding a Chlamydi pneumoniae protein (P1), given in the specification. The isolated nucleic dis useful for diagnostic and analytical methods, such as, hybridization-based assays or amplification-based assays. The protein be used for diagnostic purposes, for their enzymatic or structural activity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizing fragment of N1; (2) an isolated nucleic acid (N2) that hybridizes under stringent conditions to N1; (3) an expression and the protein activity of the conditions of N1; (3) and expressions are the conditions to N1; (3) and expressions are the conditions to N1; (4) and the conditions to N1; (5) and expressions are the conditions to N1; (6) and the conditions to N1; (7) and expressions are the conditions to N1; (8) and N1; (8) and N1; (8) are the conditions to N1; (8) and N1; (8) and N1; (8) are the conditions to N1; (8) are the cond
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Nucleotide

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Best Local Similarity Matches 1548; Conserva
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ttcacaggattttctaacctttccttcattgcagctc----ctggaactacagttgct 508131
                                                     CTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCCCATCATCGGTAATCACAACCCCC 414
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                                           atgcaaccaggaacaaagctcaaagcagatactgaagctatcagtcttaccaaacttgtc
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                                                                      ATGGATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTTCC
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                                                                                                                                                          AAACGTGGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTTTATT
                                                                                                                                                                                                                     gataacttcacatctatattaaagcaaccattggctctagcctctggaaccttagcactc
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01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia antigen; diagnosis; infection; community acquired pr
therapy; upper respiratory tract disease; bronchitis; sinusiti
asthmatic bronchitis; adult-onset asthma; acute exacerbations
                                                                                                   Nucleic acids encoding preventing, diagnosing pneumonia, bronchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia
                                                                       Claim
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DB; AAY90240.
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98US-0110340.
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98US-0110428.
98US-0110438.
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                                                                                                    polypeptide antigens from Chlamydia useful and treating diseases such as community acq sinusitis and asthmatic bronchitis, adult-c
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This sequence encodes a Chlamydia antigen of the invention, designated CPN100639. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction

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Best Local Similarity
Matches 1547; Conserv
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                              gccagctcctcgattactcaaaatagctcccttttcttctctggaaacactgcaacagat
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QY δõ Ş Qy 뫄 Qy В 밁 В В Dβ Qy Дb ρy В δÃ Qy 밁 Š 밁 Qy Qy 밁 δÃ ρ 밁 δÃ δÃ 밁 Дb 밁 밁 밁 B δÃ QΥ В 1577 1337 1051 1040 GTTCCTAATAGCCTTTGGGGATCTTTTTCAGACATCCAAGCGATTCAAGGTGTCATAGAG GCTGCGGATTCTACAGATACTTTAAATCTCCAATAAGGCTGATGCAGGTAATAGTACAGAT GCGACATTAGCTTGGACCAATACAGGCTACCTTCCGAATCCTGAGCGTCAAGGACCTTTA CAAGGTACTTGGGGAATGACTTGGGTTGATGATACCGCAAGCACTCCAAAGACTAAGACA GCAACAACTACAGATGTTCCAGCGGTTCCTACAGTAGCAACTCCTACGCACTATGGGTAT AAAAATGTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATGAA AAACGTGGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATT GACAACCTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTT TATAGTGGGTCGATTGTTTTTTCTGGTGAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCA aacttaagggcagcccaaggccaatctatctatttctatgatccgattgcatctaacacc ACTACACCACAAACTACAAAAAGAAATTCTATTGACATAGGATCTACTGCAAAGATCACG AATATAGTCCAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATACTGGCAGCTGGA ggaactatgacttgggtaactacgggctacaaccctaatcctgagcgtagagcttccgta gctagcgatatttatatcgatgcgcttctcacttctccagtacaaactccagaacctcat AATCACGACTTAGGAAAAACTCAAGACTTTTCATTTGTGCAGCTCTCTGCTCTGGGTACT aaaactataactctaacctctcctcttgttttccaagatagtagcggcaatttttatgaa gttgatctttctgccttagagggaaataagagtgtgtccattgaaacagcaggagccaac ATTCCTGTAGACTCTTTAGGCGAGGGTAAGAAGTTGTAATTGCTGCTGCTGCAGCAAGT atgcaaccaggaacaaagctcaaagcagatactgaagctatcagtcttaccaaacttgtc ATGGATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTTCC aaaggaaatgtcgagttagatgtcaatggtttcacacagactgaaggctctacactcctc gataacttcacatctatattaaagcaaccattggctctagcctctggaaccttagcactc acaggag---cttcagacgttctgaccatcaaccaaccggatagcaactcgcctttagat **AATTTACGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATTACTGCTAATACG** GAGTGTAGTCTTTCAGCAGAAGCAGGGGACATTACCTTCAATGGGAATGCCATTGTTGCA aatagatgcgggaacacagctgcaggcaagggcggcgctattgcaattgccgactctgga atctctggaaataaaagtctgaccttcgccgagaactcttcagtaactcaaggcggagca ATATCTGGGAATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCC tacgggtatcaggga---cattgggaagccacttgggcagacacatcaactgcaaaatca agccatacgataaaccaagccttcacgcagcctttggtggtattcactgctgctactgct tattcaggaacgattgtattttctggggaaaagctctctgcagatgaagcgaaagctgct acctccgcgccaacatcgacacggaatgctatctacctgggatcgtcagcaaaaattacg tctttaagtctctctgcaaatcaaggagacatcacgttccttggcaacactctaacctca atctgtgcccatggtctagatctttccgctgctggccc...-taccctattttcaaat gctgcaggcaagggcggggccatttattgtgaaaaaacaggagagactcctactcttact = = = 1696 1470 1050 1873 1816 1756 1590 1636 1410 1290 1336 1230 1170 1159 1039 1650 1576 1516 1279 1219 1099

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Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding
                                                                                                                                                                                     This DNA sequence codes for the novel 97.6 kDa surface exposed protein Ompl1 (see AAW88424) of the human respiratory pathogen
                                                                                                                                                                                                                Claim 6; Page 62-63; 115pp; English.
                                                                                                                                                                                                                                                                             P-PSDB; AAW88424.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae surface exposed
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infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                 (BIRK/) BIRKELUND S.
(CHRI/) CHRISTIANSEN G.
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vaccine; atl
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atherosclerosis; asthma; ss.
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ρ В Q 밁 B δÃ CC Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) CC was obtained which reacted with outer membrane proteins. The cantibody was used to identify the genes (see AAX06816-27) encoding CC omp4-Omp15 proteins (see AAW88417-28) in an expression library of CC. pneumoniae DNA. The genes are situated in 2 gene clusters: CC omp12,11,10,5,4,13 and 14 in one cluster and omp67,78,9 and 15 in CC the other, and encode polypeptides of about 89.6-100.3 kDa and 20 about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia CC about 56.1 kDa. The test comprises detecting antibodies specific for CC omp4-Omp15 or detecting nucleic acid fragments encoding these outer CC omp4-Omp15 or detecting nucleic acid fragments encoding these outer CC membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of CC mammals, the nucleic acids being particularly useful as DNA CV accines for effecting in vivo expression of antigens. The CC vaccines for effecting in vivo expression of antigens. The state of the control o Matches 1539; Query Match Best Local Sequence 2793 BP; 803 A; 681 C; 567 G; 121 118 AGTACTAACACAGGCACCTATACTCCTAAAAATACGACTACTGGAATAGACTATACTCTG 177 61 Local Similarity 1 ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTTGGCATGTTTTACTAGTTGT 60  $\vdash$ agcattgcaacttacggagcagatgcttctttatcccctacagatagctttgatggagcg TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCCTCTGATAGCTTTGACGGA--atgaaaatacccttgcacaaactcctgatctcttcgactcttgtcactcccattctattg Conservative 23.0%; 0; Score 646.4; DB 20; Length Pred. No. 7.3e-174; Mismatches 1221; 742 T; 0 other; Indels 2793; 60; Gaps 120 117 180 60

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931 AATATAGTCCAAGGTACCACTGCAAGTAATCGTGGACCATTTCTATACTGGCAGCTGGA 990	ACAGGAGATMAACTOTGCAAAACCTTGGGGATTGGGCAGCTTTACGAAGGGTTGTTT
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TTTGGT             tcggt   trcygt   trcygt   tcggt   ctatac   ccatac           accgac   accgac           aaaaat   AATGCT	TATICCTGTAGGCCTTAGGCGAGGGTAAGAAGTTCTTTGGAAGCAACTTTAGGAAAAATGTTAGATAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAATGTTAGGAAAAAA

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          (CONN-) CONNAUGHT
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c bronchitis;
                                                                                                                                                                                                                                                                                                                            pneumoniae
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98US-0110340.
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                                                                                                                                                                                    /product= Chlamydia antigen CPN100639
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(pos:2613..2617; aa:Val)
(pos:2641..2643; aa:Cys)
(pos:2702..2704; aa:Pro)
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(PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitts and sinusitis, asthmatic bronchitts, adult-onset asthma and acute exacerbations of asthma in adults.
                                                                                                                                                                                                                                                                             This sequence encodes a Chlamydia antigen of the invention, designated CPN100639. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumonia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preventing,
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Sequence 2790 BP; 800 A; 681 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acids encoding ing, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 157-158; 174pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bronchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide antigens from Chlamydia useful for
and treating diseases such as community acquired
sinusitis and asthmatic bronchitis, adult-onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang
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566 G;
743 T; 0 other;
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                                                                                                This sequence encodes a Chlamydia antigen of the invention, designated CPN100638. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids choosing Chlamydia antigens in samples according to standard methods. The nucleic acids conding Chlamydia probes for diagnostic polymerase chain reaction to used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they concleic acids may also be used to produce the protein of antibodies proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting contibodies may also be used as diagnostic reagents for development of the proteins and the development of the protein antipodies. Chlamydia is a pathogen implicated in the development of
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                     (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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and treating diseases such as community acquired
sinusitis and asthmatic bronchitis, adult-onset
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                                               cctacgctttttaaaaacaactctggctatgatactgcagctcccttaggaggagcaatt
                                                                                                                                            aatagtgtgaccgcaacctcagctacaggggggagccatttactgtagtagtacatcagcc
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                                                                                                                                                                                                                                                                                                                                 GCTATAAATAGCACAGGAAACTGTACAATTACAGGGAATACGTCTCTTGTATTTTCTGAA
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                                                                              GGTATCTCCTTTTCTAACAATATAGTCCAAGGTACCACTGCAGGTAATGGTGGAGCCATT
                                                                                                           cccaaaccagtcttaactctatcagacaacggggaactgaactttataggaaatacagca
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                            GAAAACTTAATTAGCTTTGCCTTTTGCCAACTCTTTTGGTAGCGATAAAGATTTCTTAGTC
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                                                                                                                                        Chlamydia pneumoniae.
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                                 30-DEC-1998
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vaccine; atherosclerosis;
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677

689

737 749 617

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CThis DNA sequence codes for the novel 90.0 kDa surface exposed CC protein Omp8 (see AAW88421) of the human respiratory pathogen CC Chlamydia pneumoniae. By generating antibodies against C. Cpneumoniae outer membrane complex, a polyclonal antibody (PAB 150) CC was obtained which reacted with outer membrane proteins. The CC antibody was used to identify the genes (see AAW06816-27) encoding CC Omp4-Omp15 proteins (see AAW88417-28) in an expression library of CC Cpneumoniae DNA. The genes are situated in 2 gene clusters: CC Omp11,110,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in CC the other, and encode polypeptides of about 89.6-100.3 kDa and CC for identifying mammals (including humans) infected with Chlamydia CC for identifying mammals (including humans) infected with Chlamydia CC omp4-Omp15 or detecting nucleic acid fragments encoding these outer CC membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The cucleic acids and proteins can also be used in the immunization of CC mammals, the nucleic acids being particularly useful as DNA CV vaccines for effecting in vivo expression of antigens. The cucleic acids and prevent atherosclerosis and bronchial asthma, CX which are possibly associated with C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 52-53; 115pp; English
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DB; AAW88421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      --CAGCTTTAACGAAGGGTTGTTTTTCTGACACTACGGAATCTTTAAGCTTTGCCGGTAA
                       gaagtttgacaaaaatgtcagtttgctcttcagcaaaaacttttcaacggataatggcgg
                                                                         TACATTTGATAACAATGGAACTATTTTATTTAAACAAGATTACTGTGAGGAAAATGGCGG
                                                                                                                         gtctcctggaagttcgataactaccggcaaaggagccgttagctgctctacgggtagctt
                                                                                                                                                      ATCATCGGTAATCACAACCCCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATC---T
                                                                                                                                                                                                                           cagcagcgtggtagataaatctaccacgtttatagggttttcttcgctatcttttattgc
                                                                                                                                                                                                                                                                             TACAACTGATAAAAATCTGTCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCC
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CHRISTIANSEN
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Pred. No. 4.1e-142;
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CC the 98kba putative outer membrane protein coding sequence The 3' primer CC contains the sequence encoding the C-terminal sequence of the putative CC cuter membrane protein and a BsrG1 restriction site. The stop codon was CC excluded and an additional nucleotide was inserted to obtain an in-frame CC C-terminal fusion with the Histidine tag. The PCR product was cloned CC into a eukaryotic expression vector (pCA-Myc-His) by restricting both CC the vector and the PCR product with Not1 and BamH1 and performing a C ligation reaction. This expression vector was injected intranuscularly CC and intranasally into mice, which were subsequently inoculated with CC chamydia pneumoniae. The chamydial lung titers of the immunised mice were lower than those of the controls. Thus the 98kDa putative outer membrane protein can be used as a vaccine to provide protection against Chlamydia infections, especially Chlamydia pneumoniae infections.

The polypeptide may also be administered orally to treat Chlamydia infection. The present sequence may also be used in the construction of attenuated Chlamydia strains that can over-express the CC gene or express it in a non-toxic form.
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01-MAR-1999;
27-OCT-1999;
                                                                                                                                                                                                                                                                                              The present sequence is the 98kDa putative outer membrane protein garring Chlamydia pneumoniae. The genomic sequence was amplified using PCR primers. The 5' primer contains a NotI restriction site, a ribos binding site, an initiation codon and a sequence close to the 5' end
                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                Novel Chlamydia 98 kDa putative outer membrane protein antigen, for vaccination and protection against Chlamydia infection
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                                      tgacattgtctttttagggaatacagtcacttctactactcc---tgggacgaatagaag
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                  2754 TAATGTAGATCTTGGGGGTAAGTTCCAATTCTA 2786
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Search completed: October 2, 2001, 04:35:26
Job time: 55073 sec

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3: /cgn2_6/ptodata/2,
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6: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Compugen Ltd.
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TELEFAX: (414)...
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
TYPE: nucleic acid
TYPE: double
US-08-743-637B-1
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APPLICANT: ROY, Paul
TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                  MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Ent
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
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CORRESPONDENCE ADDRESS:
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STATE: WISCONSII
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(414)277-5591
FOR SEQ ID NO: 1:
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                                                                                 linear
                      Enterococcus faecalis
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                                                             DNA (genomic)
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Best Local
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                                                                                                                                                NFORMATION FOR SEQ ID NO:
                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                          NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
                                                                     STRANDEDNESS:
                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/304,732 FILING DATE: 12-SEP-1994
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                                                       TOPOLOGY:
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Similarity 51.1%;
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                                                                                                                                                                    : (414) 277-5000
(414) 277-5591
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                                                       linear
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Enterococcus faecalis
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AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
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Pred. No. 0.012;
"""matches 92; Indels
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Best Local Similarity
Matches 96; Conserv
                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 30472/114 IMMUTELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
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MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                              FILING DATE:
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6

PTI.TNG DATE: 26-AUG-1991
                                                        STRANDEDNESS:
                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Alexandria
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                                         TOPOLOGY:
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                                                                                           LENGTH:
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                                                                                           7218 base pairs
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                                                                                                                                                               (703)683-4109
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51.1%;
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                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,172
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/849,411
FILING DATE: 07-JUL-1992
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TELECOMMUNICATION INFORMATION:
                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
                                                                                         FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                            CITY:
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                                                                                                                                                                                                                                                                                                                                            Toronto
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                                                                                                                                                                                                                                                                                                                                                         Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                           Canada
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Klein, Michel
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(416) 595-1155
                                                                                                                                                                                                                                                              Floppy disk
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Patent No. 5656423
GENERAL INFORMATION:
APPLICANT: Orth,
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Best Local Similarity
Matches 109; Conserv
                 TELEFAX: 202-4(
INFORMATION FOR SEQ
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                                                               REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,879
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                         APPLICATION NUMBER: WO 92/1136
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Volpers, Chr
APPLICANT: Streek, Rolf
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SEQUENCE CHARACTERISTICS
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                                                TELEPHONE:
                                                                                                                                                                                                                                     FILING DATE: 16-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, ADDRESSEE: Dunner
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STRANDEDNESS: single
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1300 I Street,
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                                  202-408-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papillomavirus HPV39, Their Use in In Vitro Diag for the Production of an Immunogenic Composition
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                                                                                        02356.0066-00000
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US-08-468-057A-9
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Best Local Similarity
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                                                                                                             INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: the
TITLE OF INVENTION: and
TITLE OF INVENTION: 11
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TOPOLOGY: 11r
MOLECULE TYPE:
                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 16-JUN-1
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              MOLECULE TYPE:
                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                           TELEPHONE: 202-408-4400
                                                                                                                                                                                                                             APPLICATION NUMBER: WO 92/1136 FILING DATE: 09-JUI-1000
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300
CITY: Washington
                                                                                                                                                                      REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 06-JUI
                             TOPOLOGY:
                                          STRANDEDNESS:
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o. 5665535
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                                          nucleic acid
EDNESS: single
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1300 I Street, N.W
                                                                        7833 base pairs
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Volpers, Christoph
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             DNA (genomic)
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the Papillomavirus HPV39, Their Use in In Vitro Diagnosis
and for the Production of an Immunogenic Composition
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Pred. No. 1
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Query Match

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                                                                                                    Query Match
Best Local Similarity
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                                                                                           Matches
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                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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                                                   1018 GACATTACCTTCAATGGGAATGCCATTGTTGCAACTACACCACAAACTACAAAAAGAAAT 1077
                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 595-1155
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TITLE OF INVENTION:
TITLE OF INVENTION:
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 1078 TCTATTGACATAGGATCTACTGCAAAGATCACGAATTTACGTGCAATATCTGGGCATAGC 1137
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: UFILING DATE: 07-JUL-1
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                 223 GATTCTAGAATTAATATGAATGGTGATGTAGCTGCTTCTATAAAAGGTGCTACAATGAAC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 ATCATCGGTAATCACAACCCCCTCAGGAAAAGGTGCAGTTAAAT 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Application US/08472172 5985288
                                                                                                                                                                                                nucleic acid
EDNESS: single
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Suite 701, 330 Un
                                                                                                                                                                                                                            1347 base pairs
                                                                                                                                                                                                                                                                          (416) 595-1163
63-24567 SIMBAS
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                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canada
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Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grass, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Munson,
                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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                                                                                                      1.2%;
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of Haemophilus Influenzae
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                                                                                                      Score 34.2;
Pred. No. 1.
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                                                                                           Mismatches
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Type B
                                                                                                                       Length 1347;
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RESULT 8
US-07-876-280-5
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TELEPAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Appl Patent No. 52621
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/8: FILING DATE: 19920430 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                            ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 33f2
IMMEDIATE SOURCE:
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TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Controlling Acarides
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                                                                                          LOCATION: 4..24
OTHER INFORMATION:
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OTHER INFORMATION:
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CITY: Gainesville
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                            CLONE: E. coli NM522(pMYC 2316) B-18785
                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: do TOPOLOGY: linear
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                                     NAME/KEY: misc_feature LOCATION: 13..33
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                   double
/function= "oligonucleotide
hybridization probe"
                                                                                                                                                /function= "oligonucleotide hybridization probe"
                                                                                           /product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT"
/standard_name= "probe a"
/note= "Probe A"
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 32606
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,783
FILING DATE: 19930419
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                                                                                                                                                                                                                                                               TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                   ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 33f2
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: NO
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ADDRESSEE: Jeff Lloyd
STREET: 2421 N.W. 41s1
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APPLICANT: Schwab, George
APPLICANT: Payne, Jewel M
TITLE OF INVENTION: Gene Encoding
TITLE OF INVENTION: Toxins Cloned
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                                     FEATURE:
                                                                                                                                 ORIGINAL SOURCE:
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                                                       CLONE:
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TOPOLOGY: li
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OTHER INFORMATION:
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NAME/KEY: misc_feature LOCATION: 4..24
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/standard_name= "Probe B"
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Pred. No. 2
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Patent No. 559607
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APPLICANT:
APPLICANT:
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NO. 5596071el Bacillus thu: TITLE OF INVENTION: Against Hymenopteran Pests NUMBER OF SEQUENCES: 51
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LOCATION: 13..33
OTHER INFORMATION: /func
OTHER INFORMATION: /pbri
OTHER INFORMATION: /prod
OTHER INFORMATION: /stan
OTHER INFORMATION: /labe
OTHER INFORMATION: /note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 TTTTAGATGTTGCATGGACTTATATAACTACAGGAGAAATTGACCCTTTAAATGTAATTA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 AAGGTGTTTTATCTGTATTAACTTTAATTCCTGAAGTTGGTACTGTGGCCTCTGCAGCAA 274
                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
84; Conserv
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                                                                                                                                                                                                                                                                                                                                           Gainesville
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Schnepf, H. Ernest
Schwab, George E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fu, Jenny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uick, Heidi Jane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kennedy, M. Keith
Randall, John Brooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Payne,
                                                                                                                                                                                                                                               Floppy disk
25-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Jewel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 5596071el Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function= "oligonucleotide hybridization probe" /product= "AAT GAA GTA/T TAT CCA/T GTA/T AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function= "oligonucleotide
hybridization probe"
/product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT"
/standard_name= "probe a"
/note= "Probe A"
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/label= probe-b
/note= "probe b"
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Pred. No. 2.4;
0; Mismatches
                                                                                                                                                                                        Version #1.
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Sequence 5, Patent No. !

5616495

Application US/08304626

GENERAL INFORMATION:
APPLICANT: Payne,
APPLICANT: Kenned

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Schnepf, Harry

Foncerrada, Luis

Rannedy, M. Keith Kennedy, M. Keith Randall, John Brooks Meier, Henry Uick, Heidi Jane

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US-08-304-626-5
               RESULT 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DI HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                       1529 GTAAAAATGTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAA 1575
                                                                                                                                                                              1469 CCATTCCTGTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTGCTGCAGCAA 1528
                                                                                                                                                                                                                                                    1409 TTATGGATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTT 1468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: E. coli
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LENGTH: 3771 base pairs
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TELEPHONE: 904-375-8100
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ATTORNEY/AGENT INFORMATION:
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LOCATION: 4..24
OTHER INFORMATION: /func
OTHER INFORMATION: /proc
OTHER INFORMATION: /proc
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                                                                                                                                                                                                                  155 TTTTAGATGTTGCATGGACTTATATAACTACAGGAGAAATTGACCCCTTTAAATGTAATTA 214
                                                                                                                                           215 AAGGTGTTTTATCTGTATTAACTTTAATTCCTGAAGTTGGTACTGTGGCCTCTGCAGCAA 274
                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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                                                                       GTACTATTGTAAGTTTTATTTGGCCTAAAATATTTGGAGATAAACCA 321
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R INFORMATION:
R INFORMATION:
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ION: 13..33
INFORMATION: /fun
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                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                       1.2%;
                                                                                                                                                                                                                                                                                                                                                                                           hybridization probe"

product "AAT GAA GTA/T TAT CCA/T GTA/T
/standard_name= "Probe B"
/label= probe-b
/note= "probe b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybridization probe"
/product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT"
/standard_name= "probe a"
/note= "Probe A"
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BER: M/SCJ104.C1
                                                                                                                                                                                                                                                                                                         Score 34.2;
Pred. No. 2
                                                                                                                                                                                                                                                                                          Mismatches
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Best Local
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                            1409 TTATGGATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTT 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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APPLICATION NUMBER:
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APPLICATION NUMBER: US
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155 TTTTAGATGTTGCATGGACTTATATAACTACAGGAGAAATTGACCCTTTAAATGTAATTA 214
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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OTHER INFORMATION:
OTHER INFORMATION:
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CTTY: Gainesville
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OTHER INFORMATION:
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                                                                                    Local Similarity
                                                                                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                              NAME/KEY:
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VENTION: No. 5616495el Bacillus thuringiensis Isolates
VENTION: Active Against Hymenopteran Pests and Genes Encoding
VENTION: Hymenopteran-Active Toxins
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                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                  1.2%;
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                                                                                                                                                                                                                                                                                                                             /function= "oligonucleotide
hybridization probe"
/product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT"
/standard_name= "probe a"
/note= "Probe A"
                                                                                                                                                                                                      /function= "oligonucleotide
hybridization probe"
/product- "AAT GAA GTA/T TAT CCA/T GTA/T AAT"
/standard_name- "Probe B"
                                                                                                                                                                    /label= probe-b
/note= "probe b"
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                                                                                  Score 34.2;
Pred. No. 2
                                                                    Pred. No. 2.4
); Mismatches
                                                                                                   DB 1;
                                                                                                   Length 3771;
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Patent No.
                                                                                                 TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5
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                                                                                                                                 REFERENCE/DOCKET NUMBER: MATELECOMMUNICATION INFORMATION: 904-375-8100
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pair
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Lloyd, Jeff
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APPLICATION NUMBER:
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              STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/8:
FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                                                                                                                             FILING DATE: 12-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/693,018 FILING DATE: 03-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 23-APF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/316,301A FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 4
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                                           nucleic acid
TYPE:
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Payne, Jewel M.
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                                                                base pairs
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                                double
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RESULT 13
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Best Local (
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                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    TITLE OF INVENTION: No. 5824792el Bacillus thuringiensis Toxins Active TITLE OF INVENTION: Against Hymenopteran Pests NUMBER OF SEQUENCES: 51 CORRESPONDENCE ADDRESS: ANDRESCEPT. PAUL OF A STANDESCEPT. PAUL OF A STANDESCEPT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 GTACTATTGTAAGTTTTATTTGGCCTAAAATATTTGGAGATAAACCA 321
                                                                                                                                                   CITY: Gainesville
STATE: FL
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OTHER INFORMATION: /fun OTHER INFORMATION: hybr
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LOCATION:
                 SOFTWARE:
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                                                                                                                               COUNTRY:
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APPLICATION DATA:
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                                                                                                                                                                                      E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                               USA
                                                                                                                                                                                                                                                                                                  Fu, Jenny
                                                                                                                                                                                                                                                                                                              Schnepf, H. Ernes
Schwab, George E.
                                                                                                                                                                                                                                                                                                                                     Foncerrada, Luis
Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                        Uick, Heidi Jane
                                                                                                                                                                                                                                                                                                                                                                                           Meier, Henry
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Randall, John Brooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Payne, Jewel
                   PatentIn Release #1.0,
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hybridization probe"
/product= AAT GAA GTA/T TAT CCA/T GTA/T AAT"
/standard_name= Probe B"
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/standard_name= probe a"
/note= Probe A"
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Pred. No. 2.4;
0; Mismatches
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                   Version #1.25
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US-08-611-928-5
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Best Local Similarity
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IMMEDIATE SOURCE:
CLONE: E. COli w//
FEATURE:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 25-NOV-1S
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                    1529
                                                                                                                                                                                    1409 TTATGGATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTT 1468
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TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
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TYPE: nucleic acid
STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: M/
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GTACTATTGTAAGTTTTATTTGGCCTAAAATATTTGGAGATAAACCA
                                    GTAAAAATGTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAA 1575
                                                                      AAGGTGTTTTATCTGTATTAACTTTAATTCCTGAAGTTGGTACTGTGGCCTCTGCAGCAA
                                                                                                           CCATTCCTGTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTTCTGCAGCAA 1528
                                                                                                                                                 TTTTAGATGTTGCATGGACTTATATAACTACAGGAGAAATTGACCCTTTAAATGTAATTA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function= "oligonucleotide
hybridization probe"
/product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT"
/standard_name= "probe a"
/note= "Probe A"
                                                                                                                                                                                                                                                                                                                              hybridization probe"
/product= "AAT GAA GTA/T TAT CCA/T GTA/T
/standard_name= "Probe B"
/label= probe-b
/note= "probe b"
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Pred. No. 2.
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                                                                                                                                                                                                                                                             Length 3771;
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RESULT 14
US-09-173-891-5
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APPLICATION NUMBER: US 0//00//--
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/797,645
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,891
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ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-NOV-1991 PRIOR APPLICATION DATA:
                                                                                                 FEATURE:
                                                                                                                                                                                                               MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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 OTHER INFORMATION:
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                                                         NAME/KEY: misc_feature
LOCATION: 4..24
                                                                                                                   CLONE:
                                                                                                                                                       ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 33F2
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Schnepf, H. Ernest
Schwab, George E.
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Uick, Heidi Jane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kennedy, M. Keith
Randall, John Bro
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/function= "oligonucleotide hybridization probe" /product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT"
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GENERAL INFORMATION:
APPLICANT: Schwab, George E.
APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Foncerrada, Luis
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                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 3771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09076137B Patent No. 6166195
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 6166195el Nematode-Active Toxins and Genes Which Code TITLE OF INVENTION: Therefor FILE REFERENCE: MA-20CCCD2
                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1994-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 42
IOCATION: (13)..(33)..(33)
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LOCATION: (4)..(24)
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OTHER INFORMATION: /standard_name= "probe a" /note= "Probe A"
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1469 CCATTCCTGTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTGCTGCAGCAA 1528
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hybridization probe"
/product= "AAT GAA GTA/T TAT CCA/T GTA/T AAT"
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/note= "Probe A"
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/label= probe-b
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Pred. No. 2.4;
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Query Match Best Local Similarity Matches 84; Conserve

Conservative

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Score 34.2; DB Pred. No. 2.4; 0; Mismatches

DB

4; Length 3771;

Indels

0,

Gaps

Search completed: October 2, 2001, 03:26:18 Job time: 50171 sec

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Maximum I
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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191 gd.bhc:*
192 em.gus.fun:*
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195 em.gus.huml:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                 GSS; genome.survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 1 (bases 1 to 773)
Roest-Crollius, H.,
                                                                                                                                                                  CNS01VTG
                        Tetraodontidae;
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 Dasilva,C.,
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 Fizames, C., Fisher, C.,
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BE015877 fk61c08 y
AI436994 fb36f02 y
AZ908189 RPCI-24-1
AZ908171 RPCI-24-1
AQ934958 CPC2341A
AL299119 Tetracdon
AL011359 F.rubripe
AU03974 AU039974
BE437493 SFR004.C1
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AU03973 BU03973
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                                   ACATACTACTGCTACTACTACTACTGCTACTACTGCTACTACTACTACTACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bouneau,L., Billault,A., Quetier,F., Weissenbach,J.
Charaterization and repeat analysis of freshwater pufferfish Tetraodon nigro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome. For more information, please t
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct
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/db_xref="taxon:99883"
/clone="199C24"
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                                               TCTGGAGATGCCGATGTTACCATATCTGGGAATCAGAGTGTAACTTTCTCAGGAAACCAA
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3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project
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AU061466 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLE356, mRNA sequence.
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Yoshino, R., Morio, T. and Tanaka, Y.
Developmental CDNA in Dictyostelium
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/dev_stage="slug"
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/clone="SLE356"
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/strain="AX4"
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GGTGCTGCAAATGG
                                GCTGTAGCTAATGG
                                                                  ACTGGAGCAAATAGTGGTGCTGCAACTGGTGCAAATAGTGGAAACAATGCCGCTGTAACT
                                                                                                  TCTGGAGATGCCGATGTTACCATATCTGGGAATCAGAGTGTAACTTTCTCAGGAAACCAA 849
                                                                                                                                      AGTGGTGCTGCAACTGGAGCAAATAGTGGTGCTGCAACTGGAGCAAATAGTGGCGCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                   146;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 623)
Yoshino,R., Morio,T. and Tanaka,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discoideum cDNA clone : AU060774 AU060774.1 GI:4881878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU060774 623 bp mRNA EST 20-MAY-1999
AU060774 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLB441, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki
Email: d402nu@sakura.cc.tsukuba.ac.
PROJECT = Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Hideko Urushihara
Institute of Biological Sciences
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Dictyostelium discoideum.
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/dev_stage="9lug"
104 c 214 g 136 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium discoideum'
/strain="AX4"
/db_xref="taxon:44689"
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Pred. No. 0.
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                                                                                                                                                                                                                                                                               TCTGGAGATGCCGATGTTACCATATCTGGGAATCAGAGTGTAACTTTCTCAGGAAACCAA 849
                                                                                                                                                                                                                                                                                                                AGTGGTGCTGCAACTGGAGCAAATAGTGGTGCTGCAACTGGAGCAAATAGTGGCGCTGCA
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                                                                    AU060177 540 bp mRNA EST 20-MAY-1999
AU060177 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLA520, mRNA sequence.
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AU060168 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLA507, mRNA sequence.
AU060168
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Tsukuba, Ibaraki 305, 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
                Dictyostelium discoideum
                                                 AU060177.1
                                                              AU060177
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Institute of Biological Sciences
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T = Dictyostelium discoideum
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/clone="SLA507"
/clone_lib="Dictyostelium d
/dev_stage="slug"
a 139 c 237 g 171 t
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                                               GI:4881281
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Pred. No. 0.11;
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170; Conserv
                                                                                                                                                  BF422671 660 bp mkNA LT_ad_A35_T3 Earthworm Lambda Zap Express Library Lumbricus rubellus cDNA clone Lr_ad_A35_5' similar to gb|AAF49822.1| (AE003538) CG10724 gene product - Drosophila melanogaster, mRNA
1 (bases 1 to 660)
Sturzenbaum, S., Parkinson, J.,
Schaffner, W. and Georgiev, O.
                                             humus earthworm.
Lumbricus rubellus
Eukaryota; Metazoa; Annel
Lumbricina; Lumbricidae;
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3-3-10 Ten-nodai, Tsukuba,
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Yoshino, R., Morio, T.
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d402hu@sakura.cc.tsukuba.ac.jp
T = Dictyostelium discoideum cDNA project
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76 c 209 g
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/clone="SLA520"
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/strain="AX4"
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                                                Lumbricus.
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Human gene number estimate provided by genome wiretracdon nigroviridis DNA sequence
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3 (bases 1
                                                                                                                                                           Charaterization and repeat analysis of the confreshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                 1 (bases 1 to 989)
Roest-Crollius, H., Jaillon, O.,
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Tetraodon nigroviridis genome survey sequence T7
139021 of library G from Tetraodon nigroviridis,
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                                                                                                                                        Unpublished
                                                                                                                                                                                                                Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot
                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis
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Seq primer: T3 sequencing primer
High quality sequence stop: 526.
                                                                                                                                                                                                 Weissenbach,J
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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/dev_stage="adult"
/note="vector: pBK-CMV; The library was
protocol given by supplier (Stratagene)
144 c 178 g 158 t
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/clone_lib="Earthworm Lambda Zap
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/db_xref="taxon:35632"
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Plasmid Drosophila melanogaster

Plasmid Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;

Eukaryota; Neoptera; Endopteryota; Diptera; Brachyce

Pterygota; Neoptera; Endopteryota; Drosophila.
                                                                                                    fly), genom
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                                                                                                                                                 Drosophila melanogaster genome survey sequence T7
BACN03K20 of DrosBAC library from Drosophila melan
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/clone_lib="G"
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/db_xref="taxon:99883"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                   AU061937
                                                                        Dictyostelium discoideum.
Dictyostelium discoideum
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                    Yoshino, R., Morio, T. and Tanaka, Y.
                                                       Eukaryota;
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Takifugu rubripes
Eukaryota; Metazoa; Chordata; Cr
Eukaryota; Metazoa; Chordata; Cr
Actinopterygii; Tel
Acanthomorpha; Acanthopterygii;
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Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA
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University of Tsukuba
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Contact: Hideko Urushihara
                                                                                              Z90754.1 GI:1867968
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/clone="SLG686"
/clone_lib="Dictyostelium d
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                           1 (bases 1 to 450) Elgar,G., Clark,M., Smith,S., Meek,S., Williams,G. and Brenner,S.
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                Takifugu rubripes.
Takifugu rubripes
                                                                                                                                                                                               F.rubripes GSS sequence, AL018519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk Vector: pBluescript II KS
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Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S.
Direct Submission
 Submitted (08-DEC-1997) MRC Human
                                                                                                                                                                GSS; genome survey sequence.
                                                                                                                                                                                 AL018519.1 GI:2684887
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                                                                       Tetraodontidae; Takifugu.
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/db_xref="taxon:31033"
/clone_lib="cosmid 133B16"
/clone="133B16aC7"
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Query Match
Best Local Similarity
Matches 137; Conserv
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                  High quality sequence start: 18
High quality sequence stop: 846
Location/Qualifiers
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                                                                                               Seq primer: M13-Forward
                                                                                                                 DNA library
                                                                                                                                    Clones are derived
                                                                                                                                                                            Fax: 301 838 0208
                                                                                                                                                                                                                 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                          Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                              1 (bases 1 to 887)
Loftus, B., van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
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                                                                           Class: shotgun
                                                                                                                                                        Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Entamoebidae;
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/db_xref="taxon:31033"
/clone_lib="cosmid 154E17"
/clone="154E172C12"
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Best Local :
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                                                                                               Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Ur
                                                                                                                                                                                                                                                                                                                                       Bos taurus
                                      Tel: 217 333 5998
Fax: 217 244 5617
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                           Unpublished (2000)
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                      h-lewin@uiuc.edu
for cattle EST sequencing was provided by the USDA National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin an Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                    Rebeiz, M., Pardinas, J.,
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                                                                                               Dr., Urbana,
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                                                                                                                                                                                                                                  and Larson
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JOURNAL
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                       GSS; genome survey
Takifugu rubripes
Takifugu rubripes
                                                                                                     biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II
                                                                                                                                      Submitted (11-OCT-1999) MRC Human Genome Mapping Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
                                                                                                                                                                                                        l (bases 1 to 550)
Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S.,
Umrania,Y., Williams,G. and Brenner,S.
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae; Takifugu.

1 (bases 1 to 550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRE from Washington University Genome Center. Vector Trimmi g: Cross_match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.
                   One pass dye-terminator sequencing
                                                           V_type: phagemid PRIMER: KS
                                                                                                                                                                                        Direct Submission
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Plate: BP230020B20
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                                                                                                                                                                                                                                                                                                                                                                                                   genome survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
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/db_xref="taxon:9913"
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                      genomic
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Best Local
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Local Similarity 47.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                           Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. The Dictyostelium developmental CDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetoga; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU033711. 607 bp mRNA EST '28-APR-1999 AU033711 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLB346, mRNA sequence.
AU033711
                                                                                                                                                                                                                           Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA proje
                                                                                                                                                                                                                                                                                                                                                        DNA Res. 5 (6), 335-340 (1998)
99156227
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                 /strain="AX4"
/db_xref="taxon:44689"
/clone="SLB346"
/clone_1bb="Dictyostelium discoideum SL (H.Urushihara)"
/clone_Lib="Slug"
/dev_stage="slug"
125 c 134 g 145 t
                                                                                                                                                                                  Location/Qualifiers
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/db_xref="taxon:31033"
/clone_11b="cosmid 161G06"
/clone="161G06aC7"
155 c 82 g 163 t
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Best Local Similarity 54.6
Matches 106; Conservative
                                                                                                                                                              666 CAATATTGCTGAAGCTGCAGGTGGAGCTATAAATAGCACACGGAAACTGTACAATTACAGG 725
218 TGGTGCTGCAACTG 231
                                                                     158 TGCTGCAAATAGTGGTGCTGCAACTGCTGCAAATAGTGGTGCTGCAGCTGGAGCAAATAG
                                                                                        726 G-----AATACGTCTCTTGTATTTTCTGAAAATAGTGTGACAGCGACCGCAGGAAATGG 779
                                                                                                                                                                                                                                                   606 TATTTGTGCTACTGGTACTGTAGATATTACAAATAATACGGCTCCTACCCTCTTCTCGAA 665
                                780 AGGAGCTCTTTCTG 793
                                                                                                                                           98 TGGAAATAATGGCGCTGCAGCTGGAGCAAATAGTGGTGCCGCAACTGCTGCAAATAGTGG 157
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Pred. No. 1.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                     Query Match 5.0%;
Best Local Similarity 21.1%;
Matches 134; Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08469880 Patent No. 5876733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 1554 - PC-
POPERATING SYSTEM: PC-
PATENTIA RE: Patentin Re-
PATENTA RE: PATENTIA RE-
PATENTA RE: PATENTA DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
FILING DATE: 16-SEP-
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APPLICATION NUMBER:
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                                     889
                                                                                                                                            137
240 FEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHAKK--LALSSGGF 297
                                                                      192
                                                                                                       851 VTINNNANVTLIGSDFDNHQKPL-----
                                                                                                                                                                          793 SIEKDLTLNATGGNITLLQVE-GTDGMIGKGIVAKKNITFEGGN-ITFGSRKAVTEIEGN 850
                                                                                                                                                                                                                                                  736 SENGNISVSGGGSVDFTLLASSSNVQTPGVVINSKYFNVSTGSSLR---FKTSGSTKTGF
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                                                                                                                                                                                                             79 -- TDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQ 136
                                                                                                                                                                                                                                                                                34 SFNGNID-----SGTFTPKTSATTYSLTGDVF---FYEPGKGTPLSDSCFKQT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 06-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                        GTLSSAGGVNL-----ENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTK 191
                                                                    GGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSILS------NKFLY 239
                                 GGNIVNIAGNLTVESNANFKAITNFTFNVGGLFDNKGNSNISIAKGGARFKDIDNSKNLS 948
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31 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                                                                                                                                                                                                   Pred. No. 2.66
9; Mismatches
                                                                                                                                                                                                                                                                                                                                     Score 238; DB 2;
Pred. No. 2.6e-09;
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                                                                                                     -----TIKKDVIINSGNLTA 888
                                                                                                                                                                                                                                                                                                                                                        Length 1536;
                                                                                                                                                                                                                                                                                                                     Indels 168;
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                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                       NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 ---TLTTTGSTDTPKRNAINIGSNGK---FTELR----AAKNHTIFFYDPITSEGTSSDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US PILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 16-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2001
STREET: Bldg.
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5. 5928651
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                         (703)
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                                                                                                                                                                                                                                                                                                                                   16-MAR-1993
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High Molecular Weight Surface Proteins
of No. 5928651-Typeable Haemophilus
                                                                                                                                                                                                                                                                                    US PCT/US93/02166
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RESULT 9
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Best Local :
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                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: BARENK
APPLICANT: ST. GE
COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
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                                                                                    CITY: Arlington STATE: Virginia
                                                                                                                       STREET: 2001 Je
STREET: Bldg. 1
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Local Similarity 21.1%;
                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDLTIGNTNSAD------GINAKKVTFNQVKDSKISADGHKVTLHSKVETSGSNNNT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIKG-TESVTTSSQSG--DIGGTISGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAKGASNKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGNVEITAQTGSILGGIESSSGSVTLTATEGALAVSNISGNTVTVTANSGALTTLAGS 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STS----FSQEAGSLLG---MDSGT-TLSTTAGSITITNLG-----INVDSLGLKQPVSL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTLE 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TLTTTGSTDTPKRNAINIGSNGK---FTELR----AAKNHTIFFYDPITSEGTSSDV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSILS-----NKFLY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTLSSAGGVNL-----ENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFNGNISVSGGGSVDFTLLASSSNVQTPGVVINSKYFNVSTGSSLR---FKTSGSTKTGF 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDSSDNNAGL------TIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTIN 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NITKQITIKAGYDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITAKDG 1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHAKK--LALSSGGF 297
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                                                                                Virginia
                                                                                                                                       2001 Jefferson Davis Hwy.,
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                                                                                                                                     Shoemaker and Mattare, Ltd
01 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                               -- TGEANVTSATGTIGGTISGNTVNVTA 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 238; DB 1;
Pred. No. 2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 235; Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TIKKDVIINSGNLTA 888
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Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,198
FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:

NAME: BERKSTRESSER, JERY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: JWB-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 115-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                            388
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mes 134; Conserv
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                                                                                                                                   TAKGASNKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVP 554
                                                                                                                                                                                 ATTGNVEITAQTGSILGGIESSSGSYTLTATEGALAVSNISGNTVTVTANSGALTTLAGS 1216
                                                                                                                                                                                                                                                                                                      LKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTLE 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITAKDG 1058
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AT-----TGEANVTSATGTIGGTISGNTVNVTA 1287
                                                                                                                                                                                                                              STS----FSQEAGSLLG---MDSGT-TLSTTAGSITITNLG----INVDSLGLKQPVSL 494
                                                                                                                                                                                                                                                                              EDSSDNNAGL------TIDAKNVTVNNNITSHKAVSISATSGEITTKTGTTIN 1156
                                                                                                                                                                                                                                                                                                                                                                                                                    ---TLTTTGSTDTPKRNAINIGSNGK----FTELR----AAKNHTIFFYDPITSEGTSSDV 387
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                                        AEDPNSEYGFQGQWNVNWTTDT----ATNTKEATA
                                                                                        TIKG-TESVTTSSQSG--DIGGTISGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEFLRNNVSSATPKGGA----ISIDASGELSLSAETGNITFVRN---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.0%; Score 238; DB 2; Length 1536; ilarity 21.1%; Pred. No. 2.6e-09; Conservative 99; Mismatches 235; Indels 16
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                                             585
                                                                                        ----TVEVKATESLTTQSNSKIK 1259
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US-08-038-682-2
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                                                                                                                                                                                                                                                                                                                         Matches 134;
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1356 IGNSA 1360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                     889
                                                                                                                                                                                                                                                     736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                       851 VTINNNANVTLIGSDFDNHQKPL-
                                                                                                                                         137 GTLSSAGGVNL-----ENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTK 191
                                                                                                                                                                             793 SIEKDLTLNATGGNITLLQVE-GTDGMIGKGIVAKKNITFEGGN-ITFGSRKAVTEIEGN 850
240 FEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHAKK--LALSSGGF 297
                                                                192 GGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSILS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                         79 --TDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 16-MA
                                                                                                                                                                                                                                                                                     34 SFNGNID-----SGTFTPKTSATTYSLTGDVF---FYEPGKGTPLSDSCFKQT----- 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                   SFNGNISVSGGGSVDFTLLASSSNVQTPGVVINSKYFNVSTGSSLR---FKTSGSTKTGF 792
                                 GGNIVNIAGNLTVESNANFKAITNFTFNVGGLFDNKGNSNISIAKGGARFKDIDNSKNLS 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible YSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                       99;
                                                                                                                                                                                                                                                                                                                                Score 238; Db 1,
No. 2.6e-09;
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                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                         235;
                                                                                                                                                                                                                                                                                                                                                         Length 1536;
                                                                                                                                                                                                                                                                                                                         Indels 168;
                                                                                                     -TIKKDVIINSGNLTA 888
                                                                     --NNKFLY 239
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GENERAL INFORMATION:
                                                                                  TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260
                                                                                                                                          NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia COUNTRY: U.S.A.
STRANDEDNESS:
                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US pct/us93/02166 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2001
STREET: Bldg.
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                                                                                                                         TELEPHONE:
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                                           LENGTH:
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                       amino acid
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                                           1536 amino acids
                                                                                                          (703)
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Shoemaker and Mattare, Ltd.
Shoemaker and Mattare, Ltd.
                                                                                                                           (703)
  single
                                                                                                     415-0813
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5. 5603938-Typeable Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08617697 Patent No. 5977336
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
COMPUTER: FC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HI
TITLE OF INVENTION: of
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1128
                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
APPLICATION NUMBER:
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                                                                                                                                                ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVSLSGGKLLLQKGVTLESTSFSQEA----GSLLG--MDSGTTLSTTAGSITITNLGINV 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SNFSLKQTKDSFYNEYSKHAINSSHNLTILGG--NVTLG-----GENSSSSITGNINI 782
                                                                                                                                                                                                                                   Bldg. 1
                                                                                                                                                                                                                                                     E: Shoemaker and Mattare, Ltd.
2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                    Barenkamp, Stephen J
VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FVRNTLTTTGSTDTPKRNAINIGSNGK---FTELRAAKNHTI 372
US/08/617,697
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Best Local S
Matches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 415-081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-OCT-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                1056 TAKNGSDLTIGN--ASGGNADAKKVT------FDKVKDSK-----ISTDGHNV 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                 1252 TTAGSTISATTG-----NANITTKTGDINGKVESSSGSVTLVATG------ATLAVGN 1291
                                                                                                                                                                                                                                          1151 GTTINATTGSVEVTAQNGTIKGNITSQNVTVTATENLVTTENAVINATS----GTVNIST 1206
                                                                                                                                                                                                                                                                                                                                        1096 TLNSEVKTSNGSSNAGNDNS-----TGLTISAKDVTVNNNVTSHKTINISAAAGNVTTKE 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            607 LWG----VFTDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGDENRKGFRHTSGGYV 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  914 ASDNLNITGT-----FTNNGTANINIKGVVKLGDI------NNKGGLNITTNASGTQ
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STRANDEDNESS: si
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 Match 5.1%; Score 244.5; DB 2 Local Similarity 21.9%; Pred. No. 8.9e-10; Local Similarity 21.9%; Pred. No. 8.9e-10; Mismatches 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                   TSSDVLKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQK 442
                                                                                                                                                                                           KGASNK---VIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKIT--VDADVDTNVDISSLI 551
                                                                                                                                                                                                                                                                                    GVTLESTSFSQEA----GSLLG--MDSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGKFTELRAAKNHTIFFYDPITSEG--- 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SNFSLKQTKDSFYNEYSKHAINSSHNLTILGG--NVTLG-----GENSSSSITGNINI 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FA-----SNVAETSGGAIHAKKLALSSGGFTEFLRNNVSSATPKGGAISIDASGELSL 325
                                                                                           PVPAEDPNSEYGFQGQWNVNWTTDTA----TNTKEATATWTKTGFVPSPERKSALVCNT 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTIINGNITNEKGDLNIKNIK-----ADAEIQIGGNISQKEGNLTISSDKVNITNQITIK 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SFLLTGTSGDALFSNNSSS-----TKGGAIATTAGARIANNTGYVRFLSNIAST- 219
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                                                                                                                                            KTGDIKGGIESTSGNVN-ITASGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SGGAIDDEGTSILSNNKFLYFEGNAAKTTGGAICNTKAS---GSPELIISNNKTLI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNKANVTLQADTSNSNTGLKKRTLTLGNISVEGNLSLTGANANIV-GNLSIAEDSTFKGE 913
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                             1018
  1128 TS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US PETILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA:
                                                                           1068 NISAAAGNVTTKEGTTINATTGSVEVTAQNGTIKGNITSQNVTVTATENLVTTENAVINA 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                          484
                                                                                                                   430 PVSLSGGKLLLQKGVTLESTSFSQEA----GSLLG--MDSGTTLSTTAGSITITNLGINV 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       732
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                                                                                                                                                                                                     373
                                                                                                                                                                                                                                                                                     332 IT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783
                                                                                                                                                                                                                                           962 LTIQTKELKLAGDLNISGFNKAEITAKNGSDLTIGNASGGNADAKKVTFDKVKDSK---- 1017
                                                                                                                                                                                                                                                                                                                       916 QIGGNISQKEG-----NLTISSDKV-----NITNQITIKAG---VEGGRSDSSEAENAN 961
                                                                                                                                                                                                                                                                                                                                                                                                                                             228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                842 ASDNLNITGT-----FTNNGT------ANINIKQGVVKLQGDI------
                                                                                                                                                                                                                                                                                                                                                             272 IFASNVAETSGGAIHAKKLALSSGGFTEFLRNNVSSATPKGGAISIDASGELSLSAETGN 331
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REGISTRATION NUMBER: 22,651
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STRANDEDNESS: si
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                                                                                                                                                                                FFYDPITSEG---TSSDVLKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQ 429
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                                     DSLGLKQPVSLTAKGASNK----VIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKIT---VD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNKANVTLQADTSNSNTGLKKRTLTLGNISVEGNLSLTGANANIV-GNLSIAEDSTFKGE 841
                                                                                                                                                           -----ISTDGHNVTLNSEVKTSNGSSNAGNDNS-----TGLTISAKDVTVNNNVTSHKTI 1067
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  -GTVNISTKTGDIKGGIESTSGNVN-ITASGN------
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-TLKVSNITG 1168
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                   Query Match
Best Local Similarity
   Matches
                                                                                                                                                                                                       TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                      NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1222
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1529 amino aci
                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerr
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1273 NTVNVTASTGDLTIGNSA 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1169 QDVTVTADAGALTTTAGSTISATTG-----NANITTKTGDINGKVESSSGSVTLVATG-- 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650 NRKGFRHTSGGYVIGGSA 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 ADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTA-----TNTKEATATWTKTGFV 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2001 .
STREET: Bldg.
                                                                                                            TOPOLOGY:
                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ATLAYGNISGNTYTITADSGKLTSTV--GST-INGTNSYTTSSQSGDIEGTISG 1272
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   162;
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                  1529 amino acids
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                                                                                                              linear
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                                                                                                                             single
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                   5.2%;
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                                                                                                                                                                                                         10:
   99;
                   Score 247.5;
Pred. No. 4.9
                                                                                                                                                                                                                                                                                1038-625
   Mismatches
5; DB 4;
4.9e-10;
hes 272;
                                    Length
   Indels
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                                      1529;
 205;
Gaps
   35;
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35;

P 65

677

11 SSVLAFSCHLQSLANEELLSPDD-SFNGNIDSGTFTPKTSATTYSLTGDVFFYEPGKGTP 69

SSVM-FDIHANLTSRAAGINMDSINITGGLDFSITSHNRNSNAFEIKKDLTINATG---- 731

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                                                                                                              ; TOPOLOGY: US-08-617-697-9
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US-08-617-697-9
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                               Query Match
Best Local Similarity
Matches 165; Conserv
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                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-APR-1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barenkam
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1080 SGNTVNVTASTGDLTIGNSA 1099
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   11 SSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTSATTYSLTGDVF----FYEPG- 65
                                                                                                                                                                                                                                                                         NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/617,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 22202-0286
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                                                                                                                                                                         1599 amino acids
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                            (703) 415-0813
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VENTION: High Molecular Weight Surface Proteins

VENTION: of No. 5977336-Typeable Haemophilus
                                Conservative
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                                                                                                                              linear
                                                                                                                                                                                                                                           (703) 415-0810
                                                                                                                                                                                                                                                                                                                                       NUMBER: US PCT/US93/02166
16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1996
                                                                                                                                            single
                               5.2%; Score 250; DB 2; 22.3%; Pred. No. 3.4e-10; tive 103; Mismatches 284
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                                                                                                                                                                                                                                                                          1038-557
                                284; Indels 188;
                                                            Length 1599;
                               Gaps
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                             CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          NUMBER OF SEQUENCES:
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COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                           STREET: 2001 .
STREET: Bldg.
                                                                                                                                                              ADDRESSEE:
   PC-DOS/MS-DOS
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Sequence 10, Application US/08728470 Patent No. 5928651
                                                                                                                        APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1340 SGNTVNVTASTGDLTIGNSA 1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASIMPF----KSNANYALFNEDISVSGG-GSVNFKLNASSSNIQTPGVIIKSQNFNVSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GGAIHAKK--LALSSGGFTEFLRNNVSSATPKGGAISIDASGELSLSAET 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---NISIARGGAKFKDINNTSSLN----ITTNSDTTYRTIIKGNISNKSGDLNII 976
E: Shoemaker and Mattare, Ltd.
2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ATLAVGNISGNTVTITADSGKLTSTV--GST-INGTNSVTTSSQSGDIEGTI 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       667
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RESULT 2
US-08-719-641-9
; Sequence 9, Application US/08719641
; Patent No. 6218141
; GENERAL INFORMATION:
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Best Local Similarity
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                                                       TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of NO. 6218141-Typeable Haemophilus NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSE: Shoemarca
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   CITY:
STATE:
                                 ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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                                                                                                                                                                                                                                                                                                      SGNTVNVTASTGDLTIGNSA 1099
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 Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US PCT
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 920
FILING DATE: 16-MAR-1992
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1338 amino acids
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APPLICATION NUMBER: US 0
FILING DATE: 16-SEP-1994
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428 TQPVSLSGGKLLLQKGVTLESTSFSQEA----GSLLG--MDSGTTLSTTAGSITITNLGI 481
                                                                                                               371 TIFFYDPITSEG---TSSDVLKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSF 427
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16-MAR-1992
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Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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Patent No. 5928651
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/302/832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
I6-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
APPLICATION UNMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/ACENT INFORMATION:
NAME: BETKSTRATION UNMBER: 22,551
REFERENCE/DOCKET NUMBER: 1038-633
                                                                                                                  TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
CIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                     TELEPHONE: (703) 415-0810
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                             TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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STREET: 2001 Jefferson Davis Hwy.; 1203 Crystal Plaza
STREET: Bldg. 1
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Search completed: October 2, 2001, 03:31:52 Job time: 227 sec

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RESULT 15
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01-APR-1990
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use
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                           "Cloning, expression and sequence analysis of the gene encoding the 120 kD surface-exposed protein of Rickettsia rickettsii."; MO1. Microbiol. 3:1579-1586(1989).

-i- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAVER WITH HEXAGONAL SYMMETRY.

-I- DISEASE: RICKETTSIA RICKETTSII IS THE CAUSATIVE AGENT OF ROCKY MOUNTAIN SPOTTED FEVER (RMSF).
                                                                                                                                                                                 Gilmore R.D. Jr.,
                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1105
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NCBI_TaxID=783;
                                                                                                                                                                                                                                                                          Rickettsia rickettsii
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FACE-EXPOSED PROTEIN.
                                                        OUS: ITS C-TERMINUS POTENTIAL ANTIGENICITY TO THE PROTEIN.
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              STRAINER;
STRAINE 92167802; PubMed=1724278;
MEDLINE=92167802; PubMed=1724278;
Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor.";
Mnl. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
00TER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
[CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
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Q53047;
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Gilmore R.D. Jr., Joste N., McDonald G.A.;
"Cloning, expression and sequence analysis of the gene encoding the surface-exposed protein of Rickettsia rickettsii.";
Mol. Microbiol. 3:1579-1586(4989).
Mol. PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUROGEN DURING INFECTION.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY LAYER WITH HEXAGONAL SYMMETRY.
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SQEAGSLLGMDSGTTLSTTAGSITITNLGINVDS-LGLKQPVSLTA----
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                                                                                    TVLSNG-NVAINELVIGNDGAVQFAHDTYLITRTTNAAGQGKIIFNPVVNNGTTL-----
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EMBL; X75780; CAA53406.1; -
EMBL; X28068; CAA81905.1; -
PIR; B44402; B44402.
PIR; S39173; S39173.
PIR; S44518; S44518
SGD; S0001551; NUP100.
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DOMAIN 33 571 29 x 6 AA APPROXIMATE REPEATS

G-L-F-G.
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                                                          RGSSTSNS-----ITDPE-SSYLNSNDL--LFDPDRRYLKHLV-----IKNNKNL
                                                                                       TATNTKEATATWTKTGFVPSPERKSALVCNTLWGVF-TDIRSLQQLVEIGATGMEHKQGF
                                                                                                                      SIPNSITNPVKATTSKVNADMKRNSSLTSAYRLAPKPLFAPSSNGDAKFQKWGKTLERSD
                                                                                                                                        KI-----TVDADVDTNVDISS---LIPVP--AEDPNSEYGFQGQWNVNWTTD
                                                                                                                                                                               NSSAVGSTGKLFGQNNNTLNVGTQNVPPVNNTTQNALLGTTAVPSLQQAPVTNEQLFSKI
                                                                                                                                                                                                                                            NSTSTTNTGLFGAKPDSQSKPALGGGLFGNSNSNSSTIGONKPVFGGTTQNTGLFGATGT
                                                                                                                                                                                                                                                                          -SITITNLGI---
                                                                                                                                                                                                                                                                                                                        SGGKLLLQ------KGVTLESTSFSQEAGSLLGMD-SGTTLSTTAG------
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                            WVSSMTNFLHKTGDENRK------GFRHTSGGYVIGGS-----AHTPKDDLFTFAF
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·NVINHNDDEASKVKLVTFTTESASKDDQASSSIAASKLTEKAHSPQTDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NNTQNNGAFGQSMGATQNSPFGSLN-----SSNASNGNTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99988 MW;
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21.1%;
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Pred.
                                                                                                                                                                                                                                                                          -----NVDSLGLKQP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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0.00032;
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B Qγ

344

4

SIPWVLVSSVLAFSCHLQSLANEELLSPDDSF-----NGNIDSGTFT---PK

Indels 144;

Gaps

23;

47

--IVSPSVSFVPSQSSSDVASSSTANVVSSSFSDIPPQ 393

Query Match
Best Local Similarity 18.
Matches 128; Conservative

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MSB2_YEASI

MSB2_YEASI

ID MSB2_Y

AC P32334

DT 01-OCT

DT 01-OCT

DT 01-OCT

DT 01-OCT

DT 01-OCT

CO Saccha

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                                                                                                                                  REPEAT
SEQUENCE
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REPEAT
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REPEAT
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01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MSB2 PROTEIN (MULTICOPY SUPPRESSION OF A BUDDING
MSB2 OR YGR014W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosome
reast 13:1077-1090(1997).
reast 13:1077-1090(1997).
reast 13:077-1090(1997).
reast 13:1077-1090(1997).
reast 13:1077-1090(1997).
reast 13:1077-1090(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M77354; AAA34798.1; -. EMBL; Z72799; CAA96997.1; -. PIR; S25370; S25370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97435481; PubMed=9290212;
Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
"Sequence analysis of 203 kilobases from Saccharomyces"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=92383951; PubMed=1514328.
Bender A., Pringle J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharon Saccharomycetales; Saccharomycetaceae; NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                               SGD; S0003246; MSB2.
Transmembrane; Glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome VII."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            defect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P32334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast 8:315-323(1992)
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                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                     Ä,
                                                                                                                                                                                          748
765
782
799
                              4.2%;
18.7%;
                                                                                                                                     133114 MW;
Score 202; DB 1;
Pred. No. 0.00057;
5; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                        Repeat.
7 x 17 AA TANDEM REPEATS.
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                                                                                                                                     67D5D984D5CA4A6D CRC64;
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(See http://www.isb-sib.
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Query Match
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Matches 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect.
                                                                                                                                         614
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hes 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ect. Immun. 60:159-165(1992).

FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR FUNCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European
                                                                                                                                                                                                                                                                                                                                                                                                                     NNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
   VGKGVNLYA-----
                                 NGKFTELRAAKNHTIFFYDPITSEGTSSDVLKINNGS----AGALNPYQG-----
                                                                                                   SATPKGGAISIDASGELSLSAETGNITFVRNTLTTTGSTDTP-----KRNAINIGS
                                                                                                                                       SIGTVVANTKTLA--QLNIGSSKTILNAGDVA-----INELVIENNGSVQ-LNHNTY
                                                                                                                                                                       TTGGAICNTKASGSPELIISNNKTLIFASNYAETSGGAIHAKKLALSSGGFTEFLRNNVS
                                                                                                                                                                                                           GGAIHFQANGGTIKLTNTQNNIVVNFDLDITTDKTGVVD---ASSLTNNQTLTING----
                                                                                                                                                                                                                                               GGAI----ATTAGARIAN--NTGYVRFLSNIASTSGGAIDDEGTSILSNNKFLYFEGNAAK
                                                                                                                                                                                                                                                                                 NALMNNNALAAGSTQLDGSATTTGDTGNGGVNAALQHTTLANDASKTLALDGANTTGANV
                                                                                                                                                                                                                                                                                                                                                 STDPNIAVTNINAIEAEGAGVV-ELSGIHIAELR----LGNGGSIFKLADGTVINGPVNQ
                                                                                                                                                                                                                                                                                                                                                                                   DSSPSTTVTT------GQGTLSSAGGVNLENIRKLVVAGN----FSTADGGAIKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVDVGLGGTTNFKTADSKVIITENSNFGSTNFGNLDTQIVVPDTKILKGNFIGDV----K 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVSSVLAFSCHLQSLANEELLSPDDSFN----GNIDSGTFTPKTSATTYSLTGDVFFYEP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M37647; AAA26390.1; ALT_INIT. AF161079; AAD42234.1; -. AJ235273; CAA15140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   ----NTAGVITENANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-layer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long as its content and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein of rickettsiae: identification of an avirulent mutant
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257
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                                                                     TINAANQGQIIVAADPLNTNTTLADGTNLGSAENPLSTIHFATKAANADSILN
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-NNITTNDANVGSLHFRSGGTSIVSGTVGGQQGHKLNNLILDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128;
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32 KDA BETA PEPTLDE.
V -> A (IN STRAIN BRE:
Y -> D (IN STRAIN BRE:
A -> S (IN STRAIN BRE:
A -> VC (IN REF: 1).
TTQEAPLTLGA -> INSRSS
T -> I (IN REF: 1).
Q -> L (IN REF: 1).
D -> G (IN REF: 2).
T -> S (IN REF: 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 208; DB 1;
Pred. No. 0.00036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDA SURFACE-EXPOSED PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERVE AS A MEMBRANE ANCHOR BACTERIUM IS COVERED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INSRSSSYHLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280;
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non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-slb.ch/announce/an email to license@isb-sib.ch).

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RESULT 12
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                                                                                           -!- SUBCELLULAR LOURINGS G-L-F-G REPEATS.
-!- SIMILARITY: BELONGS TO THE GLEG FAMILY OF NUCLEOPORINS.
                                                                                                                                                                                                                                            Rasmussen S.W.;
Rasmussen S.W.;
Region of yeast chromosome XI includes the "Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene, an open reading frame (ORF) possibly representing a nucleoside diphosphate kinase gene, tRNAs for His, Val and Trp in addition to seven ORFs with weak or no significant similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1995 (Rel. 34, Last annotation update)
NUCLEOPORIN NUP100/NSP100 (NUCLEAR PORE PROTEIN NUP100/NSP100).
NUP100 OR NSP100 OR YKL068W OR YKL336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N100_YEAST
Q02629;
                                                                           This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE=93054906; PubMed=1385442;
Wente S.R., Rout M.P., Blobel G.;
"A new family of yeast nuclear pore complex
J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1053
                                                                                                                                                                                                                       known proteins.";
Yeast 10:S69-S74(1994).
                                                                                                                                                                                                                                                                                                                                   MEDLINE=94378724; PubMed=8091863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
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Saccharomycetales;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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NUCLEOPORINS MAY BE INVOLVED IN BOTH BINDING AND TRANSLOCATION
THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.
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-SALVCN----TLWGVF-TDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGDENRK
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                                                                                                                                                                                                                                 Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding si-
the S-layer protein antigens of Rickettsia
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    Hackstadt
                                    MEDLINE=92104668;
                                                                                                                                                                                                                                                                                                                                                STRAIN-BREINL;
MEDLINE-92114896;
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Infect. Immun. 60:159-165(1992).
-i- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
-i- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
-i- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
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Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene e
surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
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"Mapping of monoclonal antibody binding sites on CNBr fragments
the S-layer protein antigens of Rickettsia typhi and Rickettsia
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live 81; Mismatches 223
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MEMBRANE ANCHOR (POTENTIAL).
H -> N (IN REF. 2).
V -> I (IN REF. 2).
G -> A (IN REF. 2).
G -> K (IN REF. 2).
MW; OCB5641C7EB185EE CRC64;
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            Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655;

MEDLINE=99426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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HYPOTHETICAL 98.4 KDA PROTEIN I
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SEQUENCE
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STRAIN-2787 (0126:H27);

MEDLINE-92326638; PubMed-1625582;

Benz I., Schmidt M.A.;

Benz I., Schmidt M.A.;

"AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli strain 2787 (0126:H27), is synthesized via a precursor molecule.";

MOI. Microbiol. 6:1539-1546(1992).

-I- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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LIFASNVAETSGGAIHAKKLALSSGGFTEFL---
                                                                                                                                                           LTGTSGDALFSNNSSSTKGGAIATT-----AGARIANNTGYVRFLSNIASTSGGA
                                                                                                                                                                                          ---GAQNILSEEGAISTHISSGGNQYISAGANATETI---VNSGGFQRVNSGAVATGTVL
                                                                                                                                                                                                                              LTFSGFSLLSFDSSPSTTVTTGQGTLSSAGGVNLENIRKLVVAGNFSTADGGAIKGASFL
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                                                                                                                                                                                                                                                                                                                                                                        NGNIDSG-----TFTPKTSATTYSLTGDVFFYEPG------KGTP
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                                                  IVSETTVNVSGTQNIYSGGSALSANIKGSQIVNSEGTAINTLVSDGGYQHIRNGGIASGT
                                                                                    IDDEGTSILSNNKFLYFEGNA--AKTTGGAICNTKASGSPELI-----ISN----NKT
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(Rel. 29, Last annotation
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Rickettsiaceae; NCBI\_TaxID=785; Bacteria;

Proteobacteria; alpha subdivision; aceae; Rickettsieae; Rickettsia.

Rickettsiales,

SEQUENCE FROM N.A.

RICTY

OMPB\_RICTY

STANDARD;

PRT;

1645 Ŗ

P96989;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
00TER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGE)

120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].

PROTEIN ANTIGEN)

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                                                                  NTQPESASVWMKITGGISSGK--LNDGQNKTTTNQFINQLGGDIYKFHAEQLGDFTLGIM 105
                                                                                                   ATLVMSPDSW-KIRGGNLSRQAFLLRGSNNY------VYNSNCELFGHYAMELR 912
                                                                                                                                       ESGTDNKGW---
                                                                                                                                                                        ESSSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDL---SGFFVSDVYRN---NPQST
                                                                                                                                                                                                           SGQSDIVYVNEDGSGGQTRDGINIISVEGNSDAEF----SLKNRVVAGAYDYTLQKG-N
                                                                                                                                                                                                                                              LPESEGSWSNECIAGG---IGLDLPFVLSNPHPLFKTFIPQMKVEMV----YVSQNSFF
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                                                                                                                                     "The Caulobacter crescentus paracrystalline S-layer protein is secreted by an ABC transporter (type I) secretion apparatus.";

J. Bacteriol. 180:3062-3069(1998).

-i- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBL OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.

-i- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.

-i- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
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01-JUN-1994 (Rel. 29, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
S-LAYER PROTEIN (PARACRYSTALLINE SURFACE LAYER PROTEIN).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gilchrist A., Fisher J.A., Smit J.K.; "Nucleotide sequence analysis of the gene encoding the crescentus paracrystalline surface layer protein."; Can. J. Microbiol. 38:193-202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98292737; Pu
Awram P., Smit J.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
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Fisher J.A., Smit J.K., Agabian N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-313 FROM N.A., AND STRAIN=ATCC 19089 / CB15;
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STRAIN-ATCC 19089 /
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Matches 169
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Cell wall; S-Layer; Calcium-binding.
INIT_MET 0 0
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   NRKGFRHTSGGYVIGGS----AHTPKDDLFT
                                                                                                                                     VD-ADVDTN----VDISSLIPVPAED--PNSEYGFQGQWNVNWTTDTATNTKEATATWTK 589
                                                                                                                                                                                                      VSLT-----AKG-----ASNKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKIT 536
                                                                                                                                                                                                                                         AFGGFETLRVAGAAAQG---SHNANGFTALQ----LGATAGATTFTNVAVNVGLTVLAAP
                                                                                                                                                                                                                                                                      SISGGKLLLQKGVTLESTSFSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQP 491
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                                                                     TGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGDE
                                                                                                      VNIAATDTNTTAHVDTLTLQATSAKSIVVTGNAGL----NLTNTGNTAVTSFDASAV---
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                                      TGTAPAVTFVSA----NTTVGEVVTIR------GGAGADSLTG
                                                                                                                                                                      TGTTTVTLANATGTSDVFNLTLSSSAALAAGTVALAGVE:
                                                                                                                                                                                                                                                                                                                                        YDPITSEGTSSDVLKINN---GSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPV 431
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-!- SIMILARITY: TO S. TYPHIMURIUM ORF NEAR CYSG (AC P25928)

-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CO
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                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makin K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Wada C., Yamamoto Y., Horiuchi T., Wada C., Sesherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92190338; PubMed=1665988; Moszer I., Glaser P., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corresponding to the 28.0 DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97251357; PubMed-9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                       Escherichia coli K–1
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"Multiple IS insertion sequences near the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 464-2003 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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 FAFCHLFA---RDKDCFIAHNNSRTYGGTL---
                                                                               GKLTVVSDSEVTSRQSNL-FDGSAEKTSGLVVIGDGNTV
                                                                                                         ---TATNTKEATATWTKTGFVPSPERKSALVC----NTLWGVFTDIRSLQQLVEIGATGM
                                                                                                                                                             YESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVPAE---DPNSEYGFQGQWNVNWTTD
                                                                                                                                                                                         --SLAGSMQVGDFSTGVDLNGNNNSVTLAAKDL--KVVGQKATGINVSGDANTVNITGNV
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D90778;
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AE000237; AAC74487.1; ALT_SEQ.
D90778; BAA15009.1; ALT_SEQ.
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EG11307; ydba.
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BAA18880.1; ALT_SEQ.
BAA18881.1; ALT_SEQ.
                           NMNGGLELIGEKNALADGSQVTSLRTGYSYTSVIVVSGESSVYLNGDTTIS
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21.4%;
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No. 3
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RESULT 5
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ID OMPB_RICJA
AC 006653;
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-EXT-2000 (Rel. 40, Last annotation update)
02TER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
03URFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
1CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
120 KDA, OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                                                                                                                                                                                                                         japonica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
STRUCTURAL PROTEIN WHICH MAY DIAY A ROLE AS A RICKETTSIAL
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                                                    (BY SIMILARITY).
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LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                              SIMILARITY).
FUNCTION: THE 32 KDA
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les 230; Conserv
                  --LFARDKDCFI---AHNNSRTYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREI
                                                                                                                                                                                                                                           LTIKSTYGNETAEGFSYPSYIYSGYDSYIADGQYIGDQNNIYGLGLGSDNGIIVNATTLY
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                                                              QVTFTTDYNNLGNIIATNTTINDGVTVTTGGIAAGGIAGTDFDGKITLGSVNGNANVRFA
                                                                                                       QGFWVSSMTNF--LHKTGDENRKGFRHTSGGYVIGGSAHTPKDDLFTFAFCH-----
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                                                                                                                                                   AGIGTINNNQ---GTVTLSGGVPNTP---
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Pred. No. 1.6e-05;
7; Mismatches 356
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MEDLING-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                  PRELIMINARY SEQUENCE OF 1-938 FROM N.A. MEDLINE-84272624; PubMed=6087316; Carlson J., Fuchs J.A., Messing J.;
                                                                                                                                                                                                                                                                    Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itch T., Kanai K., Kasai H. Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K. Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashinoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YFAL_ECOLI STANDARD; PRT; 1250 AA. P45508; P45507; P45506; P39441; P76468; P77487; 01-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) HYPOTHETICAL 131.2 KDA PROTEIN IN UBIG-NRDA INT
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Bacteria; Proteobacteria;
                                                                                                        "Primary structure of
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 three gene classes.
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88201664; pubMed=2834621;
Hussain K., Elliott E.J., Salmond
"The parD-mutant of Escherichia c
"The complete sequence of gyra,";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96032851; PubMed=7567469; Borodovsky M., McIninch J., Koonin
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MANY FRAMESHIFTS.
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; U30459;
; Y00544;
                     TDVIFSGNVAGGYGGAIYSSGTNDTGAVDLRVTNAMFRNNIANDGKGGAIYT-----IN
                                   RKLVVAGNFSTADGGAIKGASFLLTGTSG----DALFSNN-SSSTKGGAIATTAGARIAN
                                                                                   HAGAAASTTANKNLTFSGFSLLSFDSSPST----TVTTGQGTLSSAGGV-----NLENI 150
                                                                                                         PSMIASLFSANGVAAVTDSCQGYDVKASCQASRQSLSGITQDWSIADGQWLVFSDMTNNA
                                                                                                                            PKTSATTYSLTGDVFFYEPGKGTPLSDSC--FKQTTDNLT---FLGNGHSLTFGFIDAGT 100
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D90855; BAA16052.1; ALT_INIT.
D90854; BAA16050.1; ALT_INIT.
K02672; -; NOT_ANNOTATED_CDS.
U30459; AAA74094.1; -...
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EG12850; yfaL.
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o the EMBL/GenBank/DDBJ databases
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S -> Q (IN REF. 3).
AG -> SA (IN REF. 3).
A -> R (IN REF. 3).
E -> S (IN REF. 3).
V -> M (IN REF. 3).
PP -> AT (IN REF. 3).
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LRVIGG -> LLTSRC (IN REF. 4).
MW; 17F98C05E299FC95 CRC64;
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Pred.
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P15921;
01-APR-1990
                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                   Antigen; Repeat; Signal; SIGNAL 1 28
                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             repeated, near-identical sequences.";
Infect. Immun. 58:3760-3769(1990).
-i- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
-i- PTM: GLYCOSYLATED (POSSIBLE).
-i- DISEASE: PROBABLY PLAYS AN IMPORTANT ROLE IN AND IMMUNITY TO ROCKY MOUNTAIN SPOTTED FEVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seq
01-OCT-1994 (Rel. 30, Last ann
190 KDA ANTIGEN PRECURSOR (CEL
                                                        EMBL; M31227; AAA26380.1; PIR; A41477; A41477.
                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                        Anderson B.E., McDonald G.A., Jones D.C., Re
"A protective protein antigen of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90354033; PubMed=2117568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                               Chlamydia trachomatis.
Bacteria; Chlamydiales;
                                                                                                                 PUTATIVE OUTER MEMBRANE PROTEIN F
PMPF OR CT870.
 STRAIN=D/UW-3/CX;
MEDLINE=99000809;
                 SEQUENCE FROM N.A. STRAIN=D/UW-3/CX;
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Comanducci M., Christianen
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SLAP_CAUCR
AIDA_ECOLI
OMPB_RICTY
YPJA_ECOLI
TROP_HUMAN
NUP1_YEAST
HLYA_SERMA
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8%; Score 610.5; 1%; Pred. No. 2.: 146; Mismatches PGKGTPLSDSCFKQTTDITHNLTNCYLDI ANKNLTFSGFSLLSFDS:                       FAKNLTPESGGAIGYASI NLENIRKLVVAG : :	of Bioinform Institute. I Institute. I Institute. I Itions as long is not remove agreement (se isb-sib.ch)	C.J., Fan J. C.J., Fan J. ov R.L., Zhao intracellular ALL SURFACE (	96 upd on u RECU	CCLOCL YEAST YEAST RAT YEAST HUMAN HUMAN HAEIN HAEIN HAEIN HAEIN HAIN HAEIN HAEIN
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5; DB 1; Length 2.5e-27; hes 360; Indels TDNLTFLGNGHSLTFGFI    :: LDNLRYILAIL DSSPSTTVTG         ASPNSPTVEIRDTIGPVI ASPNSPTVEIRDTIGPVI	tics and the control of the control	J., Ma hao Q., lar pat	4 AA. late) pdate) RSOR. Chlamydia	
Leng Inde GHSLTFLTTGTTGTTG GGAIKG GGAIKG	and the end th	, Marathe Q., Kooni pathogen	•	
8%; Score 610.5; DB 1; Length 964; 1%; pred. No. 2.5e-27; 146; Mismatches 360; Indels 211; G PGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGA :	res the rest rest rest rest rest rest rest res	athe R., Koonin E Koonin E Ogen of		P3805; P4968; P3904, P3979; P3975; P3975; P3975; P4538; P4538; P4538; P4537771;
964; 211; IDAGTHA: : LOKTPNE IFENNTC SFLLTGT: : ::: TFVVSEN		4 N H		0000004000000
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A;Cross-references: GB:AE001586; GB:AE001363; NID:g4376263; PIDN:AAD18172.1; PID:g4376278, Experimental source: strain CWLO29 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255 A;Accession: G81541
                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-841 <REA>
A;Cross-references: GB:AE002235; GB:AE002161; NID:g7189672; PIDN:AAF38561.1; PID:g718967
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: pmp_2; CP0761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymorphic membrane protein G family CP0761 [imported] - Chlamydophila pneumoniae (stra C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: E72130; G81541
C:Accession: E72130; G81541
R:Kalman, S:: Mitchell, W.: Marathe, R.: Lammel, C.: Fan, J.: Olinger, L.: Grimwood, J.:
Nature Genet. 21, 385-389, 1999
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A;Accession: E72130
A;Molecule type: DNA
A;Residues: 1-841 <ARN>
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Best Local Similarity
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112 KNLTFSGFSLLSFDSSPSTTVTTGQGTLSSAGGVNLENIRKLVVAGNFSTADGGAIKGAS 171
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                                              KDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSEAAN 120
                                                                                    TGDVFFYE-PCKGTPLSDSCFKQ--TTDNLTFLGNGHSLTFGFIDAGTHAGAA-ASTTAN 111
                                                                                                                                          MKIPLRFLLISLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVF 60
                                                                                                                                                                                          MKTSIPWVLVSSYLAFS-CHLQSLANEELLSPDDSFNGNIDSGTFTPKTSA----TTYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSNPDCTTTLRISGDSWKTFGTNLARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNY 762
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                                                                                                                                                                                                                                             Conservative 147;
                                                                                                                                                                                                                                        30.0%; Score 1435.5; DB 2; Length 841; 35.9%; Pred. No. 1.5e-73; tive 147; Mismatches 335; Indels 125;
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B	121	TYTLSGESALSELKSPASTVINGLGAINVKGNLSLLINDXVILTONDSSTGEGGAING 190
Qy	172	
рь	181	180
Qy	232	LSNNKFLYFEGNAAKTTGGAICNTKASGSPELLISNNKTLIFASNVAETSGGAIHAKKLA 291
DЬ	181	SLKIANNKSLSFIGNSSSTRGGAIHTKNLT 210
Qy	292	LSSGGFTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTTTGSTDTPKRN 351
Db	211	LSSGGETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATGTVSHS 267
Qy	352	NHTIFFYDPITSE
Db	268	AIDLGTSAKITALRAAQGHTIYFYDPITVTGSTSVADALNINSPDTGDNKBYTGTIVFSG 327
Qy	410	ETLTADELKVADNIKSSFTQPVSLSGGKLLLQKGVTLESTSFSQEAGSILGMDSGTTLST 469
Db	328	EKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDLGTSLVA 387
VΩ	470	TAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHMFSHDQL 529
Дb	388	NTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDESFYQNGFLNEDHS 447
Qγ	530	F-SLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTATNTKEATATWT 588
Db	448	YDGILELDAGKDIVISADSRSIDAVQSPYGYQGKWTINWSTDDKKATVSWA 498
Qy	589	KTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGD 648
Δp	499	KQSFNPTAEQEAPLVPNLLWGSFIDVRSFQNFIELGTEGAPYEKRFWVAGISNVLHRSGR 558
Qy	649	ENRKGFRHTSGGYVIGGSAHTPKDDLETFAFCHLFARDKDCFIAHNNSRTYGGTLFFKHS 708
Db	559	ENQRKFRHVSGGAVVGASTRMPGGDTLSLGFAQLFARDKDYFMNTNFAKTYAGSLRLQHD 618
Qy	709	HTLQPQNYLRLGRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLP 761
Дβ	619	ASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGQLSYGHTDHRMKTESLPPPPPPTLS 676
Qy	762	ESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGFS 821
D	677	TDHTSWGGYVWAGELGTRVAVENTSGRGFFQEYTPFVKVQAVYARQDSFVELGAISRDFS 736
Qy	822	IGRILNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGN 881
Дδ	737	DSHLYNLAIPLGIK-LEKRFAEQY-YHVVAMYSPDVCRSNPKCTTTLLSNQGSWKTKGSN 794
Qy	882	LSRQAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF 928
В	795	LARQAGIVQASGFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF 841

Job time: 1295 sec 2 2001, 03:28:38

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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; H. C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Sa Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae A;Reference number: A81500; MUID:20150255
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C; Date: 31-Mar-2000
C; Accession: B81591
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A; Residues: 1-936 < REA>
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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A;Experimental source: strain AR39, HL cells
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Best Local Similarity 39.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLSRQAFILIRGSNNYYYNSNCELFGHYAMEIRGSSRNYNVDVGTKLRF
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NLARQGFSVRAANHFQVNPHMEIFGQFAFEVRSSSRNYNTNLGSKECF
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                                                                                                                                                                                                                                                                                                                                                                                                        AKKLALSSGGFTEFLRNNVSSATP---KGGAISIDASGELSLSAETGNITFVRNTLTTTG
DSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYES
                                                                                                                                                                                                                      QGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTLESTSFSQEAGSLLGM 461
                                                                                                                                                                                                                                                                                                                                                                                     GLKYSISAGGPTLF-QSNISGSSAGQGGGGAINIASAGELALSATSGDITF-NNNQVTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLSGTSQFASFSRNQAFTGKQGGVVYATGTITIENSPGIVSFSQNLAKGSGGALYSTDNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTFSGFSLLSFDSSPSTTVT-TGQGTLSSAGGVNLENIRKLVVAGNFSTADGGAIKGASF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSDVSFQNAGALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSSAGTVASTSAADKN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGDVFFYEPGK-GTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTT-ANKN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKSSVSWLFFSSIPLFSSLYAAEVTLDSSNNSYDGS-NGTTFTVFSTTDAAAGTTYSL
                                                             HNLKSASTYPLLELTT-AGANGTITLGALSTLTLQEPETHYGYQGNWQLSWA--NATSSK 590
                                                                                                                                          DGGTTLSAKEANLSLNGLAVNLSSLDGTNKAALKTEAADKNISLSGTIALIDTEGSFYEN
                                                                                                 HMFSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTATNTK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1733; DB 2;
Pred. No. 2.6e-90;
92; Mismatches 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 936;
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A;Cross-references: GB:BA000008; NID:g8978389; A;Experimental source: strain J138 C;Genetics:
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pa;Reference number: A86491; MUID:20330349
A;Accession: H86492
A;Status: preliminary
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change
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A; Residues: 1-772 <STO>
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NKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNS : :|| : | : : : | | : :: | |
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                                                                                                                                STTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGGTLSL
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                                                                          Ouchi, K.;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-936 <STO>
A;Cross-references: GB:BA000008; NID:g8978817;
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_7
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NKSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMAYGT
                                                     SIIKGSWRNDAFCADLGASLPFVISVPY-LLKEVEPFVKVQYIYAHQQDFYERYAEGRAF
                                                                                PESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGF
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                                                                                                                                                                                                                                                                                           HMFSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTATNTK
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polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: D72078
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grim Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Accession: D72078
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A;Molecule type: DNA
A;Residues: 1-930 <ARN>
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                                                                             SFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTS
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ILSNNKFLYFEGNAAKTT---GGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHA
                                                         TLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQLVFMNNKGETGGGALGFEASS
                                                                                                                           LTFTGFSNLSFIAAPGTTVASGKSTLSSAGALNLTDNGTILFSQNVSNEANNNGGAITTK 178
                                                                                                                                                 LTFSGFSLLSFDSSPSTTVTTGQGTLSSAGGVNLENIRKLVVAGNFSTA---DGGAIKGA 170
                                                                                                                                                                                                                                SLTGDVFFYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKN 113
                                                                                                                                                                                                                                                                     MKIPLHKLLISSTLYTPI-LLSIATYGADASLSPTDSFDG-AGGSTFTPKSTADANGTNY
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                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                         36.8%; Score 1761; DB 2;
41.7%; Pred. No. 6.7e-92;
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polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C;Accession: C72078 C;Accession: C72078 R;Kalman, S; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grim Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                           RESULT
C72078
                                                   A;Title: Comparative genomes of Clamydia pneumoniae A;Reference number: A72000; MUID:99206606 A;Accession: C72078
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A; Molecule type: DNA
A; Residues: 1-936 <ARN>
                                     A; Status: preliminary
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A;Cross-references: GB:AE001627; GB:AE001363; NID:g4376721; PIDN:AAD18589.1; PID:g437 A;Experimental source: strain CWLO29 C;Genetics: A;Gene: pmp\_7 Grimwood CWL029

Ş Best Local Similarity Matches 378; Conserv Query Match Best Local : MKTSIPWVLVSSYLAFSCHLQSLANEELLSPDDSFNGNIDSGTF----TPKTSATTYSL Conservative 36.3%; 182; Score 1734; DB 2; Pred. No. 2.3e-90; B2; Mismatches 356 356; 2; Length 936; Indels 32; Gaps 55

18;

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polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae (str: C:Species: Chlamydophila pneumoniae, Chlamydda pneumoniae (;)Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C:Accession: D86546
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Accession: D86546
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-930 <STO>
A;Cross-references: GB:BA000008; NID:g8978818; PIDN:BAA98654.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_8
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   LQHRAFLG--
                             FKHSHTLQPQNYLRLGRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLPESE 764
                                                            KDKSGTNQAFRHKSYGYIVGGSAEDFSENIFSVAFCQLFGKDKDLFIVENTSHNYLASLY
                                                                              MTWVTTGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGLWASGTANFFH
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-GLPMPSFGSITDMLKDIPLILNAQLSYSYTKNDMDTRYTSYPEAQ
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Pred. No. 5.2e-92;
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Local Similarity 41.7%; Pages 394; Conservative 165;

1 MKTSIPWVLVSSVLAFSCHLQSLAN---EELLSPDDSFNGNIDSGTFTPKTSA----TTY

Mismatches

Indels

30;

Gaps

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MKIPLHKLLISSTLVTPI-LLSIATYGADASLSPTDSEDG-AGGSTFTPKSTADANGTNY

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TPKRNAINIGSNGKFTELRAAKNHTIFFYDPITSEGT-SSDVLKINNGSAGALNPYQGTI 405

TSTRNAIYLGSSAKITNLRAAQGQSIYFYDPIASNTTGASDVLTINQPDSNSPLDYSGTI

417

KKLALSSGGFTEFLRNNV-SSATPKGGAISIDASGELSLSAETGNITFVRNTLTTTGSTD

HGLDLSAAGPTLFSNNRCGNTAAGKGGATATADSGSLSLSANQGDITFLGNTLTST-SAP

357 346 298

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SFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTS

LTETGESNUSEIAAPGTTVASGKSTLSSAGALNLTDNGTILFSQNVSNEANNNGGAITAK LTFSGFSLLSFDSSPSTTVTTGQGTLSSAGGVNLENIRKLVVAGNFSTA---DGGAIKGA 170

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VLSGNVYINDAGKGTALTGCCFTETTGDLTFTGKGYSFSFNTVDAGSNAGAAASTTADKA 118 SLTGDVFFYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKN 113

ILSNNKELYFEGNAAKTT----GGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHA

SITQNSSLFFSGNTATDAAGKGGAIYCEKTGETPTLTISGNKSLTFAENSSVTQGGAICA

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VFSGEKLSADEAKAADNFTSILKQPLALASGTLALKGNVELDVNGFTQTEGSTLLMQPGT LFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTLESTSFSQEAGSLLGMDSGT 465

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polymorphic membrane protein G family CP0307 [imported] - Chlamydophila pneumoniae (s C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: A81591
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81591
A;Accession: A81591
A;Accession: A81591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-930 <REA>
A;Residues: 1-930 <REA>
A;Cross-references: GB:AE002193; GB:AE002161; NID:g7189234; PIDN:AAF38164.1; PID:g718
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0307
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                      36.9%; Score 1763; 41.7%; Pred. No. 5.
DB 2;
5.2e-92;
nes 355;
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Query Match Best Local S Matches 385

Local Similarity les 385; Conser

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37.3%; Score 1785; DB 2; 40.4%; Pred. No. 2.9e-93; tive 173; Mismatches 344.

Length 928; Indels

52;

Gaps

18;

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A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-928 <REA>
A;Cross-references: GB:AE002192; GB:AE002161;
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0303
                                                                                                        R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Nucleic Acids Res. 28, 1397-1406, 200 t A;Title: Genome sequences of Chlamydia trachomatis A;Reference number: A81500; MUID:20150255 A;Accession: G81591
                                                                                                                                                                    C;Species: Chlamydophila pneumoniae, Ch
C;Date: 31-Mar-2000 #sequence_revision
C;Accession: G81591
R;Read, T.D.; Brunham, R.C.; Shen, C.;
C.; Dodson, R.; Gwinn, M.; Nelson, W.
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-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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Воу, R.;
                                              NID:g7189226;
                                                                                                                                                                    Heidelberg, J.F.; White, O.
; Kolonay, J.; McClarty, G.;
                                                                                                                                       MoPn and Chlamydia pneumoniae
                                              PIDN: AAF38160.1;
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                                                                                                                                                                                                                                                                                                            TATLAWTNTGYLPNPERQGPLVPNSLWGSFSDIQAIQGVIERSALTLCSDRGFWAAGVAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLALSS--GGFTEFLRNNVSSATP-KGGAISIDASGELSLSAETGNITFVRNTLTTTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTSGDALFSNNSSST---KGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKTSIPWVLVSSVLA--FSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTSAT--TYSLT
                            WKIRGGNLSROAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF 928
                                                            TEGRSFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPDLIRNDPKCTTALVISGAS
                                                                                                                                                   SLPESEGSWSNECIAGGIGLDLPFVLSNPHP----LFKTFIPQMKVEMVYVSQNSFFESS
                                                                                                                                                                                   AFYIQHITEC-----SGFIGCLLDKLPGSWSHKPLVLEGQLAYSHVSNDLKTKYT
                                                                                                                                                                                                                                                                           FLHKTGDENRKGERHTSGGYVIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNNSRTYGG
                                                                                                                                                                                                                                                                                                                                         EATATWTKTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTN
                                                                                                                                                                                                                                                                                                                                                                    {\tt LGKTQDFSFVQLSA-LGTATTTDVPA---VPTVATPTHYGYQGTWGMTWVDDTASTPKTK}
                                                                                                                                                                                                                                                                                                                                                                                       FSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTAT--NTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTPKRNAINIGSNGKFTELRAAKNHTIFFYDPITSE--GTSSDVLKINNGSAGALNPYQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITGNTSLVFSENSVTATAGNGGAL-----SGDADVTISGNQSVTFSGNQAVANGGAIYAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDITLONLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNIKSSAE-GAALSVTTDKNLSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSNNKFLYFEGNAAKTT----GGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHAK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDVFFYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTF
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Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and A;Accession: B81592

A;Accession: B81592

A;Residues: 1-928 <REA>

A;Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; 1

A;Scenetics: DND_9; CP0306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000; MUID:99206606
A;Accession: B72077
A;Molecule type: DNA
A;Residues: 1-928 <ARN>
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                                                                                                                                                                              LSNNKFLYFEGN---AAKTTGGAI-CNTKASGSPELIISNNKTLIFASNVAETSGGAIHA
                                                                                                                                                                                                                                                               FLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSI
QTTTRNSINIGNTNAKIVQLRASQGNTIYFYDPITTSITAALSDALNLNGPDLAGNPAYQ
                                                                                                                  KKLALSSGGFTEFLRNN-VSSATPKGGAISIDASGELSLSAETGNITFVRNTLTT-TGST
                                                                                                                                                                                                                                      ISLS-LNPNLTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAANNGGAIYTEASSF
                                                                                                                                                                                                                                                                                                                                              KNLTFSGFSLLSFDSSPSTTVTTGQGTLSSAGGVNLENIRKLVVAGNFSTADGGAIKGAS
                                                                                                                                                                                                                                                                                                                                                                                                IYNLTGDYSITNAGSPTALTASCEKETTGNLSFQGHGYQFLLQNIDAGANC-TETNTAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKTSIPWVLVSSVLAFSCHLQ----SLANEELLSPDDSFNGNIDSGTFTP-----KTSAT
                                   DTPKRNAINIG-SNGKFTELRAAKNHTIFFYDPITSEGTS--SDVLKINNGSAGALNPYQ
                                                                            DNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLSALGGDITFEGNTVVKGASSS
                                                                                                                                                         ISSNKAISFINNSVTATSATGGAIYCSSTSAPKPVLTLSDNGELNFIGNTAITSGGAIYT
                                                                                                                                                                                                                                                                                                                   KLLSFSGFSYLSL--IQTTNATTGTGAIKSTGACSIQSNYSCYFGQNFSNDNGGALQGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.5%; Score 1794; DB 2; 42.7%; Pred. No. 9.1e-94;
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A; Experimental : C; Genetics: A; Gene: pmp_10
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A, Tille: Comparison of whole genome sequences of chlamydia p. A; Reference number: A86491; MUID:20330349
A, Rocession: G86546
A, Status: preliminary
A, Molecule type: NNA
                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-928 <STO>
A;Cross references: GB:BA000008; NID:g8978821; PIDN:BAA98657.1; GSPDB:GN00142
A;Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: G86546 R;Shirai, M; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, R;Shirai, M; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba,
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                                     57
                                                                                                                                                  Match 37.3%; Score 1785; DB 2; Local Similarity 40.4%; Pred. No. 2.9e-93; Nes 385; Conservative 173; Mismatches 344
                                                                                             1 MKTSIPWVLVSSVLA--FSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTSAT--TYSLT
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                   GDVFFYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTF 116
                                                                           MKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNTTTGIDYTLT
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                                                                                                                                                                                                                                  YVIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNNSRTYGGTLFFKHSHTLQPQNYLRLG
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                                                                                                      IGDSYTYDLSGFFVSDYYRNNPQSTATLVMSPDSWKIRGGNLSRQAFLLRGSNNYYYNSN
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Pred. No. 9.7e-263;
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C;Species: Chlamydophila pneumoniae, Chlamydia pn C;Date: 02-Mar-2001 #sequence_revision 02-Mar-200 C;Accession: E86546 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of A;Reference number: A86491; MUID:20330349 A;Accession: E86546 A;Status: preliminary
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A;Residues: 1-928 <TO>
A;Cross-references: GB:BA000008; NID:g8978819;
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_9
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:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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                              LFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLPE
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EQPVLFDAQISYIYSKNTMKTYYTQAPK
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polymorphic outer membrane protein g family - Chlamydophila pneumoniae (str C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C; Accession: D72077
R; Kalman, S; Mitchell, W; Marathe, R; Lammel, C; Fan, J; Olinger, L.;
Nature Genet: 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Reference number: A72000; MUID:99206606
A; Accession: D72077
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-928 < ARN>
A; Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:AAD18593.1
A; Experimental source: strain CWL029
C; Genetics:
A; Gene: pmp_11
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RESULT 3
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P01ymorphic membrane protein G family CP0302 [imported] - Chlamydophila pneumoniae (S F801591
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000
C;Accession: F81591
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81500; MUID:20150255
A;Reference number: A81500; MUID:20150255
A;Recssion: F81591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-949 <REA>
A;Cross references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38159.1; PID:g718
A;Cross references: Strain AR39, HL cells
C;Genetics:
A;Gene: CP0302 ; Hicke Salzbe

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PID:9718

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C;Accession: H86546
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A;Fitle: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Accession: H86546
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <570>
A;Cross-references: GB:BA000008; NID:g8978822; PIDN:BAA98658.1; GSPDB:GN00142
A;Cross-references: GB:BA000008; NID:g8978822; PIDN:BAA98658.1; GSPDB:GN00142 polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001 δÃ 밁 ğ 밁 Q Вр Š 밁 Qy 밁 δÃ 밁 δÃ A; Gene: Query Match Best Local Similarity Matches 928; Conserv 361 301 301 241 241 181 181 61 : pmp\_11 61 ۲ ш LRNNYSSATPKGGAISIDASGELSLSAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK FTELRAAKNHTIFFYDPITSEGTSSDYLKINNGSAGALNPYQGTILFSGETLTADELKVA ALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSILSNNKFLYF FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFS 120 MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTSATTYSLTGDVF 60 FTELRAAKNHTIFFYDPITSEGTSSDVLKINNGSAGALNPYQGTILFSGETLTADELKVA FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFS MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTSATTYSLTGDVF Conservative 100.0%; 0; Score 4782; DB 2; Pred. No. 9.4e-263; D; Mismatches 0; Length Indels 928; 0 Gaps 360 360 300 240 60 300 240 120 0

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                                                                                  InterPro;
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TIGR; CP0761; T.
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.,
McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
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[2]
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Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMP7 OR PMP_2 OR CP0761.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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Nucleic Acids Res. 28:1397-1406(2000).
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LARQAGIVQASGFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF
                               LSRQAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF
                                                              DSHLYNLAIPLGIK-LEKRFAEQY-YHVVAMYSPDVCRSNPKCTTTLLSNQGSWKTKGSN
                                                                             IGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGN
                                                                                                                             TDHTSWGGYVWAGELGTRVAVENTSGRGFFQEYTPFVKVQAVYARQDSFVELGAISRDFS
                                                                                                                                               ESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGFS
                                                                                                                                                                                          ASLYSVVSILLGEGGLREILLPYVSKTLPCSFYGQLSYGHTDHRMKTE--SLPPPPPTLS
                                                                                                                                                                                                                       HTLQPQNYLRLGRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLP-----
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P71132;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence upon-
01-MAR-2001 (TrEMBLrel. 16, Last annotation upomp91A.
Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiaceaeae; Chlamydiaceaeae; Chlamydiaceaeae; Chlamydiaceaeae; Chlamydiaceaeae; Chlamydiaceaeae; 
SEQUENCE FROM N.A.
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EMBL: U65942: AAC15921.1; -
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InterPro; IPR003368; -.
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 SGLGNFLHKSGSDTKRKFRHNSAGYALGVYAQTPSEDVFSAAFCQLFGKDKDYLVSKNSS
                                                             SAQEKTATLTWEQTGYSPNPERQGSLVPNTLWGSFSDIRAIQNLMDISVNGADYHRGFWV
                                                                             ATNIKEATATWIKTGFVPSPERKSALVCNILWGVFIDIRSLQQLVEIGATGMEHKQGFWV
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                                                                                                                           PILAASQPFTAIEVRSGS-----SGSITKPTTNLENYTPPTHYGYQGNWTVTWKQGS
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-OVINE ENZOOTIC ABORTION ISOLATE S26/3; Longbottom D., Russell M., Jones G.E., Lainson F.A., Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databas
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NCBI_TaxID=83554;
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FLHKTGDENRKGFRHTSGGYVIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNNSRTYGG
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                                                                                                  DQLFSLLKITVDADVDTNVDISSLIPVPAED----PNSEYGFQGQWNVNWTTDTATNTK
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                        -ATLTWEQTGYSPNPERQGPLVPNTLWGAFSDLRAIQNLMDISVNGADYHRGFWVSGLAN
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37.7%;
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Pred. No. 3.1
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P71133;
01-FEB-1997 (TrEMBLrel. (
01-FEB-1997 (TrEMBLrel. (
01-MAR-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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"Identification of a multigene family coding for the 90 kDa proteins
of the ovine abortion subtype of Chlamydia psittaci.";
FEMS Microbiol. Lett. 142:277-281(1996).
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Bacteria; Chlamydiales; Chlamydiaceae; Chla
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-OVINE ENZOOTIC ABORTION ISOLATE S26/3; MEDLINE-96406378; Pubmed-8810511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02385; OMP;
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EMBL; U65943; AAC15923.1; -.
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MEDLINE=20303049; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouc. Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumonia."
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
REMBL; AP002545; BAA90226.1; -.
REINTEPTO; IPR003357; -.
RINTEPTO; IPR003358; -.
RINTEPTO; IPR003368; -.
RPfam; PF02385; OMP; I.
RPfam; PF02415; DUF145; 1.
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Q9RB71;
01-MAY-2000
01-OCT-2000
01-MAR-2001
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                STRAIN-J138;
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(TrEMBLrel. 16, Last annotation
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             SIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGG
                                          GAIVFSGEKLSPTEKAIAANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQSPGSRILM
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NKSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMAYGT
                                                                 PESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGF
                                                                                         SIYFHHTEGLFDIANFL-WGKATRAPWYLSEISQIIPLSFDAKFSYLHTDNHMKTYYTDN
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Q1-OCT-2000 (TrEMBLrel. 16, IC)
Q1-MAR-2001 (TrEMBLrel. 16, IC)
POLYMORPHIC OUTER MEMBRANE PREPROTEIN G FAMILY).

PMP_7 OR CP0308.
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InterPro; IPR003357; -.
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Pfam; PF02415; DUF145; 1.
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heide, White O., Hickey E.K., Peterson J., Umayam L.A., UT Berry K., Bass S., Linher K., Weidman J., Khouri H. Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R. McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and pneumoniae AR39.";

Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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EMBL; AE002193; AAF38165.1;
TIGR; CP0308;
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                                           LLSGTSQFASFSRNQAFTGKQGGVVYATGTITIENSPGIVSFSQNLAKGSGGALYSTDNC
                                                                     LLTGTSGDALFSNNSSST--KGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTS
                                                                                                   LLFNDFSRLSIISCPSLLLSPTGQCALKSVGNLSLTGNSQIIFTQNFSSDNGGVINTKNF
                                                                                                                              LTFSGFSLLSFDSSPSTTVT-TGQGTLSSAGGVNLENIRKLVVAGNFSTADGGAIKGASF
                                                                                                                                                           LSDVSFQNAGALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSSAGTVASTSAADKN
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Best Local Similarity 40.0
Matches 376; Conservative
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086163;
01-NOV-1998
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Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelur
Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelur
"Identification of two novel genes encoding outer membrane or
associated surface layer proteins in Chlamydia pneumoniae.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001311; CAA04671.1; -.
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Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydoj
NCBI_TaxID=83558;
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InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
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TGFSSLTFLAAPSSVITTPSGKGAVKCGGDLTFDNNGTILFKQDYCEENGGAISTKNLSL
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914 AA;
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(TIEMBLIEL 08, Last sequence update)
(TIEMBLIEL 16, Last annotation updat
ANE PROTEIN 5 PRECURSOR (FRAGMENT).
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95603
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40.0%; Pred. No. 1.3e-94;
tive 171; Mismatches 341
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Q9Z898;
Q1-MAY-1999
01-MAY-1999
01-MAR-2001
MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fa
Olinger L., Grimwood J., Davis R.W., Stephens R.S
"Comparative genomes of Chiamydia pneumoniae and
                                                                                                    Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                               PMP_7
                                                      STRAIN-CWL029
                                                                 SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=83558;
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Hyman R.W.,

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O9Z393 PRELIMINARY; PRT; 930 AA.
09Z393; PTEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
OUTER MEMBRANE PROTEIN 11 PRECURSOR.
OMP11 OR PMP_8.
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                                                                                                                                                                                            QAFLASAGSHLTLSPHVELSGEAAYELRGSAHIYNVDCGLRYSF
                                                                                                                                                                                                                             QAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF
                                                                                                                                                                                                                                                                                  LLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGNLSR
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003357; -.
InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
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                  HDQLFSL-LKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTATNTKEAT
                                                    KLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTITLTSPLVFQDSSGNFYESHTI-
                                                                                TLSTTAGSITITULGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHMFS
                                                                                                                        VFSGEKLSADEAKAADNFTSILKQPLALASGTLALKGNVELDVNGFTQTEGSTLLMQPGT
                                                                                                                                         LFSGETUTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTLESTSFSQEAGSLLGMDSGT
                                                                                                                                                                                          TSTRNAIYLGSSAKITNLRAAQGQSIYFYDPIASNTTGASDVLTINQPDSNSPLDYSGTI
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OUTER MEMBRANE PROTEIN
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A Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

A White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,

A White N., Holsey E.K., Peterson J., Khouri H., Craven B.,

A Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,

A Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.,

A McClarty G., Salzberg S.L., Elsen J., Fraser C.M.;

"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia

"T pneumoniae AR39.";

"L Nucleic Acids Res. 28:1397-1406(2000).

EMBL; AP0075246; BAA98657.1; -.

EMBL; AP0075246; BAA938160.1; -.

EMBL; AE003192; AAF38160.1; -.

EMBL; AE003193; -.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Chlamydia proteins containing the GGAI-repeat belong to of autotransporting pathogenicity factors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hjerno K., Boesen T., Daugaard L.,
Christiansen G., Birkelund S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02385; OMP;
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                                                                                                                                                                                    TILFSGETLTADELKVADNIKSSFTQPVSLSGGKLLLQKGVTLESTSFSQEAGSLLGMDS
                                                                                                                   GTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHM
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                                                                                                                                                                                                                                                       DTPKRNAINIGSNGKFTELRAAKNHTIFFYDPITSE--GTSSDVLKINNGSAGALNPYQG
                                                                                                                                                                   SIVFSGEKLSEDEAKVADNLTSTLKQPVTLTAGNLVLKRGVTLDTKGFTQTAGSSVIMDA
                                                                                                                                                                                                                                                                                                                    KLALSS--GGFTEFLRNNVSSATP-KGGAISIDASGELSLSAETGNITFVRNTLTTTGST
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 EATATWTKTGFVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTN
                                LGKTQDFSFVQLSA-LGTATTTDVPA----VPTVATPTHYGYQGTWGMTWVDDTASTPKTK
                                                                FSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTAT--NTK
                                                                                                  GTTLKASTEEYTLTGLSIPVDSLGEGKKVVIAASAASKNVALSGPILLLDNQGNAYENHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                 KNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPTLFSNNIAEAAGGAINSTGNCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGFSLLSFDSSPSTTVTT--GQGTLSSAGGVNLENIRKLVVAGNFSTADGGAIKGASFLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 928 AA;
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MKTSIPWVLVSSVLAFSCHLQSLAN---EELLSPDDSFNGNIDSGTFTPKTSA---

Query Match Best Local Matches

Similarity

Conservative 165;

Pred.

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30;

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-TTY 53 Gaps

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                                                                                                                                                                      Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                       "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AP000546; BAA98654.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Shiba T., Tohole genome sequences of Chlamydia pneum from Japan and CWL029 from USA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae (Chlamydophila pneumoniae). Bacteria; Chlamydiales; Chlamydiaceae; Chlamydop
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2010 (TrEMBLrel. 16, Last annotation update)
POLYMORPHIC OUTER MEMBRANE PROTEIN G FAMILY (POLYMORPHIC MEMBRANE
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20330349; PubMed=10871362;
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InterPro; IPR003368; -.
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CP0307; -.
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|: ||:||| :| ::| :: |: |:||:|||| ||:||
| WETYANNLARQALQVRAGSHYAFSPMFEVLGQFVFEVRGSSRIYNVDLGGKFQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLPESEGSWSNECIAGGIGLDLPFVLSNPHP----LFKTFIPQMKVEMVYVSQNSFFESS
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PF02415;
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                                                                                                                                            ; OMP; 1.
; DUF145; 1.
O AA; 97639 MW;
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                                36.9%;
41.7%;
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                             Score 1763;
Pred. No. 5
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ore 1763; DB 2;
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Mismatches 355;
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Christiansen G., Birkelung s.;
"Chlamydia proteins containing the GGAI-repeat
of autotransporting pathogenicity factors.";
cubmitted (JAN-1999) to the EMBL/GenBank/DDBJ c
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                                                                                                                                                                                                                                                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20150255; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill
White O., Hickey E.K., Peterson J., Uma
Berry K., Bass S., Linher K., Weidman J
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Shirai M., Hirakawa H., Kimoto M., Tabu
Shiba T., Ishii K., Hattori M., Kuhara
                                                                                                                                                                                                                                                                                                                                        Ptam;
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                                                                          KNLTFSGFSLLSFDSSPSTTVTTGQGTLSSAGGVNLENIRKLVVAGNFSTADGGAIKGAS
                                                                                                                       TYSLTGDVFFYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTAN
                                                                                                                                                                            MKTSIPWVLVSSVLAFSCHLQ----SLANEELLSPDDSFNGNIDSGTFTP-----KTSAT
                         FLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASTSGGAIDDEGTSI
                                                     KLLSFSGFSYLSL--IQTTNATTGTGAIKSTGACSIQSNYSCYFGQNFSNDNGGALQGSS
                                                                                                       IYNLTGDVSITNAGSPTALTASCFKETTGNLSFQGHGYQFLLQNIDAGANC-TFTNTAAN
                                                                                                                                                           MKSSLHWFLISSSIALPLSLNFSAFAAVVEINLGPTNSFSG---PGTYTPPAQTTNADGT
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CP0306; -.
ISLS-LNPNLTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAANNGGAIYTEASSF
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AJ133034; CAB37069.1;
AP002546; BAA98655.1;
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2385; OMP;
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en G., Birkelund S.;
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Q9R865; Q9R864; Q9S6P2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
POLYMORPHIC OUTER MEMBRANE PROTEIN G FAMILY (OUTER I
PRECURSOR) (POLYMORPHIC MEMBRANE PROTEIN G FAMILY).
PMP_10 OR OMP5 OR CP0303.
                                      Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kish
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa
"Comparison of whole genome sequences of Chlamydia
from Japan and CWLO29 from USA.";
Nucleic Acids Res. 28:2311-2314
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P71135;

01-FEB-1997 (TrEMBLrel. 02, Created)

10-FEB-1997 (TrEMBLrel. 02, Last sequence update)

101-MAR-2001 (TrEMBLrel. 16, Last annotation update)

101-MAR-2001 (TrEMBLrel. 16, Last annotation update)

101-MAR-2001 (TrEMBLrel. 16, Last annotation update)

102-MAR-2001 (TrEMBLrel. 16, Last annotation update)

103-MAR-2001 (TrEMBLrel. 16, Last annotation update)

104-MAR-2001 (TrEMBLrel. 16, Last annotation update)

105-MAR-2001 (TrEMBLrel. 16, Last annotation update)

106-MAR-2001 (TrEMBLrel. 16, Last annotation update)

107-MAR-2001 (TrEMBLrel. 02, Created)

108-MAR-2001 (TrEMBLrel. 02, Created)

108-MAR-2001 (TrEMBLrel. 02, Created)

109-MAR-2001 (TrEMBLrel. 02, Created)

109-MAR-2001 (TrEMBLrel. 02, Created)

109-MAR-2001 (TrEMBLrel. 02, Last sequence update)

101-MAR-2001 (TrEMBLrel. 02, Last sequence update)

101-MAR-2001 (TrEMBLrel. 02, Last sequence update)

101-MAR-2001 (TrEMBLrel. 16, Last annotation update
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Pfam;
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Longbottom D., Russell M., Dunbar S.M., Jones Submitted (SEP-1996) to the EMBL/GenBank/DDBJ EMBL; U72499; AAB18188.1;
InterPro; IPR003357;
InterPro; IPR003368;
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PF02415; DUF145; 1.
NCE 926 AA; 98439
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Similarity 40.8%;
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                                                                    Score 1802; DB 2;
Pred. No. 2.6e-98;
2; Mismatches 354;
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Q9Z398; Q9Z398; Q1-MAY-1999 Q1-MAY-1999 Q1-MAR-2001

PRELIMINARY;

928 æ

01-MAY-1999 (TREMBLrel. 10, Created)
01-MAY-1999 (TREMBLrel. 110, Last sequence update)
01-MAR-2001 (TREMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN PRECURSOR (POLYMORPHIC MEMBRANE PRANILY).
PAMILY).
0MP10 OR PMP\_9 OR CP0306.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.

MEMBRANE

PROTEIN

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RESULT 0.923.98 ID 0.923.98 AC 0.92 DT 0.1 D
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Best Local Similarity
Matches 928; Conserv
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Nucleic Acids Res. 28:2311-2314(2000).
EMBL; AJ001311; CAA04672.1; -.
EMBL; AJ133034; CAB37072.1; -.
EMBL; AE001628; AAD18593.1; -.
EMBL; AP0002546; BAA98658.1; -.
InterPro; IPR003357; -.
InterPro; IPR003358; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02385; OMP; 1.
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                           RAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLPESEGSWSNECIAGGIGLDL
                                                    VDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTATNTKEATATWTKTGFVPSPERKS
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PFVLSNPHPLFKTFIPQMKVEMVYVSQNSFFESSSDGRGFSIGRLLNLSIPVGAKFVQGD
                  RAKFSESAIEKFPREIPLALDVQVSFSHSDNRMETHYTSLPESEGSWSNECIAGGIGLDL
                                                                                                                                                               INVDSLGLKQPVSLTAKGASNKVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKITVDAD
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OUTER MEMBRANE PROTEIN 4.
788BCDD62C911402 CRC64;
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Chlamydia pneumoniae (Cn Chlamydia; Chlamydiales;
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01-OCT-2000
01-OCT-2000
01-MAR-2001
POLYMORPHIC
                                                                                                                                                                                                                                                                                                        Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20150255; PubMed-10684935;; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T. Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9K299
                                                                                                                                                                                                                                                                                              InterPro; IPR003357; -.
InterPro; IPR003368; -.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
SEQUENCE 949 AA; 101357
                                                                                                                                                                                                                                                                                                                                                EMBL; AE00219; TIGR; CP0302;
                                                                                                                                                                                                                                                                                                                                                                    pneumoniae AR39.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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322
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Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                            04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia pneumoniae
                                                 WPI; 1999-357842/30
                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                 20-NOV-1998;
                                                                                                                                                                                              98US-0107078
97FR-0014673
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frames in the complete genome (see AXX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AXX4584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae. AAY34584-Y35879 represent the proteins encoded by all the open reading 930 AA;

Conservative

42.3%; Score 2028; DB 20; 44.5%; Pred. No. 4.6e-125; ative 158; Mismatches 326;

Length

44;

Gaps

17;

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aicahgidisa--agptlfsnnrcgntaagkggaiaiadsgslslsanggditflgntlt
                                                                                                                                    AIYAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITFNGNAIV
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stsaptstrnaiylgssakitnlraaqgqsiyfydpiasnttg-asdvltinqpdsnspl
                       ATTPQTTKRNSIDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLNKADAGNST
                                                                                                                                                                                                                     easssitqnsslffsgntatdaagkggaiycektgetptltisgnksltfaenssvtqgg
                                                                                                                                                                                                                                                                                                                                  ktlsisgntssitftsnsak---klggaiyssaaasisgntgqlvfmnnkgetgggalgf
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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efgssrlvnlalpigirfdkesdcqdatynltlgytvdlvrsnpdctttlrisgdswktf
                       SFDDSNLFNLSLPIGVKFEKFSDCNDFSYDLTLSYVPDLIRNDPKCTTALVISGASWETY
                                                                                                                                                                                                     WAAGVANFLDKDKKGEKRKYRHKSGGYAIGGAAQTCSENLISFAFCQLFGSDKDFLVAKN
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                                                                                                                            qgtvyggtlyyqhnetyislpcklrpcslsyvp---teipvlfsgnlsythtdndlktky
                                                                                                                                                         HTDTYAGAFYIQH----ITECSGFIGCLLDKLPGSWSHKPLVLEGQLAYSHVSNDLKTKY
                                                                                                                                                                                    ASTPKTKTATLAWINTGYLPNPERQGPLVPNSLWGSFSDIQAIQGVIERSALTLCSDRGF
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sttfigfsslsfiaspgssitt--gkgavscstgslsltknvsllfsknfstdnggaita
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                                                                                                                                                                                                                                              \hbox{-} gtgasttatfnwtktgyipnperigslvpnslwnafidisslhylmetaneglqgdraf
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46.7%; Pred. No. 4.9e-127;
tive 142; Mismatches 320;
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RESULT 1

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ID AAY90240
ID AAY9
AC AAY9
AC AAY9
AC CAlla
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PR 01-I

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01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                          (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a Chlamydia antigen of the invention, designated CPN100639. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquired pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia antigen; diagnosis; infection; community acquired pneumonia; therapy; upper respiratory tract disease; bronchitis; sinusitis; asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma
      Sequence
                                                                   adult-onset asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Fig 7; 174pp; English.
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asthma –
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                                                                infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract lisease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
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          930 AA;
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98US-0110340.
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; bronchitis; sinusitis;
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Query Match Best Local Similarity

42.3%;

Pred. Score 2030; Pred. No. 3

Length

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Best Local Similarity
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chlamydia pneumoniae. The genomic sequence was amplified using two PCR primers. The 5' primer contains a Noti restriction site, a ribosome binding site, an initiation codon and a sequence close to the 5' end of the 98kDa putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BsrGl restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame c-terminal fusion with the Histidine tag. The PCR product was cloned into a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with Noti and BamH1 and performing a ligation reaction. This expression vector was injected intramuscularly and intermediate with the pcroposition of the pc Claim 6; Fig 1; 93pp; The present sequence is the 98kDa putative outer membrane protein from English.

and intranasally into mice, Chlamydia pneumoniae. The c

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                                                                                                                    GGAIYAKKLTLASGGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITFNGNA
IVAT-TPQTTKRNSIDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLNKADAG
                                                      ggaiytkklvlss-grggvlfsnnkaanatp-kggaiaildsgeisisadlgniifegnt
                                                                                                                                                                                 egnlvisnnqniffdgckatt---nggaldcnkaganpdpiltlsgneslhflnntagns
                                                                                                                                                                                                                                               TGNCTITGNTSLVFSENSVTATAGNGGAL-----SGDADVTISGNQSVTFSGNQAVAN 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470;
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Species-specific test for identifying mammals infected with
                                                   N-PSDB; AAX06820
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                                                                                                                                  Birkelund S, 
Mygind P;
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(CHRI/) CHRISTIANSEN
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20-AUG-1998;
20-AUG-1998;
                                                                                                                                                                                              external vicinity of the membrane structure, in the inclusion membrane structure, in the external vicinity of the inclusion membrane structure, and in the cytoplasm of the infected cell. The polypeptides may be used to prevent, treat and detect the presence of Chlamydia infection and/or the presence of Chlamydia in a sample. The polypeptides may also be used to induce an immune response in a mammal. The vaccine vector comprising the polynucleotides is used to induce an immune response in a mammal. Antibodies directed against the polypeptides may also be used therapeutically to treat and/or prevent a Chlamydia
                                                                                                                                                                                                                                                                                                                                                                          Novel antigens and corresponding DNA molecules that can prevent, treat and diagnose disease caused by Chlamydia mammals, especially humans -
                                                                                                                                                                                                                                                                                                          AAY69362-69 represent Chlamydia pneumoniae polypeptides. The polypeptides are present in the bacterial membrane structure, in the
                                                                                                                                                                                                                                                                                                                                                 Claim 19; Fig 15-E; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murdin AD,
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20-AUG-1998;
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                                                                                                                                                              Sequence
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                                             mrssfslllisssla-fpllmsvsadaadltlgsrdsyngdtstteftpkaatsdasgtt 59
                                                                      MKSQFSWLVLSSTLACFTSCSTVFAATAE-NIGPSDSFDGSTNTGTYTPKNTT---TGID
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)B; AAZ61509.
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C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX94584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Pred. No. 3.2e-207;
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AAY90238;

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121 164 61 Query Match Best Local S Matches 874

Similarity

94.0%;

Score 4508; D: Pred. No. 4.6e
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DB 21; .6e-288;

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Conservative

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YCEENGGAISTKNLSLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPTLFSNN

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This sequence is a Chlamydia antigen of the invention, designated CC CPMI00635. The nucleic acids (and their complementary sequences) may be cu used as diagnostic agents for detecting the presence of nucleic acids cand therefore, for diagnosing chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate carginates as a coording to standard methods. The nucleic acids may also be used to produce the protein antigens they concode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infections by Chlamydia. The infections. Chlamydia is a pathogen implicated in the development of the example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, candition and acute exacerbations of asthma in adults.
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01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquired pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset asthma
Sequence
                                                                                                                                                                                                                                                                                                Claim 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.
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Pred. No. 1.3e-302;
1; Mismatches 10;
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Query Match
Best Local Similarity

98.3%; 99.9%;

Score 4714; DB 20; Pred. No. 1.4e-301;

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914;

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                                                                           This polypeptide is described as a subsequence of the claimed novel surface exposed protein Omp5 (see AAW88418) of Chlamydia pneumoniae, a human respiratory pathogen. The invention provides a new species specific test for identifying mammals (including humans) infected with C. pneumoniae. The test comprises detecting antibodies specific for surface exposed proteins Omp4-Omp15 (see AAW88417-28) or detecting nucleic acid fragments encoding them (see AAX06816-27), especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the
                                      nucleic acids being particularly useful as DNA vaccines effecting in vivo expression of antigens. The vaccines prevent atherosclerosis and bronchial asthma, which are
                                                                                                                                                                                                                                                      Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding these proteins
                                                                                                                                                                                                                                                                                                                                                                                                       (BIRK/)
(CHRI/)
 Sequence
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                                                                                                                                                                                                                              Disclosure; Page 78-80;
                                                                                                                                                                                                                                                                                                                                       WPI; 1999-105610/09
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This polypeptide comprises the novel 97.2 kDa surface exposed protein Omp5 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAX06817) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.
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TGNTSLVFSENSYTATAGNGGALSGDADVTISGNQSVTFSGNQAVANGGAIYAKKLTLAS
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                                                                  SFVQLSALGTATTTDVPAVPTVATPTHYGYQGTWGMTWVDDTASTPKTKTATLAWTNTGY
                                                                                                       proteins
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Pred. No. 0;
0; Mismatches
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This sequence is a Chlamydia antigen of the invention, designated CPN100635. The nucleic acids (and their complementary sequences) used as diagnostic agents for detecting the presence of nucleic acids.

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RESULT
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01-DEC-1998;
01-DEC-1998;
01-DEC-1998;
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                                                                                                                                                                          Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquired pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
                                                                                                    Claim 16;
                                                                                                                                                                                                                                                                                                                                                 Murdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1999;
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DB; AAA30849, AA
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score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
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	Chlamydia antigen		Chlamydia pneumoni	Chlamydia pneumoni	Amino acid sequenc	Chlamydia pneumoni	Mature Chlamydia a		Chlamydia antigen	Chlamydia pneumoni	Description	

Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for  $\cdot$ 

## ALIGNMENTS

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                        WPI; 1999-105610/09.
N-PSDB; AAX06817.
                                                  Birkelund S,
Mygind P;
                                                                                                         23-JUN-1997;
                                                                                                                                                                                Chlamydia pneumoniae
                                                                                                                                                                                                   Omp5; outer membrane protein 5; surface exposed protein; antigen; infection; diagnosis; vaccine; atherosclerosis; asthma.
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                                                                                                                                                                                                                                                                  AAW88418;
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                                                                              (BIRK/) BIRKELUND S. (CHRI/) CHRISTIANSEN G.
                                                                                                                           19-JUN-1998;
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                                                            Christiansen G,
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                                                            Knudsen K,
                                                            Madsen
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